

BOS

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
28 February 2002 (28.02.2002)

PCT

(10) International Publication Number  
WO 02/16649 A2

- (51) International Patent Classification<sup>7</sup>: C12Q 1/68
- (21) International Application Number: PCT/US01/26519
- (22) International Filing Date: 27 August 2001 (27.08.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
60/227,948 25 August 2000 (25.08.2000) US  
60/228,854 29 August 2000 (29.08.2000) US
- (71) Applicant: ILLUMINA, INC. [US/US]; Suite 200, 9390 Towne Centre Drive, San Diego, CA 92121 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**  
— *without international search report and to be republished upon receipt of that report*
- (72) Inventor: GUNDERSON, Kevin; 1543 Juniper Hill Drive, Encinitas, CA 92024 (US).
- (74) Agents: BREZNER, David, J. et al.; Flehr, Hohbach, Test, Albritton & Herbert LLP, Suite 3400, 4 Embarcadero Center, San Francisco, CA 94111-4187 (US).
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*



WO 02/16649 A2

(54) Title: PROBES AND DECODER OLIGONUCLEOTIDES

(57) Abstract: The present invention is directed to improved methods and compositions for the use of adapter sequences on arrays in a variety of multiplexed nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

BEST AVAILABLE COPY

## PROBES AND DECODER OLIGONUCLEOTIDES

This application claims the benefit of U.S.N.s 60/227,948 filed August 25, 2000 and 60/228,854, filed August 29, 2001, both of which are expressly incorporated herein by reference.

5

### FIELD OF THE INVENTION

The present invention is directed to methods and compositions for the use of adapter sequences on arrays in a variety of nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

10

### BACKGROUND OF THE INVENTION

The detection of specific nucleic acids is an important tool for diagnostic medicine and molecular biology research. Gene probe assays currently play roles in identifying infectious organisms such as bacteria and viruses, in probing the expression of normal and mutant genes and identifying mutant genes such as oncogenes, in typing tissue for compatibility preceding tissue transplantation, in matching tissue or blood samples for forensic medicine, and for exploring homology among genes from different species.

20

Ideally, a gene probe assay should be sensitive, specific and easily automatable (for a review, see Nickerson, Current Opinion in Biotechnology 4:48-51 (1993)). The requirement for sensitivity (i.e. low detection limits) has been greatly alleviated by the development of the polymerase chain reaction (PCR) and other amplification technologies which allow researchers to amplify exponentially a specific nucleic acid sequence before analysis (for a review, see Abramson et al., Current Opinion in Biotechnology, 4:41-47 (1993)).

25

Specificity, in contrast, remains a problem in many currently available gene probe assays. The extent of molecular complementarity between probe and target defines the specificity of the interaction.

30

Variations in the concentrations of probes, of targets and of salts in the hybridization medium, in the reaction temperature, and in the length of the probe may alter or influence the specificity of the

probe/target interaction.

It may be possible under some circumstances to distinguish targets with perfect complementarity from targets with mismatches, although this is generally very difficult using traditional technology, since small variations in the reaction conditions will alter the hybridization. New experimental techniques for mismatch detection with standard probes include DNA ligation assays where single point mismatches prevent ligation and probe digestion assays in which mismatches create sites for probe cleavage.

Recent focus has been on the analysis of the relationship between genetic variation and phenotype by making use of polymorphic DNA markers. Previous work utilized short tandem repeats (STRs) as polymorphic positional markers; however, recent focus is on the use of single nucleotide polymorphisms (SNPs), which occur at an average frequency of more than 1 per kilobase in human genomic DNA. Some SNPs, particularly those in and around coding sequences, are likely to be the direct cause of therapeutically relevant phenotypic variants and/or disease predisposition. There are a number of well known polymorphisms that cause clinically important phenotypes; for example, the apoE2/3/4 variants are associated with different relative risk of Alzheimer's and other diseases (see Cordor et al., Science 261(1993). Multiplex PCR amplification of SNP loci with subsequent hybridization to oligonucleotide arrays has been shown to be an accurate and reliable method of simultaneously genotyping at least hundreds of SNPs; see Wang et al., Science, 280:1077 (1998); see also Schafer et al., Nature Biotechnology 16:33-39 (1998). The compositions of the present invention may easily be substituted for the arrays of the prior art.

There are a variety of particular techniques that are used to detect sequence, including mutations and SNPs. These include, but are not limited to, ligation based assays, cleavage based assays (mismatch and invasive cleavage such as Invader™), single base extension methods (see WO 92/15712, EP 0 371 437 B1, EP 0317 074 B1; Pastinen et al., Genome Res. 7:606-614 (1997); Syvänen, Clinica Chimica Acta 226:225-236 (1994); and WO 91/13075), and competitive probe analysis (e.g. competitive sequencing by hybridization; see below).

Oligonucleotide ligation amplification ("OLA", which is referred as the ligation chain reaction (LCR) when two-stranded reactions or nested reactions are done) involves the ligation of two smaller probes into a single long probe, using the target sequence as the template. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; WO 97/31256 and WO 89/09835, all of which are incorporated by reference.

Invasive cleavage technology is based on structure-specific nucleases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with a non-complementary overlap. The enzyme cleaves at the overlap due to its recognition of the "tail", and releases the "tail" with a label. This can then be

detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

5 An additional technique utilizes sequencing by hybridization. For example, sequencing by hybridization has been described (Drmanac et al., Genomics 4:114 (1989); Koster et al., Nature Biotechnology 14:1123 (1996); U.S. Patent Nos. 5,525,464; 5,202,231 and 5,695,940, among others, all of which are hereby expressly incorporated by reference in their entirety).

10 Sensitivity, i.e. detection limits, remain a significant obstacle in nucleic acid detection systems, and a variety of techniques have been developed to address this issue. Briefly, these techniques can be classified as either target amplification or signal amplification. Target amplification involves the amplification (i.e. replication) of the target sequence to be detected, resulting in a significant increase in the number of target molecules. Target amplification strategies include the polymerase chain reaction (PCR), strand displacement amplification (SDA), and nucleic acid sequence based  
15 amplification (NASBA).

Alternatively, rather than amplify the target, alternate techniques use the target as a template to replicate a signalling probe, allowing a small number of target molecules to result in a large number of signalling probes, that then can be detected. Signal amplification strategies include the ligase chain  
20 reaction (LCR), cycling probe technology (CPT), invasive cleavage techniques such as Invader™ technology, Q-Beta replicase (Q $\beta$ R) technology, and the use of "amplification probes" such as "branched DNA" that result in multiple label probes binding to a single target sequence.

The polymerase chain reaction (PCR) is widely used and described, and involves the use of primer  
25 extension combined with thermal cycling to amplify a target sequence; see U.S. Patent Nos. 4,683,195 and 4,683,202, and PCR Essential Data, J. W. Wiley & sons, Ed. C.R. Newton, 1995, all of which are incorporated by reference. In addition, there are a number of variations of PCR which also find use in the invention, including "quantitative competitive PCR" or "QC-PCR", "arbitrarily primed PCR" or "AP-PCR", "immuno-PCR", "Alu-PCR", "PCR single strand conformational polymorphism" or "PCR-SSCP", allelic PCR (see Newton et al. Nucl. Acid Res. 17:2503 91989); "reverse transcriptase PCR" or  
30 "RT-PCR", "biotin capture PCR", "vectorette PCR", "panhandle PCR", and "PCR select cDNA subtraction", among others.

Strand displacement amplification (SDA) is generally described in Walker et al., in Molecular Methods  
35 for Virus Detection, Academic Press, Inc., 1995, and U.S. Patent Nos. 5,455,166 and 5,130,238, all of which are hereby incorporated by reference.

Nucleic acid sequence based amplification (NASBA) is generally described in U.S. Patent No. 5,409,818 and "Profiting from Gene-based Diagnostics", CTB International Publishing Inc., N.J., 1996,



both of which are incorporated by reference.

Cycling probe technology (CPT) is a nucleic acid detection system based on signal or probe amplification rather than target amplification, such as is done in polymerase chain reactions (PCR).

5 Cycling probe technology relies on a molar excess of labeled probe which contains a scissile linkage of RNA. Upon hybridization of the probe to the target, the resulting hybrid contains a portion of RNA:DNA. This area of RNA:DNA duplex is recognized by RNaseH and the RNA is excised, resulting in cleavage of the probe. The probe now consists of two smaller sequences which may be released, thus leaving the target intact for repeated rounds of the reaction. The unreacted probe is removed and  
10 the label is then detected. CPT is generally described in U.S. Patent Nos. 5,011,769, 5,403,711, 5,660,988, and 4,876,187, and PCT published applications WO 95/05480, WO 95/1416, and WO 95/00667, all of which are specifically incorporated herein by reference.

The oligonucleotide ligation assay (OLA) involve the ligation of at least two smaller probes into a single  
15 long probe, using the target sequence as the template for the ligase. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; and WO 89/09835, all of which are incorporated by reference.

Invader™ technology is based on structure-specific polymerases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently  
20 hybridize to a target sequence with overlap. For mismatch discrimination, the invader technology relies on complementarity at the overlap position where cleavage occurs. The enzyme cleaves at the overlap, and releases the "tail" which may or may not be labeled. This can then be detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.  
25

"Branched DNA" signal amplification relies on the synthesis of branched nucleic acids, containing a multiplicity of nucleic acid "arms" that function to increase the amount of label that can be put onto one probe. This technology is generally described in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730,  
30 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference.

Similarly, dendrimers of nucleic acids serve to vastly increase the amount of label that can be added to a single molecule, using a similar idea but different compositions. This technology is as described  
35 in U.S. Patent No. 5,175,270 and Nilsen et al., J. Theor. Biol. 187:273 (1997), both of which are incorporated herein by reference.

U.S.S.N.s 09/189,543; 08/944,850; 09/033,462; 09/287,573; 09/151,877; 09/187,289 and 09/256,943; and PCT applications US98/09163 and US99/14387; US98/21193; US99/04473 and US98/05025, all

of which are expressly incorporated by reference, describe novel compositions utilizing substrates with microsphere arrays, which allow for novel detection methods of nucleic acid hybridization.

5 The use of adapter-type sequences that allow the use of universal arrays has been described in limited contexts; see for example Chee et al., Nucl. Acid Res. 19:3301 (1991); Shoemaker et al., Nature Genetics 14:450 (1996); U.S. Patent Nos. 5,494,810, 5,830,711, 6,027,889, 6,054,564, and 6,268,148; and EP 0 799 897 A1; WO 97/31256, all of which are expressly incorporated by reference.

10 Accordingly, it is an object of the present invention to provide methods for detecting nucleic acid reactions, and other target analytes, on arrays using adapter sequences.

#### SUMMARY OF THE INVENTION

15 In accordance with the above objects, the invention also provides a method of detecting a target nucleic acid. The method comprises contacting the target nucleic acid with an adapter sequence such that the target nucleic acid is joined to the adapter sequence to form a modified target nucleic acid. In addition, the method comprises contacting the modified target nucleic acid with an array comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the  
20 modified target nucleic acid form a complex, wherein the microspheres are distributed on the surface, and detecting the presence of the target nucleic acid. In addition the method comprises adding at least one decoding binding ligand to the array such that the identity of the target nucleic acid is determined. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

25 In addition the invention provides a method of making an array. The method comprises forming a surface comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, wherein the microspheres comprise at least a first and a second subpopulation each comprising a capture probe, wherein the capture probe is complementary  
30 to an adapter sequence, the adapter sequence joined to a target nucleic acid, and an identifier binding ligand that will bind at least one decoder binding ligand such that the identification of the target nucleic acid is elucidated. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

35 In addition the invention provides a kit comprising at least one nucleic acid selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV. In one embodiment the invention provides a kit that includes a nucleic acid that includes a sequence as set forth in Table I, Table II, Table III or Table IV and at least a first universal priming sequence.

In addition the invention includes an array composition comprising a first population of microspheres comprising first and second subpopulations, wherein the first subpopulation includes a first nucleic acid selected from the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the invention includes an array composition comprising a first sequence at a known location on a substrate, wherein the first sequence is selected from the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the invention includes a method for making an array. The method includes distributing a population of microspheres on an substrate, wherein the population includes first and second subpopulations, wherein the first subpopulation includes a first sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the method includes a method of immobilizing a target nucleic acid. The method includes hybridizing a first adapter probe with a first target nucleic acid, wherein the first adapter probe comprises a first domain that is complementary to the first target nucleic acid and a second domain, comprising a first sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV to form a first hybridization complex. In addition the method includes contacting the first hybridization complex with a first capture probe immobilized on a first substrate, wherein the first capture probe is substantially complementary to the second domain of the first adapter probe.

In addition the invention includes a method of decoding an array composition comprising providing an array composition that includes a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on the surface. The method further includes adding a plurality of decoding binding ligands to the array composition to identify the location of at least a plurality of the bioactive agents wherein at least a first decoder binding ligand comprises a sequence selected from the group consisting of the sequences of Table I, Table II, Table III or Table IV.

A method of detecting a target nucleic acid sequence, said method comprising attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein the first adapter nucleic acid includes a sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV. The method further includes contacting the modified first target nucleic acid sequence with an array comprising a substrate with a patterned surface

comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified first target nucleic acid sequence form a hybridization complex; wherein the microspheres are distributed on the surface and detecting the presence of the modified first target nucleic acid sequence.

5

#### DETAILED DESCRIPTION OF THE FIGURES

Figure 1 depicts a method of selecting oligonucleotide sequences.

10

Figure 2 depicts a scheme for selection of probes and decoder oligonucleotides.

Figure 3 demonstrates hybridization intensity comparison of immobilized beads using non-purified oligonucleotides with HPLC purified oligonucleotides.

15

Figure 4 depicts different oligonucleotide sequences immobilized onto silica beads at various salt concentration. Average intensity indicates hybridization intensity of beads in a BeadArray.

Figure 5 depicts immobilization of oligonucleotides in increasing salt concentrations.

20

#### DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to the use of adapter sequences, and optionally capture extender probes, that allow the use of "universal" arrays. That is, a "universal" array is an array with a set of capture probes that will hybridize to adapter sequences, for use in any number of different reactions, including the binding of nucleic acid reactions and other target analytes comprising a nucleic acid adapter sequence that can hybridize to the array. In this way, a manufacturer of arrays can make one type of array that may be used in a variety of applications, thus reducing the manufacturing costs associated with the array. In addition, in the case of bead arrays, the decoding steps as outlined below can be simplified, as one set of decoding probes can be made.

25

30

In general, the use of adapter sequences can be described as follows for nucleic acid reactions. An adapter sequence can be added exogenously to a target nucleic acid sequence using any number of different techniques, including, but not limited to, amplification reactions as described in U.S.S.N. 09/425,633, filed October 22, 1999; 09/513,362, filed February 25, 2000; 09/517,945, filed March 3, 2000; 09/535,854, filed March 27, 2000; 09/553,993, filed April 20, 2000; 09/556,463, filed April 21, 2000; 60/135,051, filed May 20, 1999; 60/135,053, filed May 20, 1999; 60/135,123, filed May 20, 1999; 60/130,089, filed April 20, 1999; 60/160,917, filed October 22, 1999; 60/160,927, filed October 22,

35

1999; 60/161,148, filed October 22, 1999; and 60/244,119, filed October 26, 2000 all of which are hereby incorporated by reference. In addition, the adapter can be added to an extension probe. The adapter sequence can then be used to target to its complementary capture probe on the surface.

- 5 Alternatively, the adapter sequences can be added to other target analytes, to generate unique and reproducible arrays of target analytes in a similar manner. By adding the nucleic acid to the target analyte (for example to an antibody in an immunoassay), the target analytes may then be arrayed.

10 Accordingly, the present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and  
15 soil samples); biological warfare agent samples; research samples; purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.); As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

20 The present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. By "target analyte" or "analyte" or grammatical equivalents herein is meant any molecule, compound or particle to be detected. As outlined below, target analytes preferably bind to binding ligands, as is more fully described below. As will be appreciated by those in the art, a large number of analytes may be detected using the present methods; basically, any target  
25 analyte for which a binding ligand, described below, may be made may be detected using the methods of the invention.

Suitable analytes include organic and inorganic molecules, including biomolecules. In a preferred embodiment, the analyte may be an environmental pollutant (including pesticides, insecticides, toxins, etc.); a chemical (including solvents, polymers, organic materials, etc.); therapeutic molecules  
30 (including therapeutic and abused drugs, antibiotics, etc.); biomolecules (including hormones, cytokines, proteins, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc); whole cells (including procaryotic (such as pathogenic bacteria) and eukaryotic cells, including mammalian tumor cells); viruses  
35 (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.); and spores; etc. Particularly preferred analytes are environmental pollutants; nucleic acids; proteins (including enzymes, antibodies, antigens, growth factors, cytokines, etc); therapeutic and abused drugs; cells; and viruses.

In a preferred embodiment, the target analyte is a protein. As will be appreciated by those in the art,

there are a large number of possible proteinaceous target analytes that may be detected using the present invention. By "proteins" or grammatical equivalents herein is meant proteins, oligopeptides and peptides, derivatives and analogs, including proteins containing non-naturally occurring amino acids and amino acid analogs, and peptidomimetic structures. The side chains may be in either the (R) or the (S) configuration. In a preferred embodiment, the amino acids are in the (S) or L-configuration. As discussed below, when the protein is used as a binding ligand, it may be desirable to utilize protein analogs to retard degradation by sample contaminants.

Suitable protein target analytes include, but are not limited to, (1) immunoglobulins, particularly IgEs, IgGs and IgMs, and particularly therapeutically or diagnostically relevant antibodies, including but not limited to, for example, antibodies to human albumin, apolipoproteins (including apolipoprotein E), human chorionic gonadotropin, cortisol,  $\alpha$ -fetoprotein, thyroxin, thyroid stimulating hormone (TSH), antithrombin, antibodies to pharmaceuticals (including antiepileptic drugs (phenytoin, primidone, carbamazepine, ethosuximide, valproic acid, and phenobarbital), cardioactive drugs (digoxin, lidocaine, procainamide, and disopyramide), bronchodilators (theophylline), antibiotics (chloramphenicol, sulfonamides), antidepressants, immunosuppressants, abused drugs (amphetamine, methamphetamine, cannabinoids, cocaine and opiates) and antibodies to any number of viruses (including orthomyxoviruses, (e.g. influenza virus), paramyxoviruses (e.g. respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses (including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picornaviruses, and the like), and bacteria (including a wide variety of pathogenic and non-pathogenic prokaryotes of interest including *Bacillus*; *Vibrio*, e.g. *V. cholerae*; *Escherichia*, e.g. Enterotoxigenic *E. coli*, *Shigella*, e.g. *S. dysenteriae*; *Salmonella*, e.g. *S. typhi*; *Mycobacterium* e.g. *M. tuberculosis*, *M. leprae*; *Clostridium*, e.g. *C. botulinum*, *C. tetani*, *C. difficile*, *C. perfringens*; *Corynebacterium*, e.g. *C. diphtheriae*; *Streptococcus*, *S. pyogenes*, *S. pneumoniae*; *Staphylococcus*, e.g. *S. aureus*; *Haemophilus*, e.g. *H. influenzae*; *Neisseria*, e.g. *N. meningitidis*, *N. gonorrhoeae*; *Yersinia*, e.g. *G. lamblia*; *Y. pestis*, *Pseudomonas*, e.g. *P. aeruginosa*, *P. putida*; *Chlamydia*, e.g. *C. trachomatis*; *Bordetella*, e.g. *B. pertussis*; *Treponema*, e.g. *T. palladium*; and the like); (2) enzymes (and other proteins), including but not limited to, enzymes used as indicators of or treatment for heart disease, including creatine kinase, lactate dehydrogenase, aspartate amino transferase, troponin T, myoglobin, fibrinogen, cholesterol, triglycerides, thrombin, tissue plasminogen activator (tPA); pancreatic disease indicators including amylase, lipase, chymotrypsin and trypsin; liver function enzymes and proteins including cholinesterase, bilirubin, and alkaline phosphatase; aldolase, prostatic acid phosphatase, terminal deoxynucleotidyl transferase, and bacterial and viral enzymes such as HIV protease; (3) hormones and cytokines (many of which serve as ligands for cellular receptors) such as erythropoietin (EPO), thrombopoietin (TPO), the interleukins

(including IL-1 through IL-17), insulin, insulin-like growth factors (including IGF-1 and -2), epidermal growth factor (EGF), transforming growth factors (including TGF- $\alpha$  and TGF- $\beta$ ), human growth hormone, transferrin, epidermal growth factor (EGF), low density lipoprotein, high density lipoprotein, leptin, VEGF, PDGF, ciliary neurotrophic factor, prolactin, adrenocorticotrophic hormone (ACTH),  
 5 calcitonin, human chorionic gonadotropin, cortisol, estradiol, follicle stimulating hormone (FSH), thyroid-stimulating hormone (TSH), luteinizing hormone (LH), progesterone, testosterone, ; and (4) other proteins (including  $\alpha$ -fetoprotein, carcinoembryonic antigen CEA.

10 In addition, any of the biomolecules for which antibodies may be detected may be detected directly as well; that is, detection of virus or bacterial cells, therapeutic and abused drugs, etc., may be done directly.

Suitable target analytes include carbohydrates, including but not limited to, markers for breast cancer (CA15-3, CA 549, CA 27.29), mucin-like carcinoma associated antigen (MCA), ovarian cancer  
 15 (CA125), pancreatic cancer (DE-PAN-2), and colorectal and pancreatic cancer (CA 19, CA 50, CA242).

In a preferred embodiment, the target analyte (and various adapters and other probes of the invention), comprise nucleic acids. By "nucleic acid" or "oligonucleotide" or grammatical equivalents  
 20 herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl.  
 25 Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 (1986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoramidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones  
 30 and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., Angew. Chem. Intl. Ed.  
 35 English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S.

Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within the definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done to facilitate the addition of labels, alter the hybridization properties of the nucleic acids, or to increase the stability and half-life of such molecules in physiological environments.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made. Alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. This allows for better detection of mismatches. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribonucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. A preferred embodiment utilizes isocytosine and isoguanine in nucleic acids designed to be complementary to other probes, rather than target sequences, as this reduces non-specific hybridization, as is generally described in U.S. Patent No. 5,681,702. As used herein, the term "nucleoside" includes nucleotides as well as nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

In general, probes of the present invention (including adapter sequences and capture probes, described below) are designed to be complementary to a target sequence (either the target sequence of the sample or to other probe sequences, for example adapter sequences) such that hybridization of the target and the probes of the present invention occurs. This complementarity need not be perfect;



there may be any number of base pair mismatches that will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by

5 "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under the selected reaction conditions.

When nucleic acids are to be detected, they are referred to herein as "target nucleic acids" or "target sequences". The term "target sequence" or "target nucleic acid" or grammatical equivalents herein

10 means a nucleic acid sequence on a single strand of nucleic acid. The target sequence may be a portion of a gene, a regulatory sequence, genomic DNA, cDNA, RNA including mRNA and rRNA, or others. As is outlined herein, the target sequence may be a target sequence from a sample, or a derivative target such as a product of a reaction such as a detection sequence from an Invader™ reaction, a ligated probe from an OLA reaction, an extended probe from an SBE reaction, etc. It may

15 be any length, with the understanding that longer sequences are more specific. As will be appreciated by those in the art, the complementary target sequence may take many forms. For example, it may be contained within a larger nucleic acid sequence, i.e. all or part of a gene or mRNA, a restriction fragment of a plasmid or genomic DNA, among others. As is outlined more fully below, probes are made to hybridize to target sequences to determine the presence or absence of the target sequence in

20 a sample. Generally speaking, this term will be understood by those skilled in the art. The target sequence may also be comprised of different target domains; for example, a first target domain of the sample target sequence may hybridize to a capture probe, a second target domain may hybridize to a portion of a label probe, etc. The target domains may be adjacent or separated as indicated. Unless specified, the terms "first" and "second" are not meant to confer an orientation of the sequences with

25 respect to the 5'-3' orientation of the target sequence. For example, assuming a 5'-3' orientation of the complementary target sequence, the first target domain may be located either 5' to the second domain, or 3' to the second domain. In addition, as will be appreciated by those in the art, the probes on the surface of the array (e.g. attached to the microspheres) may be attached in either orientation, either such that they have a free 3' end or a free 5' end.

30 As is more fully outlined below, the target sequence may comprise a position for which sequence information is desired, generally referred to herein as the "detection position" or "detection locus". In a preferred embodiment, the detection position is a single nucleotide, although in some embodiments, it may comprise a plurality of nucleotides, either contiguous with each other or separated by one or more

35 nucleotides. By "plurality" as used herein is meant at least two. As used herein, the base which basepairs with a detection position base in a hybrid is termed a "readout position" or an "interrogation position".

In some embodiments, as is outlined herein, the target sequence may not be the sample target

sequence but instead is a product of a reaction herein, sometimes referred to herein as a "secondary" or "derivative" target sequence. Thus, for example, in SBE, the extended primer may serve as the target sequence; similarly, in invasive cleavage variations, the cleaved detection sequence may serve as the target sequence.

If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification as needed, as will be appreciated by those in the art.

Once prepared, the target sequence can be used in a variety of reactions for a variety of reasons. For example, in a preferred embodiment, genotyping reactions are done. Similarly, these reactions can also be used to detect the presence or absence of a target sequence. Sequencing or amplification reactions are also preferred. In addition, in any reaction, quantitation of the amount of a target sequence may be done.

Furthermore, as outlined below for each reaction, many of these techniques may be used in a solution based assay, wherein the reaction is done in solution and a reaction product is bound to the array for subsequent detection, or in solid phase assays, where the reaction occurs on the surface and is detected.

In general, the present invention provides pairs of capture probes (nucleic acids that are attached to addresses on arrays) and adapter sequences (sequences that are either perfectly or substantially complementary to the capture probe sequences) that can be used in a wide variety of ways, to immobilize target nucleic acids (either primary targets, such as genomic DNA, mRNA or cDNA, or secondary targets such as amplicons from a nucleic acid amplification or extension reaction, as outlined herein) to the addresses of the array. Thus, all the sequences in the Tables include their complements, and either sequence can be used as a capture probe (e.g. spotted onto a surface or attached to a microsphere of an array) or as the adapter sequence that binds to the capture probe.

Accordingly, by "adapter sequences" or "adapters" or grammatical equivalents is meant a nucleic acid segment generally non-native or exogenous to a target molecule that is used to immobilize the target molecule to a solid support via binding to a capture probe sequence. In a preferred embodiment the adapter sequences and capture probes are selected from the sequences set forth in Table I, Table II, Table III or Table IV.

Table I includes the sequence of the preferred 4000 sequences labeled "Decoder (5'-3')", and inherent in this table are the complementary sequences as well. In addition, the invention includes oligonucleotides that are complementary to those depicted in Table 1.

Table II includes the sequence of the preferred adapter/capture probe sequences and their complementary sequence. Table 2 depicts a preferred subset of 3172 decoder oligonucleotides and their complementary probe oligonucleotides. Accordingly, the invention provides compositions comprising a sequence as outlined in Table 2. In addition, the invention provides a composition comprising a complementary binding pair as outlined in Table 2.

Table 3 includes a preferred subset of 768 decoder oligonucleotides and complementary probe sequences. In some embodiments it may be desirable to include a uniform base at a terminus of the oligonucleotide, such as a T at the 5' end as depicted in Table 4. The inclusion of this uniform or constant base facilitates uniform labeling of the oligonucleotides.

These sequences are used as decoder probes, capture probes or adapter sequences as outlined in U.S.S.N. 09/344,526 and PCT/US99/14387, and U.S.S.N.s 60/160,917 and 09/5656,463 all of which are expressly incorporated by reference in their entirety.

As will be appreciated by those in the art, the length of the capture probe/adapter sequences will vary, depending on the desired "strength" of binding and the number of different adapters desired. In a preferred embodiment, adapter sequences range from about 5 to about 500 basepairs in length, with from about 8 to about 100 being preferred, and from about 10 to about 50 being particularly preferred.

As will be appreciated by those in the art, it is desirable to have adapter sequences that do not have significant homology to naturally occurring target sequences, to avoid non-specific or erroneous binding of target sequences to the capture probes. Accordingly, preferred embodiments utilize some method to select useful adapter sequences. In a preferred embodiment the method is outlined in Figure 1. Briefly, random 24-mer (or could be any desired length as outlined herein), sequences were assembled and subjected to certain defined screening procedures including such steps as requiring that the T<sub>m</sub> of each of the sequence be within a pre-defined range. In addition the GC content must be balanced with the AT content and the self-complementarity must be minimized. In addition GC runs should be minimized, that is, runs of Gs or Cs should be reduced. In addition, decoder (adapter) to decoder (adapter) complementarity should be reduced so that the adapters do not hybridize with each other. Finally, the sequences are screened against a specified genomic database. In a preferred embodiment the adapters comprise at least one sequence selected from the sequences in Table I, Table II, Table III or Table IV.

In a preferred embodiment, the adapter sequences are chosen on the basis of a decoding step. As is more fully outlined below, a decoding step is used to decode random bead arrays. In this embodiment, a set of candidate capture probes is chosen; this may be done in a variety of ways. In a preferred embodiment, the sequences are generated randomly, each of a sufficient length to ensure a

low probability of occurring naturally. In some embodiments, for example when the array will be used with a particular organism's genome (e.g. the human genome, the *Drosophila* genome, etc. ), the sequences are compared to the genome as a first filter, for example to remove sequences that would cross hybridize. Additionally, further filtering may be done using well-known methods, such as known  
5 methods for selecting good PCR primers. These techniques generally include steps that remove sequences that may have a propensity to form secondary structures or otherwise to cross-hybridize. Additionally, sequences that have extremes of melting temperatures can be optionally discarded, depending on the planned assay conditions.

10 Once a set of candidate capture probes is obtained, an array comprising the capture probes is made, and a matching set of decoding probes comprising the adapter sequences (e.g. the complements of the capture probes), as more fully outlined below, is made. Decoding then proceeds. Probes that do not hybridize well, for whatever reason, will not decode well, generally due to weak signals, and are generally discarded. Probes that cross-hybridize will also not decode well, as they will give ambiguous  
15 or mixed decoding signals. Only probes that hybridize sufficiently strongly and specifically will decode. Thus, by setting suitable thresholds for signal strength and signal purity, adapter sequences that perform according to specified criteria are identified. Additionally, by setting a range on signal strength, capture probe/adapter sequence pairs that perform similarly (but hybridize specifically) are identified. In a preferred embodiment, decoding reactions are repeated, under a variety of conditions,  
20 to test the robustness of the sequence pair.

Once identified, the adapter sequences are added to target sequences in a variety of ways, as will be appreciated by those in the art. In a preferred embodiment, nucleic acid amplification reactions are done, as is generally outlined in "Detection of Nucleic Acid Amplification Reactions Using Bead Arrays"  
25 and "Sequence Determination of Nucleic Acids using Arrays with Microspheres", both of which were filed on October 22, 1999, (U.S.S.N.'s 60/161,148 and 09/425,633, respectively), both of which are hereby incorporated by reference in their entirety. These may be either target amplification or signal amplification. In general, the techniques can be described as follows. Most amplification techniques require one or more primers hybridizing to all or part the target sequence (e.g. that hybridize to a target  
30 domain). The adapter sequences can be added to one or more of the primers (depending on the configuration/orientation of the system and need) and the amplification reactions are run. Thus, for example, PCR primers comprising at least one adapter sequence (and preferably one on each PCR primer) may be used; one or both of the ligation probes of an OLA or LCR reaction may comprise an adapter sequence; the sequencing primers for pyrosequencing, single-base extension, reversible  
35 chain termination, etc., reactions may comprise an adapter sequence; either the invader probe or the signalling probe of invasive cleavage reactions can comprise an adapter sequence; etc. Similarly, for signal detection techniques, the probes may comprise adapter sequences, with preferred methods utilizing removal of the unreacted probes. In addition, primers may include universal priming sequences. That is, the adapters may additionally contain universal priming sequences for universal

amplification of products of any of the reactions described herein. Universal priming sequences are further outlined in 09/779376, filed February 7, 2001; 09/779202, filed February 7, 2001; 09/915231, filed July 24, 2001; 60/180810, filed February 7, 2000; and 60/297609, filed June 11, 2001; and 60/311194 filed August 9, 2001, all of which are expressly incorporated herein by reference.

5

In an alternative embodiment, non-nucleic acid reactions are used to add adapter sequences to the nucleic acid targets. For example, for the direct detection of non-amplified target sequences (e.g. genomic DNA samples, etc. ) on universal arrays, non-amplification methods are required. In this embodiment, binding partner pairs or chemical methods may be used. For example, one member of a binding partner pair may be attached to the adapter sequence and the other member attached to the target sequence. For example, the binding partner be a hapten or antigen, which will bind its binding partner. For example, suitable binding partner pairs include, but are not limited to: antigens (such as proteins (including peptides)) and antibodies (including fragments thereof (FABs, etc.)); proteins and small molecules, including biotin/streptavidin and digoxigenin and antibodies; enzymes and substrates or inhibitors; other protein-protein interacting pairs; receptor-ligands; and carbohydrates and their binding partners, are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. In general, the smaller of the pair is attached to the NTP (or the probe) for incorporation into the extension primer. Preferred binding partner pairs include, but are not limited to, biotin (or imino-biotin) and streptavidin, digoxigenin and Abs, and Prolinx™ reagents.

20

In a preferred embodiment, chemical attachment methods are used. In this embodiment, chemical functional groups on each of the target sequences and adapter sequences are used. As is known in the art, this may be accomplished in a variety of ways. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the two sequences are joined together; for example, amino groups on each nucleic acid may be attached, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).

30

In a preferred embodiment, aptamers are used in the system. Aptamers are nucleic acids that can be made to bind to virtually any target analyte; see Bock et al., Nature 355:564 (1992); Femulok et al., Current Op. Chem. Biol. 2:230 (1998); and U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference.

35

In a preferred embodiment, an array comprising capture probes that hybridize to adapter sequences is made, as outlined herein. In one embodiment aptamers, comprising adapter sequences, can be added. As will be appreciated by those in the art, the aptamers may be preassociated with their binding partners, e.g. target analytes, prior to introduction to the array, or not. In addition, the association between the adapter sequences on the aptamers and the capture probes can be made

covalent, for example through the use of reactive groups (e.g. psoralen) and appropriate activation.

In addition, the present invention is directed to the use of adapter sequences to assemble arrays comprising other target analytes.

5

The adapter sequences may be chosen as outlined above. Preferably the adapters are selected from the sequences set forth in Table I, Table II, Table III or Table IV. These adapter sequences can then be added to the target analytes using a variety of techniques. In general, as described above, non-covalent attachment using binding partner pairs may be done, or covalent attachment using chemical moieties (including linkers).

10

Advantages of using adapters include but are not limited to, for example, the ability to create universal arrays. That is, a single array is utilized with each capture probe designed to hybridize with a specific adapter. The adapters are joined to any number of target analytes, such as nucleic acids, as is described herein. Thus, the same array is used for vastly different target analytes. Furthermore, hybridization of adapters with capture probes results in non-covalent attachment of the target nucleic acid to the address of the array (e.g. a microsphere in some embodiments). As such, the target nucleic/adapter hybrid is easily removed, and the microsphere/capture probe can be re-used. In addition, the construction of kits is greatly facilitated by the use of adapters. For example, arrays or microspheres can be prepared that comprise the capture probe; the adapters can be packaged along with the microspheres for attachment to any target analyte of interest. Thus, one need only attach the adapter to the target analyte and disperse on the array for the construction of an array of target analytes.

15

20

25

Accordingly the present invention provides kits comprising adapters. Preferably the kits include at least 1 nucleic acid sequence as set forth in Table 1. More preferably the kits include at least 10-25 nucleic acids, with at least 50 nucleic acids more preferred. Even more preferable are kits that include at least 100 nucleic acids with more than 1000 even more preferred and more than 2000 even more preferred.

30

It should also be noted that the sequences defined herein can also be used in "sandwich" assay formats, wherein a capture extender probe comprising a first domain that will hybridize to the capture probe and a second domain that has a target specific domain is used. The capture extender probe hybridizes both to the target sequence and the capture probe, thereby immobilizing the target sequence on the array.

35

Once the adapter sequences are associated with the target analyte, including target nucleic acids, the compositions are added to an array comprising addresses comprising capture probes. In one embodiment a plurality of hybrid adapter sequence/target analytes are pooled prior to addition to an

array. All of the methods and compositions herein are drawn to compositions and methods for detecting the presence of target analytes, particularly nucleic acids, using adapter arrays.

Accordingly, the present invention provides array compositions comprising at least a first substrate with a surface comprising individual sites. The present system finds particular utility in array formats, i.e. wherein there is a matrix of capture probes (herein generally referred to "pads", "addresses" or "micro-locations"). By "array" or "biochip" herein is meant a plurality of nucleic acids in an array format; the size of the array will depend on the composition and end use of the array. Nucleic acids arrays are known in the art, and can be classified in a number of ways; both ordered arrays (e.g. the ability to resolve chemistries at discrete sites), and random arrays are included. Ordered arrays include, but are not limited to, those made using photolithography techniques (Affymetrix GeneChip™), spotting techniques (Synteni and others), printing techniques (Hewlett Packard and Rosetta), three dimensional "gel pad" arrays, etc. In one embodiment the ordered arrays include arrays that contain nucleic acids at known locations. That is, the adapters or capture probes described herein are immobilized at known locations on a substrate. By "known" locations is meant a site that is known or has been known.

In addition, adapters find use "liquid arrays". By "liquid arrays" is meant an array in solution for analysis, for example, by flow cytometry.

A preferred embodiment utilizes microspheres on a variety of substrates including fiber optic bundles, as are outlined in PCTs US98/21193, PCT US99/14387 and PCT US98/05025; WO98/50782; and U.S.S.N.s 09/287,573, 09/151,877, 09/256,943, 09/316,154, 60/119,323, 09/315,584; all of which are expressly incorporated by reference. While much of the discussion below is directed to the use of microsphere arrays on fiber optic bundles, any array format of nucleic acids on solid supports may be utilized.

Arrays containing from about 2 different bioactive agents (e.g. different beads, when beads are used) to many millions can be made, with very large arrays being possible. Generally, the array will comprise from two to as many as a billion or more, depending on the size of the beads and the substrate, as well as the end use of the array, thus very high density, high density, moderate density, low density and very low density arrays may be made. Preferred ranges for very high density arrays are from about 10,000,000 to about 2,000,000,000, with from about 100,000,000 to about 1,000,000,000 being preferred (all numbers being in square cm). High density arrays range about 100,000 to about 10,000,000, with from about 1,000,000 to about 5,000,000 being particularly preferred. Moderate density arrays range from about 10,000 to about 100,000 being particularly preferred, and from about 20,000 to about 50,000 being especially preferred. Low density arrays are generally less than 10,000, with from about 1,000 to about 5,000 being preferred. Very low density arrays are less than 1,000, with from about 10 to about 1000 being preferred, and from about 100 to about 500 being particularly preferred. In some embodiments, the compositions of the invention may

not be in array format; that is, for some embodiments, compositions comprising a single bioactive agent may be made as well. In addition, in some arrays, multiple substrates may be used, either of different or identical compositions. Thus for example, large arrays may comprise a plurality of smaller substrates.

5

In addition, one advantage of the present compositions is that particularly through the use of fiber optic technology, extremely high density arrays can be made. Thus for example, because beads of 200  $\mu\text{m}$  or less (with beads of 200 nm possible) can be used, and very small fibers are known, it is possible to have as many as 40,000 or more (in some instances, 1 million) different elements (e.g. fibers and beads) in a 1  $\text{mm}^2$  fiber optic bundle, with densities of greater than 25,000,000 individual beads and fibers (again, in some instances as many as 50-100 million) per 0.5  $\text{cm}^2$  obtainable (4 million per square cm for 5  $\mu$  center-to-center and 100 million per square cm for 1  $\mu$  center-to-center).

10

By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of beads and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates is very large. Possible substrates include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers. In general, the substrates allow optical detection and do not themselves appreciably fluoresce.

15

20

25

Generally the substrate is flat (planar), although as will be appreciated by those in the art, other configurations of substrates may be used as well; for example, three dimensional configurations can be used, for example by embedding the beads in a porous block of plastic that allows sample access to the beads and using a confocal microscope for detection. Similarly, the beads may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Preferred substrates include optical fiber bundles as discussed below, and flat planar substrates such as glass, polystyrene and other plastics and acrylics.

30

In a preferred embodiment, the substrate is an optical fiber bundle or array, as is generally described in U.S.S.N.s 08/944,850 and 08/519,062, PCT US98/05025, and PCT US98/09163, all of which are expressly incorporated herein by reference. Preferred embodiments utilize preformed unitary fiber optic arrays. By "preformed unitary fiber optic array" herein is meant an array of discrete individual fiber optic strands that are co-axially disposed and joined along their lengths. The fiber strands are generally individually clad. However, one thing that distinguished a preformed unitary array from other fiber optic formats is that the fibers are not individually physically manipulatable; that is, one strand

35



generally cannot be physically separated at any point along its length from another fiber strand.

At least one surface of the substrate is modified to contain discrete, individual sites for later association of microspheres. These sites may comprise physically altered sites, i.e. physical configurations such as wells or small depressions in the substrate that can retain the beads, such that a microsphere can rest in the well, or the use of other forces (magnetic or compressive), or chemically altered or active sites, such as chemically functionalized sites, electrostatically altered sites, hydrophobically/ hydrophilically functionalized sites, spots of adhesive, etc.

The sites may be a pattern, i.e. a regular design or configuration, or randomly distributed. A preferred embodiment utilizes a regular pattern of sites such that the sites may be addressed in the X-Y coordinate plane. "Pattern" in this sense includes a repeating unit cell, preferably one that allows a high density of beads on the substrate. However, it should be noted that these sites may not be discrete sites. That is, it is possible to use a uniform surface of adhesive or chemical functionalities, for example, that allows the attachment of beads at any position. That is, the surface of the substrate is modified to allow attachment of the microspheres at individual sites, whether or not those sites are contiguous or non-contiguous with other sites. Thus, the surface of the substrate may be modified such that discrete sites are formed that can only have a single associated bead, or alternatively, the surface of the substrate is modified and beads may go down anywhere, but they end up at discrete sites.

In a preferred embodiment, the surface of the substrate is modified to contain wells, i.e. depressions in the surface of the substrate. This may be done as is generally known in the art using a variety of techniques, including, but not limited to, photolithography, stamping techniques, molding techniques and microetching techniques. As will be appreciated by those in the art, the technique used will depend on the composition and shape of the substrate.

In a preferred embodiment, physical alterations are made in a surface of the substrate to produce the sites. In a preferred embodiment, the substrate is a fiber optic bundle and the surface of the substrate is a terminal end of the fiber bundle, as is generally described in 08/818,199 and 09/151,877, both of which are hereby expressly incorporated by reference. In this embodiment, wells are made in a terminal or distal end of a fiber optic bundle comprising individual fibers. In this embodiment, the cores of the individual fibers are etched, with respect to the cladding, such that small wells or depressions are formed at one end of the fibers. The required depth of the wells will depend on the size of the beads to be added to the wells.

Generally in this embodiment, the microspheres are non-covalently associated in the wells, although the wells may additionally be chemically functionalized as is generally described below, cross-linking agents may be used, or a physical barrier may be used, i.e. a film or membrane over the beads.

In a preferred embodiment, the surface of the substrate is modified to contain chemically modified sites, that can be used to attach, either covalently or non-covalently, the microspheres of the invention to the discrete sites or locations on the substrate. "Chemically modified sites" in this context includes, but is not limited to, the addition of a pattern of chemical functional groups including amino groups, carboxy groups, oxo groups and thiol groups, that can be used to covalently attach microspheres, which generally also contain corresponding reactive functional groups; the addition of a pattern of adhesive that can be used to bind the microspheres (either by prior chemical functionalization for the addition of the adhesive or direct addition of the adhesive); the addition of a pattern of charged groups (similar to the chemical functionalities) for the electrostatic attachment of the microspheres, i.e. when the microspheres comprise charged groups opposite to the sites; the addition of a pattern of chemical functional groups that renders the sites differentially hydrophobic or hydrophilic, such that the addition of similarly hydrophobic or hydrophilic microspheres under suitable experimental conditions will result in association of the microspheres to the sites on the basis of hydroaffinity. For example, the use of hydrophobic sites with hydrophobic beads, in an aqueous system, drives the association of the beads preferentially onto the sites. As outlined above, "pattern" in this sense includes the use of a uniform treatment of the surface to allow attachment of the beads at discrete sites, as well as treatment of the surface resulting in discrete sites. As will be appreciated by those in the art, this may be accomplished in a variety of ways.

In a preferred embodiment, the compositions of the invention further comprise a population of microspheres. By "population" herein is meant a plurality of beads as outlined above for arrays. Within the population are separate subpopulations, which can be a single microsphere or multiple identical microspheres. That is, in some embodiments, as is more fully outlined below, the array may contain only a single bead for each capture probe; preferred embodiments utilize a plurality of beads of each type.

By "microspheres" or "beads" or "particles" or grammatical equivalents herein is meant small discrete particles. The composition of the beads will vary, depending on the class of capture probe and the method of synthesis. Suitable bead compositions include those used in peptide, nucleic acid and organic moiety synthesis, including, but not limited to, plastics, ceramics, glass, polystyrene, methylstyrene, acrylic polymers, paramagnetic materials, thoria sol, carbon graphite, titanium dioxide, latex or cross-linked dextrans such as Sepharose, cellulose, nylon, cross-linked micelles and Teflon may all be used. *"Microsphere Detection Guide"* from Bangs Laboratories, Fishers IN is a helpful guide.

The beads need not be spherical; irregular particles may be used. In addition, the beads may be porous, thus increasing the surface area of the bead available for either capture probe attachment or tag attachment. The bead sizes range from nanometers, i.e. 100 nm, to millimeters, i.e. 1 mm, with beads from about 0.2 micron to about 200 microns being preferred, and from about 0.5 to about 5

micron being particularly preferred, although in some embodiments smaller beads may be used.

It should be noted that a key component of this embodiment of the invention is the use of a substrate/bead pairing that allows the association or attachment of the beads at discrete sites on the surface of the substrate, such that the beads do not move during the course of the assay.

Each microsphere comprises a capture probe, although as will be appreciated by those in the art, there may be some microspheres which do not contain a capture probe, depending on the synthetic methods. Alternatively, some have more than one capture probe.

Attachment of the nucleic acids may be done in a variety of ways, as will be appreciated by those in the art, including, but not limited to, chemical or affinity capture (for example, including the incorporation of derivatized nucleotides such as AminoLink or biotinylated nucleotides that can then be used to attach the nucleic acid to a surface, as well as affinity capture by hybridization), cross-linking, and electrostatic attachment, etc. In a preferred embodiment, affinity capture is used to attach the nucleic acids to the beads. For example, nucleic acids can be derivatized, for example with one member of a binding pair, and the beads derivatized with the other member of a binding pair. Suitable binding pairs are as described herein for IBL/DBL pairs. For example, the nucleic acids may be biotinylated (for example using enzymatic incorporation of biotinylated nucleotides, for by photoactivated cross-linking of biotin). Biotinylated nucleic acids can then be captured on streptavidin-coated beads, as is known in the art. Similarly, other hapten-receptor combinations can be used, such as digoxigenin and anti-digoxigenin antibodies. Alternatively, chemical groups can be added in the form of derivatized nucleotides, that can then be used to add the nucleic acid to the surface.

Preferred attachments are covalent, although even relatively weak interactions (i.e. non-covalent) can be sufficient to attach a nucleic acid to a surface, if there are multiple sites of attachment per each nucleic acid. Thus, for example, electrostatic interactions can be used for attachment, for example by having beads carrying the opposite charge to the bioactive agent.

Similarly, affinity capture utilizing hybridization can be used to attach nucleic acids to beads. For example, as is known in the art, polyA+RNA is routinely captured by hybridization to oligo-dT beads; this may include oligo-dT capture followed by a cross-linking step, such as psoralen crosslinking). If the nucleic acids of interest do not contain a polyA tract, one can be attached by polymerization with terminal transferase, or via ligation of an oligoA linker, as is known in the art.

Alternatively, chemical crosslinking may be done, for example by photoactivated crosslinking of thymidine to reactive groups, as is known in the art.

In a preferred embodiment, each bead comprises a single type of capture probe, although a plurality of

individual capture probes are preferably attached to each bead. Similarly, preferred embodiments utilize more than one microsphere containing a unique capture probe; that is, there is redundancy built into the system by the use of subpopulations of microspheres, each microsphere in the subpopulation containing the same capture probe.

5

In an alternative embodiment, each bead comprises a plurality of different capture probes.

10

As will be appreciated by those in the art, the capture probes may either be synthesized directly on the beads, or they may be made and then attached after synthesis. In a preferred embodiment, linkers are used to attach the capture probes to the beads, to allow both good attachment, sufficient flexibility to allow good interaction with the target molecule, and to avoid undesirable binding reactions.

15

In a preferred embodiment, the capture probes are synthesized directly on the beads. As is known in the art, many classes of chemical compounds are currently synthesized on solid supports, such as peptides, organic moieties, and nucleic acids. It is a relatively straightforward matter to adjust the current synthetic techniques to use beads.

20

25

In a preferred embodiment, the capture probes are synthesized first, and then covalently attached to the beads. As will be appreciated by those in the art, this will be done depending on the composition of the capture probes and the beads. The functionalization of solid support surfaces such as certain polymers with chemically reactive groups such as thiols, amines, carboxyls, etc. is generally known in the art. Accordingly, "blank" microspheres may be used that have surface chemistries that facilitate the attachment of the desired functionality by the user. Some examples of these surface chemistries for blank microspheres include, but are not limited to, amino groups including aliphatic and aromatic amines, carboxylic acids, aldehydes, amides, chloromethyl groups, hydrazide, hydroxyl groups, sulfonates and sulfates.

30

In a preferred embodiment the attachment of nucleic acids to substrates includes contacting the oligonucleotide and the solid support in the presence of high salt concentrations. As is appreciated by those skilled in the art, salt includes, but is not limited to sodium chloride, potassium chloride, calcium chloride, magnesium chloride, lithium chloride, rubidium chloride, cesium chloride, barium chloride and the like. In a preferred embodiment, salt as used in the invention includes sodium chloride.

35

By high salt concentrations is meant salt that is more concentrated than about 0.1 M salt. In a preferred embodiment, by high salt concentrations is meant greater than about 0.2 M salt. In a particularly preferred embodiment, high salt concentrations include from about 0.5 to 3M salt, with about 1M to 2M being most preferred.

By solid support or other grammatical equivalents herein is meant any material that can be modified

to contain oligonucleotides. As will be appreciated by those in the art, the number of possible solid supports is very large. Possible solid supports include, but are not limited to beads, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers.

Once formed, the support containing the oligonucleotides finds use in a variety of systems including decoding arrays as described in more detail in U.S.S.N. 09/344,526, and U.S.S.N. 09/574, 117, both of which are expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in microfluidic systems as described in U.S.S.N. 09/306,369 which is expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in composite array systems as described in U.S.S.N. 09/606,369, which is expressly incorporated herein by reference. In addition the support containing the oligonucleotides finds use in a variety of assays as outlined in more detail in U.S.S.N.s 09/513,362, 09/517,945, 09/535,854, 60/160,917, 60/180,810, 60/182,955, and 09/566,463, all of which are expressly incorporated herein by reference in their entirety. In addition, the support containing the oligonucleotides finds use in array based sensors as described in more detail in 09/287,573, 09/260,963, 09/450,829, 09/151,877, 09/187,289 and 08/519,062, all of which are expressly incorporated herein by reference in their entirety.

Accordingly the invention provides a method of attaching oligonucleotides to a solid support. The method includes contacting the oligonucleotides with the support in the presence of high salt as described herein. Once attached, as discussed in the examples, the attached oligonucleotides readily hybridize to targets, probes and the like. Attachment of crude oligonucleotides in the presence of high salt is as efficient as attaching purified oligonucleotides. Thus, the invention also contemplates a method of attachment of oligonucleotides to a solid support without prior purification of the oligonucleotides. Again, the method includes contacting the crude oligonucleotides with a solid support in the presence of high salt as described herein.

The capture probes are designed to be substantially complementary to the adapter sequences, to allow for a minimum of cross reactivity.

When microsphere arrays are used, an encoding/decoding system must be used. That is, since the beads are generally put onto the substrate randomly, there are several ways to correlate the functionality on the bead with its location, including the incorporation of unique optical signatures, generally fluorescent dyes, that could be used to identify the chemical functionality on any particular bead. This allows the synthesis of the candidate agents (i.e. compounds such as nucleic acids and

antibodies) to be divorced from their placement on an array, i.e. the candidate agents may be synthesized on the beads, and then the beads are randomly distributed on a patterned surface. Since the beads are first coded with an optical signature, this means that the array can later be "decoded", i.e. after the array is made, a correlation of the location of an individual site on the array with the bead or candidate agent at that particular site can be made. This means that the beads may be randomly distributed on the array, a fast and inexpensive process as compared to either the in situ synthesis or spotting techniques of the prior art.

However, the drawback to these methods is that for a large array, the system requires a large number of different optical signatures, which may be difficult or time-consuming to utilize. Accordingly, the present invention provides several improvements over these methods, generally directed to methods of coding and decoding the arrays. That is, as will be appreciated by those in the art, the placement of the capture probes is generally random, and thus a coding/decoding system is required to identify the probe at each location in the array. This may be done in a variety of ways, as is more fully outlined below, and generally includes: a) the use a decoding binding ligand (DBL), generally directly labeled, that binds to either the capture probe or to identifier binding ligands (IBLs) attached to the beads; b) positional decoding, for example by either targeting the placement of beads (for example by using photoactivatable or photocleavable moieties to allow the selective addition of beads to particular locations), or by using either sub-bundles or selective loading of the sites, as are more fully outlined below; c) selective decoding, wherein only those beads that bind to a target are decoded; or d) combinations of any of these. In some cases, as is more fully outlined below, this decoding may occur for all the beads, or only for those that bind a particular target sequence. Similarly, this may occur either prior to or after addition of a target sequence. In addition, as outlined herein, the target sequences detected may be either a primary target sequence (e.g. a patient sample), or a reaction product from one of the methods described herein (e.g. an extended SBE probe, a ligated probe, a cleaved signal probe, etc.).

Once the identity (i.e. the actual agent) and location of each microsphere in the array has been fixed, the array is exposed to samples containing the target sequences, although as outlined below, this can be done prior to or during the analysis as well. The target sequences can hybridize (either directly or indirectly) to the capture probes as is more fully outlined below, and results in a change in the optical signal of a particular bead.

In the present invention, "decoding" may not rely on the use of optical signatures, but rather on the use of decoding binding ligands that are added during a decoding step. The decoding binding ligands will bind either to a distinct identifier binding ligand partner that is placed on the beads, or to the capture probe itself. In this embodiment the decoding binding ligand either is complementary to the capture probe. In this embodiment the decoding binding ligand has the sequence of the adapter that also binds to the capture probe. In a preferred embodiment the decoder binding ligand is a nucleic acid

that has the sequence of at least one of the nucleic acids set forth in Table 1.

The decoding binding ligands are either directly or indirectly labeled, and thus decoding occurs by detecting the presence of the label. By using pools of decoding binding ligands in a sequential fashion, it is possible to greatly minimize the number of required decoding steps.

In some embodiments, the microspheres may additionally comprise identifier binding ligands for use in certain decoding systems. By "identifier binding ligands" or "IBLs" herein is meant a compound that will specifically bind a corresponding decoder binding ligand (DBL) to facilitate the elucidation of the identity of the capture probe attached to the bead. That is, the IBL and the corresponding DBL form a binding partner pair. By "specifically bind" herein is meant that the IBL binds its DBL with specificity sufficient to differentiate between the corresponding DBL and other DBLs (that is, DBLs for other IBLs), or other components or contaminants of the system. The binding should be sufficient to remain bound under the conditions of the decoding step, including wash steps to remove non-specific binding.

In some embodiments, for example when the IBLs and corresponding DBLs are proteins or nucleic acids, the dissociation constants of the IBL to its DBL will be less than about  $10^{-4}$ - $10^{-6}$  M<sup>-1</sup>, with less than about  $10^{-5}$  to  $10^{-9}$  M<sup>-1</sup> being preferred and less than about  $10^{-7}$ - $10^{-9}$  M<sup>-1</sup> being particularly preferred.

IBL-DBL binding pairs are known or can be readily found using known techniques. For example, when the IBL is a protein, the DBLs include proteins (particularly including antibodies or fragments thereof (FABs, etc.)) or small molecules, or vice versa (the IBL is an antibody and the DBL is a protein). Metal ion- metal ion ligands or chelators pairs are also useful. Antigen-antibody pairs, enzymes and substrates or inhibitors, other protein-protein interacting pairs, receptor-ligands, complementary nucleic acids, and carbohydrates and their binding partners are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. Similarly, as is generally described in U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference, nucleic acid "aptamers" can be developed for binding to virtually any target; such an aptamer-target pair can be used as the IBL-DBL pair. Similarly, there is a wide body of literature relating to the development of binding pairs based on combinatorial chemistry methods.

In a preferred embodiment, the IBL is a molecule whose color or luminescence properties change in the presence of a selectively-binding DBL. For example, the IBL may be a fluorescent pH indicator whose emission intensity changes with pH. Similarly, the IBL may be a fluorescent ion indicator, whose emission properties change with ion concentration.

Alternatively, the IBL is a molecule whose color or luminescence properties change in the presence of various solvents. For example, the IBL may be a fluorescent molecule such as an ethidium salt whose

fluorescence intensity increases in hydrophobic environments. Similarly, the IBL may be a derivative of fluorescein whose color changes between aqueous and nonpolar solvents.

5 In one embodiment, the DBL may be attached to a bead, i.e. a "decoder bead", that may carry a label such as a fluorophore.

10 In a preferred embodiment, the IBL-DBL pair comprise substantially complementary single-stranded nucleic acids. In this embodiment, the binding ligands can be referred to as "identifier probes" and "decoder probes". Generally, the identifier and decoder probes range from about 4 basepairs in length to about 1000, with from about 6 to about 100 being preferred, and from about 8 to about 40 being particularly preferred. What is important is that the probes are long enough to be specific, i.e. to distinguish between different IBL-DBL pairs, yet short enough to allow both a) dissociation, if necessary, under suitable experimental conditions, and b) efficient hybridization.

15 In a preferred embodiment, as is more fully outlined below, the IBLs do not bind to DBLs. Rather, the IBLs are used as identifier moieties ("IMs") that are identified directly, for example through the use of mass spectroscopy.

20 Alternatively, in a preferred embodiment, the IBL and the capture probe are the same moiety; thus, for example, as outlined herein, particularly when no optical signatures are used, the capture probe can serve as both the identifier and the agent. For example, in the case of nucleic acids, the bead-bound probe (which serves as the capture probe) can also bind decoder probes, to identify the sequence of the probe on the bead. Thus, in this embodiment, the DBLs bind to the capture probes.

25 In one embodiment, the microspheres may contain an optical signature. That is, as outlined in U.S.S.N.s 08/818,199 and 09/151,877, previous work had each subpopulation of microspheres comprising a unique optical signature or optical tag that is used to identify the unique capture probe of that subpopulation of microspheres; that is, decoding utilizes optical properties of the beads such that a bead comprising the unique optical signature may be distinguished from beads at other locations with different optical signatures. Thus the previous work assigned each capture probe a unique optical signature such that any microspheres comprising that capture probe are identifiable on the basis of the signature. These optical signatures comprised dyes, usually chromophores or fluorophores, that were entrapped or attached to the beads themselves. Diversity of optical signatures utilized different fluorochromes, different ratios of mixtures of fluorochromes, and different concentrations (intensities) of fluorochromes.

30

35

In a preferred embodiment, the present invention does not rely solely on the use of optical properties to decode the arrays. However, as will be appreciated by those in the art, it is possible in some embodiments to utilize optical signatures as an additional coding method, in conjunction with the



present system. Thus, for example, as is more fully outlined below, the size of the array may be effectively increased while using a single set of decoding moieties in several ways, one of which is the use of optical signatures on some beads. Thus, for example, using one "set" of decoding molecules, the use of two populations of beads, one with an optical signature and one without, allows the effective doubling of the array size. The use of multiple optical signatures similarly increases the possible size of the array.

In a preferred embodiment, each subpopulation of beads comprises a plurality of different IBLs. By using a plurality of different IBLs to encode each capture probe, the number of possible unique codes is substantially increased. That is, by using one unique IBL per capture probe, the size of the array will be the number of unique IBLs (assuming no "reuse" occurs, as outlined below). However, by using a plurality of different IBLs per bead,  $n$ , the size of the array can be increased to  $2^n$ , when the presence or absence of each IBL is used as the indicator. For example, the assignment of 10 IBLs per bead generates a 10 bit binary code, where each bit can be designated as "1" (IBL is present) or "0" (IBL is absent). A 10 bit binary code has  $2^{10}$  possible variants. However, as is more fully discussed below, the size of the array may be further increased if another parameter is included such as concentration or intensity; thus for example, if two different concentrations of the IBL are used, then the array size increases as  $3^n$ . Thus, in this embodiment, each individual capture probe in the array is assigned a combination of IBLs, which can be added to the beads prior to the addition of the capture probe, after, or during the synthesis of the capture probe, i.e. simultaneous addition of IBLs and capture probe components.

Alternatively, the combination of different IBLs can be used to elucidate the sequence of the nucleic acid. Thus, for example, using two different IBLs (IBL1 and IBL2), the first position of a nucleic acid can be elucidated: for example, adenosine can be represented by the presence of both IBL1 and IBL2; thymidine can be represented by the presence of IBL1 but not IBL2, cytosine can be represented by the presence of IBL2 but not IBL1, and guanosine can be represented by the absence of both. The second position of the nucleic acid can be done in a similar manner using IBL3 and IBL4; thus, the presence of IBL1, IBL2, IBL3 and IBL4 gives a sequence of AA; IBL1, IBL2, and IBL3 shows the sequence AT; IBL1, IBL3 and IBL4 gives the sequence TA, etc. The third position utilizes IBL5 and IBL6, etc. In this way, the use of 20 different identifiers can yield a unique code for every possible 10-mer.

In this way, a sort of "bar code" for each sequence can be constructed; the presence or absence of each distinct IBL will allow the identification of each capture probe.

In addition, the use of different concentrations or densities of IBLs allows a "reuse" of sorts. If, for example, the bead comprising a first agent has a 1X concentration of IBL, and a second bead comprising a second agent has a 10X concentration of IBL, using saturating concentrations of the

corresponding labelled DBL allows the user to distinguish between the two beads.

Once the microspheres comprising the capture probes are generated, they are added to the substrate to form an array. It should be noted that while most of the methods described herein add the beads to the substrate prior to the assay, the order of making, using and decoding the array can vary. For example, the array can be made, decoded, and then the assay done. Alternatively, the array can be made, used in an assay, and then decoded; this may find particular use when only a few beads need be decoded. Alternatively, the beads can be added to the assay mixture, i.e. the sample containing the target sequences, prior to the addition of the beads to the substrate; after addition and assay, the array may be decoded. This is particularly preferred when the sample comprising the beads is agitated or mixed; this can increase the amount of target sequence bound to the beads per unit time, and thus (in the case of nucleic acid assays) increase the hybridization kinetics. This may find particular use in cases where the concentration of target sequence in the sample is low; generally, for low concentrations, long binding times must be used.

In general, the methods of making the arrays and of decoding the arrays is done to maximize the number of different candidate agents that can be uniquely encoded. The compositions of the invention may be made in a variety of ways. In general, the arrays are made by adding a solution or slurry comprising the beads to a surface containing the sites for attachment of the beads. This may be done in a variety of buffers, including aqueous and organic solvents, and mixtures. The solvent can evaporate, and excess beads are removed.

In a preferred embodiment, when non-covalent methods are used to associate the beads with the array, a novel method of loading the beads onto the array is used. This method comprises exposing the array to a solution of particles (including microspheres and cells) and then applying energy, e.g. agitating or vibrating the mixture. This results in an array comprising more tightly associated particles, as the agitation is done with sufficient energy to cause weakly-associated beads to fall off (or out, in the case of wells). These sites are then available to bind a different bead. In this way, beads that exhibit a high affinity for the sites are selected. Arrays made in this way have two main advantages as compared to a more static loading: first of all, a higher percentage of the sites can be filled easily, and secondly, the arrays thus loaded show a substantial decrease in bead loss during assays. Thus, in a preferred embodiment, these methods are used to generate arrays that have at least about 50% of the sites filled, with at least about 75% being preferred, and at least about 90% being particularly preferred. Similarly, arrays generated in this manner preferably lose less than about 20% of the beads during an assay, with less than about 10% being preferred and less than about 5% being particularly preferred.

In this embodiment, the substrate comprising the surface with the discrete sites is immersed into a solution comprising the particles (beads, cells, etc.). The surface may comprise wells, as is described

herein, or other types of sites on a patterned surface such that there is a differential affinity for the sites. This differential affinity results in a competitive process, such that particles that will associate more tightly are selected. Preferably, the entire surface to be "loaded" with beads is in fluid contact with the solution. This solution is generally a slurry ranging from about 10,000:1 beads:solution (vol:vol) to 1:1. Generally, the solution can comprise any number of reagents, including aqueous buffers, organic solvents, salts, other reagent components, etc. In addition, the solution preferably comprises an excess of beads; that is, there are more beads than sites on the array. Preferred embodiments utilize two-fold to billion-fold excess of beads.

10 The immersion can mimic the assay conditions; for example, if the array is to be "dipped" from above into a microtiter plate comprising samples, this configuration can be repeated for the loading, thus minimizing the beads that are likely to fall out due to gravity.

15 Once the surface has been immersed, the substrate, the solution, or both are subjected to a competitive process, whereby the particles with lower affinity can be disassociated from the substrate and replaced by particles exhibiting a higher affinity to the site. This competitive process is done by the introduction of energy, in the form of heat, sonication, stirring or mixing, vibrating or agitating the solution or substrate, or both.

20 A preferred embodiment utilizes agitation or vibration. In general, the amount of manipulation of the substrate is minimized to prevent damage to the array; thus, preferred embodiments utilize the agitation of the solution rather than the array, although either will work. As will be appreciated by those in the art, this agitation can take on any number of forms, with a preferred embodiment utilizing microtiter plates comprising bead solutions being agitated using microtiter plate shakers.

25 The agitation proceeds for a period of time sufficient to load the array to a desired fill. Depending on the size and concentration of the beads and the size of the array, this time may range from about 1 second to days, with from about 1 minute to about 24 hours being preferred.

30 It should be noted that not all sites of an array may comprise a bead; that is, there may be some sites on the substrate surface which are empty. In addition, there may be some sites that contain more than one bead, although this is not preferred.

35 In some embodiments, for example when chemical attachment is done, it is possible to attach the beads in a non-random or ordered way. For example, using photoactivatable attachment linkers or photoactivatable adhesives or masks, selected sites on the array may be sequentially rendered suitable for attachment, such that defined populations of beads are laid down.

The arrays of the present invention are constructed such that information about the identity of the

capture probe is built into the array, such that the random deposition of the beads in the fiber wells can be "decoded" to allow identification of the capture probe at all positions. This may be done in a variety of ways, and either before, during or after the use of the array to detect target molecules.

5 Thus, after the array is made, it is "decoded" in order to identify the location of one or more of the capture probes, i.e. each subpopulation of beads, on the substrate surface.

In a preferred embodiment, pyrosequencing techniques are used to decode the array, as is generally described in "Nucleic Acid Sequencing using Microsphere Arrays", filed October 22, 1999 (no U.S.S.N. received yet), hereby incorporated by reference.

10

In a preferred embodiment, a selective decoding system is used. In this case, only those microspheres exhibiting a change in the optical signal as a result of the binding of a target sequence are decoded. This is commonly done when the number of "hits", i.e. the number of sites to decode, is generally low. That is, the array is first scanned under experimental conditions in the absence of the target sequences. The sample containing the target sequences is added, and only those locations exhibiting a change in the optical signal are decoded. For example, the beads at either the positive or negative signal locations may be either selectively tagged or released from the array (for example through the use of photocleavable linkers), and subsequently sorted or enriched in a fluorescence-activated cell sorter (FACS). That is, either all the negative beads are released, and then the positive beads are either released or analyzed in situ, or alternatively all the positives are released and analyzed. Alternatively, the labels may comprise halogenated aromatic compounds, and detection of the label is done using for example gas chromatography, chemical tags, isotopic tags mass spectral tags.

15

20

As will be appreciated by those in the art, this may also be done in systems where the array is not decoded; i.e. there need not ever be a correlation of bead composition with location. In this embodiment, the beads are loaded on the array, and the assay is run. The "positives", i.e. those beads displaying a change in the optical signal as is more fully outlined below, are then "marked" to distinguish or separate them from the "negative" beads. This can be done in several ways, preferably using fiber optic arrays. In a preferred embodiment, each bead contains a fluorescent dye. After the assay and the identification of the "positives" or "active beads", light is shown down either only the positive fibers or only the negative fibers, generally in the presence of a light-activated reagent (typically dissolved oxygen). In the former case, all the active beads are photobleached. Thus, upon non-selective release of all the beads with subsequent sorting, for example using a fluorescence activated cell sorter (FACS) machine, the non-fluorescent active beads can be sorted from the fluorescent negative beads. Alternatively, when light is shown down the negative fibers, all the negatives are non-fluorescent and the the positives are fluorescent, and sorting can proceed. The characterization of the attached capture probe may be done directly, for example using mass

25

30

35

spectroscopy.

Alternatively, the identification may occur through the use of identifier moieties ("IMs"), which are similar to IBLs but need not necessarily bind to DBLs. That is, rather than elucidate the structure of the capture probe directly, the composition of the IMs may serve as the identifier. Thus, for example, a specific combination of IMs can serve to code the bead, and be used to identify the agent on the bead upon release from the bead followed by subsequent analysis, for example using a gas chromatograph or mass spectroscope.

Alternatively, rather than having each bead contain a fluorescent dye, each bead comprises a non-fluorescent precursor to a fluorescent dye. For example, using photocleavable protecting groups, such as certain ortho-nitrobenzyl groups, on a fluorescent molecule, photoactivation of the fluorochrome can be done. After the assay, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. The illuminated precursors are then chemically converted to a fluorescent dye. All the beads are then released from the array, with sorting, to form populations of fluorescent and non-fluorescent beads (either the positives and the negatives or vice versa).

In an alternate preferred embodiment, the sites of attachment of the beads (for example the wells) include a photopolymerizable reagent, or the photopolymerizable agent is added to the assembled array. After the test assay is run, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. As a result of the irradiation, either all the positives or all the negatives are polymerized and trapped or bound to the sites, while the other population of beads can be released from the array.

In a preferred embodiment, the location of every capture probe is determined using decoder binding ligands (DBLs). As outlined above, DBLs are binding ligands that will either bind to identifier binding ligands, if present, or to the capture probes themselves, preferably when the capture probe is a nucleic acid or protein.

In a preferred embodiment, as outlined above, the DBL binds to the IBL.

In a preferred embodiment, the capture probes are single-stranded nucleic acids and the DBL is a substantially complementary single-stranded nucleic acid that binds (hybridizes) to the capture probe, termed a decoder probe herein. A decoder probe that is substantially complementary to each candidate probe is made and used to decode the array. In this embodiment, the candidate probes and the decoder probes should be of sufficient length (and the decoding step run under suitable conditions) to allow specificity; i.e. each candidate probe binds to its corresponding decoder probe with sufficient specificity to allow the distinction of each candidate probe.

In a preferred embodiment, the DBLs are either directly or indirectly labeled. In a preferred embodiment, the DBL is directly labeled, that is, the DBL comprises a label. In an alternate embodiment, the DBL is indirectly labeled; that is, a labeling binding ligand (LBL) that will bind to the DBL is used. In this embodiment, the labeling binding ligand-DBL pair can be as described above for IBL-DBL pairs.

Accordingly, the identification of the location of the individual beads (or subpopulations of beads) is done using one or more decoding steps comprising a binding between the labeled DBL and either the IBL or the capture probe (i.e. a hybridization between the candidate probe and the decoder probe when the capture probe is a nucleic acid). After decoding, the DBLs can be removed and the array can be used; however, in some circumstances, for example when the DBL binds to an IBL and not to the capture probe, the removal of the DBL is not required (although it may be desirable in some circumstances). In addition, as outlined herein, decoding may be done either before the array is used to in an assay, during the assay, or after the assay.

In one embodiment, a single decoding step is done. In this embodiment, each DBL is labeled with a unique label, such that the the number of unique tags is equal to or greater than the number of capture probes (although in some cases, "reuse" of the unique labels can be done, as described herein; similarly, minor variants of candidate probes can share the same decoder, if the variants are encoded in another dimension, i.e. in the bead size or label). For each capture probe or IBL, a DBL is made that will specifically bind to it and contains a unique tag, for example one or more fluorochromes. Thus, the identity of each DBL, both its composition (i.e. its sequence when it is a nucleic acid) and its label, is known. Then, by adding the DBLs to the array containing the capture probes under conditions which allow the formation of complexes (termed hybridization complexes when the components are nucleic acids) between the DBLs and either the capture probes or the IBLs, the location of each DBL can be elucidated. This allows the identification of the location of each capture probe; the random array has been decoded. The DBLs can then be removed, if necessary, and the target sample applied.

In a preferred embodiment, the number of unique labels is less than the number of unique capture probes, and thus a sequential series of decoding steps are used. In this embodiment, decoder probes are divided into  $n$  sets for decoding. The number of sets corresponds to the number of unique tags. Each decoder probe is labeled in  $n$  separate reactions with  $n$  distinct tags. All the decoder probes share the same  $n$  tags. The decoder probes are pooled so that each pool contains only one of the  $n$  tag versions of each decoder, and no two decoder probes have the same sequence of tags across all the pools. The number of pools required for this to be true is determined by the number of decoder probes and the  $n$ . Hybridization of each pool to the array generates a signal at every address. The sequential hybridization of each pool in turn will generate a unique, sequence-specific code for each candidate probe. This identifies the candidate probe at each address in the array. For example, if four

tags are used, then  $4 \times n$  sequential hybridizations can ideally distinguish  $4^n$  sequences, although in some cases more steps may be required. After the hybridization of each pool, the hybrids are denatured and the decoder probes removed, so that the probes are rendered single-stranded for the next hybridization (although it is also possible to hybridize limiting amounts of target so that the available probe is not saturated. Sequential hybridizations can be carried out and analyzed by subtracting pre-existing signal from the previous hybridization).

An example is illustrative. Assuming an array of 16 probe nucleic acids (numbers 1-16), and four unique tags (four different fluors, for example; labels A-D). Decoder probes 1-16 are made that correspond to the probes on the beads. The first step is to label decoder probes 1-4 with tag A, decoder probes 5-8 with tag B, decoder probes 9-12 with tag C, and decoder probes 13-16 with tag D. The probes are mixed and the pool is contacted with the array containing the beads with the attached candidate probes. The location of each tag (and thus each decoder and candidate probe pair) is then determined. The first set of decoder probes are then removed. A second set is added, but this time, decoder probes 1, 5, 9 and 13 are labeled with tag A, decoder probes 2, 6, 10 and 14 are labeled with tag B, decoder probes 3, 7, 11 and 15 are labeled with tag C, and decoder probes 4, 8, 12 and 16 are labeled with tag D. Thus, those beads that contained tag A in both decoding steps contain candidate probe 1; tag A in the first decoding step and tag B in the second decoding step contain candidate probe 2; tag A in the first decoding step and tag C in the second step contain candidate probe 3; etc. In one embodiment, the decoder probes are labeled in situ; that is, they need not be labeled prior to the decoding reaction. In this embodiment, the incoming decoder probe is shorter than the candidate probe, creating a 5' "overhang" on the decoding probe. The addition of labeled ddNTPs (each labeled with a unique tag) and a polymerase will allow the addition of the tags in a sequence specific manner, thus creating a sequence-specific pattern of signals. Similarly, other modifications can be done, including ligation, etc.

In addition, since the size of the array will be set by the number of unique decoding binding ligands, it is possible to "reuse" a set of unique DBLs to allow for a greater number of test sites. This may be done in several ways; for example, by using some subpopulations that comprise optical signatures. Similarly, the use of a positional coding scheme within an array; different sub-bundles may reuse the set of DBLs. Similarly, one embodiment utilizes bead size as a coding modality, thus allowing the reuse of the set of unique DBLs for each bead size. Alternatively, sequential partial loading of arrays with beads can also allow the reuse of DBLs. Furthermore, "code sharing" can occur as well.

In a preferred embodiment, the DBLs may be reused by having some subpopulations of beads comprise optical signatures. In a preferred embodiment, the optical signature is generally a mixture of reporter dyes, preferably fluorescent. By varying both the composition of the mixture (i.e. the ratio of one dye to another) and the concentration of the dye (leading to differences in signal intensity), matrices of unique optical signatures may be generated. This may be done by covalently attaching the

dyes to the surface of the beads, or alternatively, by entrapping the dye within the bead.

5 In a preferred embodiment, the encoding can be accomplished in a ratio of at least two dyes, although more encoding dimensions may be added in the size of the beads, for example. In addition, the labels are distinguishable from one another; thus two different labels may comprise different molecules (i.e. two different fluors) or, alternatively, one label at two different concentrations or intensity.

10 In a preferred embodiment, the dyes are covalently attached to the surface of the beads. This may be done as is generally outlined for the attachment of the capture probes, using functional groups on the surface of the beads. As will be appreciated by those in the art, these attachments are done to minimize the effect on the dye.

15 In a preferred embodiment, the dyes are non-covalently associated with the beads, generally by entrapping the dyes in the pores of the beads.

Additionally, encoding in the ratios of the two or more dyes, rather than single dye concentrations, is preferred since it provides insensitivity to the intensity of light used to interrogate the reporter dye's signature and detector sensitivity.

20 In a preferred embodiment, a spatial or positional coding system is done. In this embodiment, there are sub-bundles or subarrays (i.e. portions of the total array) that are utilized. By analogy with the telephone system, each subarray is an "area code", that can have the same tags (i.e. telephone numbers) of other subarrays, that are separated by virtue of the location of the subarray. Thus, for example, the same unique tags can be reused from bundle to bundle. Thus, the use of 50 unique tags in combination with 100 different subarrays can form an array of 5000 different capture probes. In this embodiment, it becomes important to be able to identify one bundle from another; in general, this is done either manually or through the use of marker beads, i.e. beads containing unique tags for each subarray.

30 In alternative embodiments, additional encoding parameters can be added, such as microsphere size. For example; the use of different size beads may also allow the reuse of sets of DBLs; that is, it is possible to use microspheres of different sizes to expand the encoding dimensions of the microspheres. Optical fiber arrays can be fabricated containing pixels with different fiber diameters or cross-sections; alternatively, two or more fiber optic bundles, each with different cross-sections of the individual fibers, can be added together to form a larger bundle; or, fiber optic bundles with fiber of the same size cross-sections can be used, but just with different sized beads. With different diameters, the largest wells can be filled with the largest microspheres and then moving onto progressively smaller microspheres in the smaller wells until all size wells are then filled. In this manner, the same dye ratio could be used to encode microspheres of different sizes thereby expanding the number of

35



different oligonucleotide sequences or chemical functionalities present in the array. Although outlined for fiber optic substrates, this as well as the other methods outlined herein can be used with other substrates and with other attachment modalities as well.

5 In a preferred embodiment, the coding and decoding is accomplished by sequential loading of the microspheres into the array. As outlined above for spatial coding, in this embodiment, the optical signatures can be "reused". In this embodiment, the library of microspheres each comprising a different capture probe (or the subpopulations each comprise a different capture probe), is divided into a plurality of sublibraries; for example, depending on the size of the desired array and the number of  
10 unique tags, 10 sublibraries each comprising roughly 10% of the total library may be made, with each sublibrary comprising roughly the same unique tags. Then, the first sublibrary is added to the fiber optic bundle comprising the wells, and the location of each capture probe is determined, generally through the use of DBLs. The second sublibrary is then added, and the location of each capture probe is again determined. The signal in this case will comprise the signal from the "first" DBL and the  
15 "second" DBL; by comparing the two matrices the location of each bead in each sublibrary can be determined. Similarly, adding the third, fourth, etc. sublibraries sequentially will allow the array to be filled.

In a preferred embodiment, codes can be "shared" in several ways. In a first embodiment, a single  
20 code (i.e. IBL/DBL pair) can be assigned to two or more agents if the target sequences differ sufficiently in their binding strengths. For example, two nucleic acid probes used in an mRNA quantitation assay can share the same code if the ranges of their hybridization signal intensities do not overlap. This can occur, for example, when one of the target sequences is always present at a much higher concentration than the other. Alternatively, the two target sequences might always be present  
25 at a similar concentration, but differ in hybridization efficiency.

Alternatively, a single code can be assigned to multiple agents if the agents are functionally equivalent. For example, if a set of oligonucleotide probes are designed with the common purpose of detecting the presence of a particular gene, then the probes are functionally equivalent, even though they may  
30 differ in sequence. Similarly, an array of this type could be used to detect homologs of known genes. In this embodiment, each gene is represented by a heterologous set of probes, hybridizing to different regions of the gene (and therefore differing in sequence). The set of probes share a common code. If a homolog is present, it might hybridize to some but not all of the probes. The level of homology might be indicated by the fraction of probes hybridizing, as well as the average hybridization intensity.  
35 Similarly, multiple antibodies to the same protein could all share the same code.

In a preferred embodiment, decoding of self-assembled random arrays is done on the bases of pH titration. In this embodiment, in addition to capture probes, the beads comprise optical signatures, wherein the optical signatures are generated by the use of pH-responsive dyes (sometimes referred to

herein as "pH dyes") such as fluorophores. This embodiment is similar to that outlined in PCT US98/05025 and U.S.S.N. 09/151,877, both of which are expressly incorporated by reference, except that the dyes used in the present invention exhibit changes in fluorescence intensity (or other properties) when the solution pH is adjusted from below the pKa to above the pKa (or vice versa). In a preferred embodiment, a set of pH dyes are used, each with a different pKa, preferably separated by at least 0.5 pH units. Preferred embodiments utilize a pH dye set of pKa's of 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11, and 11.5. Each bead can contain any subset of the pH dyes, and in this way a unique code for the capture probe is generated. Thus, the decoding of an array is achieved by titrating the array from pH 1 to pH 13, and measuring the fluorescence signal from each bead as a function of solution pH.

Thus, the present invention provides array compositions comprising a substrate with a surface comprising discrete sites. A population of microspheres is distributed on the sites, and the population comprises at least a first and a second subpopulation. Each subpopulation comprises a capture probe, and, in addition, at least one optical dye with a given pKa. The pKas of the different optical dyes are different.

In a preferred embodiment, "random" decoding probes can be made. By sequential hybridizations or the use of multiple labels, as is outlined above, a unique hybridization pattern can be generated for each sensor element. This allows all the beads representing a given clone to be identified as belonging to the same group. In general, this is done by using random or partially degenerate decoding probes, that bind in a sequence-dependent but not highly sequence-specific manner. The process can be repeated a number of times, each time using a different labeling entity, to generate a different pattern of signals based on quasi-specific interactions. In this way, a unique optical signature is eventually built up for each sensor element. By applying pattern recognition or clustering algorithms to the optical signatures, the beads can be grouped into sets that share the same signature (i.e. carry the same probes).

In order to identify the actual sequence of the clone itself, additional procedures are required; for example, direct sequencing can be done, or an ordered array containing the clones, such as a spotted cDNA array, to generate a "key" that links a hybridization pattern to a specific clone.

Alternatively, clone arrays can be decoded using binary decoding with vector tags. For example, partially randomized oligos are cloned into a nucleic acid vector (e.g. plasmid, phage, etc.). Each oligonucleotide sequence consists of a subset of a limited set of sequences. For example, if the limited set comprises 10 sequences, each oligonucleotide may have some subset (or all of the 10) sequences. Thus each of the 10 sequences can be present or absent in the oligonucleotide. Therefore, there are  $2^{10}$  or 1,024 possible combinations. The sequences may overlap, and minor variants can also be represented (e.g. A, C, T and G substitutions) to increase the number of possible

combinations. A nucleic acid library is cloned into a vector containing the random code sequences. Alternatively, other methods such as PCR can be used to add the tags. In this way it is possible to use a small number of oligo decoding probes to decode an array of clones.

5 As will be appreciated by those in the art, the systems of the invention may take on a large number of different configurations, as is generally depicted in the Figures. In general, there are three types of systems that can be used: (1) "non-sandwich" systems (also referred to herein as "direct" detection) in which the target sequence itself is labeled with detectable labels (again, either because the primers  
10 comprise labels or due to the incorporation of labels into the newly synthesized strand); (2) systems in which label probes directly bind to the target analytes; and (3) systems in which label probes are indirectly bound to the target sequences, for example through the use of amplifier probes.

Detection of the reactions of the invention, including the direct detection of products and indirect  
15 detection utilizing label probes (i.e. sandwich assays), is preferably done by detecting assay complexes comprising detectable labels, which can be attached to the assay complex in a variety of ways.

In a preferred embodiment, an array of different and usually artificial capture probes are made; that is,  
20 the capture probes do not have complementarity to known target sequences. The adapter sequences can then be added to any target sequences, or soluble capture extender probes are made; this allows the manufacture of only one kind of array, with the user able to customize the array through the use of adapter sequences or capture extender probes. This then allows the generation of customized soluble probes, which as will be appreciated by those in the art is generally simpler and less costly.

25 When capture extender probes are used, in one embodiment, microsphere arrays containing a single type of capture probe are made; in this embodiment, the capture extender probes are added to the beads prior to loading on the array. The capture extender probes may be additionally fixed or crosslinked, as necessary.

30 Accordingly, the present invention provides compositions and methods for detecting the presence or absence of target analytes, including nucleic acid sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being  
35 preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples (i.e. in the case of nucleic acids, the sample may be the products of an amplification reaction, including both target and signal amplification); purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the

art, virtually any experimental manipulation may have been done on the sample.

The present invention provides compositions and methods for detecting the presence or absence of target nucleic acid sequences in a sample.

5

In a preferred embodiment, several levels of redundancy are built into the arrays of the invention. Building redundancy into an array gives several significant advantages, including the ability to make quantitative estimates of confidence about the data and significant increases in sensitivity. Thus, preferred embodiments utilize array redundancy. As will be appreciated by those in the art, there are at least two types of redundancy that can be built into an array: the use of multiple identical sensor elements (termed herein "sensor redundancy"), and the use of multiple sensor elements directed to the same target analyte, but comprising different chemical functionalities (termed herein "target redundancy"). For example, for the detection of nucleic acids, sensor redundancy utilizes of a plurality of sensor elements such as beads comprising identical binding ligands such as probes. Target redundancy utilizes sensor elements with different probes to the same target: one probe may span the first 25 bases of the target, a second probe may span the second 25 bases of the target, etc. By building in either or both of these types of redundancy into an array, significant benefits are obtained. For example, a variety of statistical mathematical analyses may be done.

10

15

20

In addition, while this is generally described herein for bead arrays, as will be appreciated by those in the art, this techniques can be used for any type of arrays designed to detect target analytes. Furthermore, while these techniques are generally described for nucleic acid systems, these techniques are useful in the detection of other binding ligand/target analyte systems as well.

25

In a preferred embodiment, sensor redundancy is used. In this embodiment, a plurality of sensor elements, e.g. beads, comprising identical bioactive agents are used. That is, each subpopulation comprises a plurality of beads comprising identical bioactive agents (e.g. binding ligands). By using a number of identical sensor elements for a given array, the optical signal from each sensor element can be combined and any number of statistical analyses run, as outlined below. This can be done for a variety of reasons. For example, in time varying measurements, redundancy can significantly reduce the noise in the system. For non-time based measurements, redundancy can significantly increase the confidence of the data.

30

35

In a preferred embodiment, a plurality of identical sensor elements are used. As will be appreciated by those in the art, the number of identical sensor elements will vary with the application and use of the sensor array. In general, anywhere from 2 to thousands may be used, with from 2 to 100 being preferred, 2 to 50 being particularly preferred and from 5 to 20 being especially preferred. In general, preliminary results indicate that roughly 10 beads gives a sufficient advantage, although for some applications, more identical sensor elements can be used.

Once obtained, the optical response signals from a plurality of sensor beads within each bead subpopulation can be manipulated and analyzed in a wide variety of ways, including baseline adjustment, averaging, standard deviation analysis, distribution and cluster analysis, confidence interval analysis, mean testing, etc.

5

In a preferred embodiment, the first manipulation of the optical response signals is an optional baseline adjustment. In a typical procedure, the standardized optical responses are adjusted to start at a value of 0.0 by subtracting the integer 1.0 from all data points. Doing this allows the baseline-loop data to remain at zero even when summed together and the random response signal noise is canceled out. When the sample is a fluid, the fluid pulse-loop temporal region, however, frequently exhibits a characteristic change in response, either positive, negative or neutral, prior to the sample pulse and often requires a baseline adjustment to overcome noise associated with drift in the first few data points due to charge buildup in the CCD camera. If no drift is present, typically the baseline from the first data point for each bead sensor is subtracted from all the response data for the same bead. If drift is observed, the average baseline from the first ten data points for each bead sensor is subtracted from all the response data for the same bead. By applying this baseline adjustment, when multiple bead responses are added together they can be amplified while the baseline remains at zero. Since all beads respond at the same time to the sample (e.g. the sample pulse), they all see the pulse at the exact same time and there is no registering or adjusting needed for overlaying their responses. In addition, other types of baseline adjustment may be done, depending on the requirements and output of the system used.

Once the baseline has been adjusted, a number of possible statistical analyses may be run to generate known statistical parameters. Analyses based on redundancy are known and generally described in texts such as Freund and Walpole, Mathematical Statistics, Prentice Hall, Inc. New Jersey, 1980, hereby incorporated by reference in its entirety.

In a preferred embodiment, signal summing is done by simply adding the intensity values of all responses at each time point, generating a new temporal response comprised of the sum of all bead responses. These values can be baseline-adjusted or raw. As for all the analyses described herein, signal summing can be performed in real time or during post-data acquisition data reduction and analysis. In one embodiment, signal summing is performed with a commercial spreadsheet program (Excel, Microsoft, Redmond, WA) after optical response data is collected.

Methods for signal summing and analyses are included in U.S.S.N. 08/944,850, filed October 6, 1997; 09/287,573, filed April 6, 1999; and 60/238,866, filed October 6, 2000; an PCT Nos. US98/21193, filed October 6, 1998; and US00/09183, filed April 6, 2000.

Once made, the methods and compositions of the invention find use in a number of applications. In a

preferred embodiment, the compositions are used to probe a sample solution for the presence or absence of a target sequence, including the quantification of the amount of target sequence present. The compositions and methods find utility in the detection of genotyping assays and sequencing assays, and in all sorts of target analyte assays, including immunoassays.

5 For SNP analysis, the ratio of different labels at a particular location on the array indicates the homozygosity or heterozygosity of the target sample, assuming the same concentration of each readout probe is used. Thus, for example, assuming a first readout probe comprising a first base at the readout position with a first detectable label and a second readout probe comprising a second  
10 base at the readout position with a second detectable label, equal signals (roughly 1:1 (taking into account the different signal intensities of the different labels, different hybridization efficiencies, and other reasons)) of the first and second labels indicates a heterozygote. The absence of a signal from the first label (or a ratio of approximately 0:1) indicates a homozygote of the second detection base; the absence of a signal from the second label (or a ratio of approximately 1:0) indicates a homozygote  
15 for the first detection base. As is appreciated by those in the art, the actual ratios for any particular system are generally determined empirically.

Generally, a sample containing a target analyte (whether for detection of the target analyte or screening for binding partners of the target analyte) is added to the array, under conditions suitable for  
20 binding of the target analyte to at least one of the capture probes, i.e. generally physiological conditions. The presence or absence of the target analyte is then detected. As will be appreciated by those in the art, this may be done in a variety of ways, generally through the use of a change in an optical signal. This change can occur via many different mechanisms. A few examples include the binding of a dye-tagged analyte to the bead, the production of a dye species on or near the beads, the  
25 destruction of an existing dye species, a change in the optical signature upon analyte interaction with dye on bead, or any other optical interrogatable event.

In a preferred embodiment, the change in optical signal occurs as a result of the binding of a target analyte that is labeled, either directly or indirectly, with a detectable label, preferably an optical label  
30 such as a fluorochrome. Thus, for example, when a proteinaceous target analyte is used, it may be either directly labeled with a fluor, or indirectly, for example through the use of a labeled antibody. Similarly, nucleic acids are easily labeled with fluorochromes, for example during PCR amplification as is known in the art. Alternatively, upon binding of the target sequences, a hybridization indicator may be used as the label. Hybridization indicators preferentially associate with double stranded  
35 nucleic acid, usually reversibly. Hybridization indicators include intercalators and minor and/or major groove binding moieties. In a preferred embodiment, intercalators may be used; since intercalation generally only occurs in the presence of double stranded nucleic acid, only in the presence of target hybridization will the label light up. Thus, upon binding of the target analyte to a capture probe, there is a new optical signal generated at that site, which then may be detected.

Alternatively, in some cases, as discussed above, the target analyte such as an enzyme generates a species that is either directly or indirectly optical detectable.

Furthermore, in some embodiments, a change in the optical signature may be the basis of the optical signal. For example, the interaction of some chemical target analytes with some fluorescent dyes on the beads may alter the optical signature, thus generating a different optical signal.

As will be appreciated by those in the art, in some embodiments, the presence or absence of the target analyte may be done using changes in other optical or non-optical signals, including, but not limited to, surface enhanced Raman spectroscopy, surface plasmon resonance, radioactivity, etc.

The assays may be run under a variety of experimental conditions, as will be appreciated by those in the art. A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding. Various blocking and washing steps may be utilized as is known in the art.

The following examples serve to more fully describe the manner of using the above-described invention, as well as to set forth the best modes contemplated for carrying out various aspects of the invention. It is understood that these examples in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references cited herein are incorporated by reference in their entirety.

## Examples

## Example 1

## Immobilization of Crude Oligonucleotides to a Solid Support

1. Introduce chemical functional group (such as -NH<sub>2</sub>, -COOH, -NCO, -NHS, -SH, -CHO, etc. ) onto solid support.

2. Activate the functional group before oligonucleotide attachment.

3. 5'-terminal modified oligonucleotide attachment.

Crude Oligonucleotides were attached to supports and compared to results from attachment of purified oligonucleotides. As demonstrated in Figure 3, in the presence of 2M salt, crude oligonucleotides were immobilized as efficiently as purified oligonucleotides.

IN addition, the improved attachment of oligonucleotides to a solid support in the presence of increased salt was sequence and length independent. Thus, the method finds use in attachment of all oligonucleotides to a solid support (see Figure 4).

In addition, when 0.5 M to 3 M NaCl was used for attachment of oligonucleotides, non-purified oligonucleotides were attached with comparable efficiency when compared to purified oligonucleotides (see Figure 5).



TABLE 1

Seq. ID No.	Decoder (5'-3')
17	GGCTGGTTCGGCCCGAAAGCTTAG
18	GTTCCCAGTGAAGCTGCGATCTGG
19	TACTTGGCATGGAATCCCTTACGC
20	ACTAGCATATTTTCAGGGCACC GGC
21	GAACGGTCAATGAACCCGCTGTGA
22	GCGGCCTTGGTTCAATATGAATCG
23	GATCGTTAGAGGGACCTTGCCCGA
24	TGGACCTAGTCCGGCAGTGACGAA
25	ATAAACTACCCAGGACGGGCGGAA
26	CATCGGTTGCGGCCAATCCAGATA
27	GTCGGGCATAGAGCCGACCACCCT
28	CTTGGGTCATGATTCACCGTGCTA
29	TGCCTAACGTGCTAATCAGCAGCG
30	CGCATGTTGGAGCATATGCCCTGA
31	AGCCACTGCATCAGTGCTGTTCAA
32	GGTTGTTTTGAGGCGTCCCACACT
33	TCGACCAAGAGCAAGGGCGGACCA
34	GACATCGCTATTGCGCATGGATCA
35	GAAATACGAAGTCTGCGGGAGTCG
36	TGTCATGAATGATTGATCGCGCGA
37	ATATCGGGATTTCGTTCCCGGTGAA
38	GCGAGCGTACCGAAGGGCCTAGAA
39	TTACCGGCAGCGGACTTCCGAATT
40	GTAATCGAGAGCTGCGCGCCGTCT
41	TCCCTGAGGTCGGAAGCTTCCGAC
42	CCTGTTAGCGTAGGCGAGTCGATC
43	TAGCGGACCGGCAGAATGAGTTCC
44	GGTACATGCACTACGCGCACTCGG
45	AATTCATCTCGGACTCCCGCGGTA
46	GCCAAATCTGGATTGGCAGGAATG
47	TGCATTTTCGGTTGAGGCACATCC
48	CCGCTCAATTCACCATGCTTCGCT
49	CTCGGAAAGGTGCAACTTTGGTGT
50	AATTCGACCAGCAGAACGTCCCAT
51	GCCAGAGTCTCAACCTCACGGGAT
52	CCAACAACCTGGAACGGGAACCCGC
53	GAGAACTGATCGCTGAGGGGCATG
54	GGCACACTAGACTTGTGGCACCGA

55	CTTGGGCAAACGCTTCAGCCACAA
56	TCACATCCAAATATGGTCCGCGAA
57	GTCTGCCGGTGTGACCGCTTCATT
58	CATCGCAGAGCATAAACACCCTCA
59	GTTGGTATCTATGGCAGAGGCGGA
60	ACGAGGTGCCGCTGAGGTTCCATT
61	GGAATGAGTGGACCCAGGCACATT
62	TGTCAATATGCGTCCGTGTCGTCT
63	TGATGAGCCTCAGGGTACGAGGCA
64	CACCGCGGTGTTCTACAGAATGA
65	TTGTTGCCAATGGTGTCCGCTCGG
66	TTAACCTGCGTCTGCCCCTTTCCT
67	AGGCGCGTTCCTGCCTTAGTGACG
68	TAGGGCGATGGCACGAAGCTTCAA
69	TGCATAGAGCCAAAGTCGGCGATG
70	TTGAGAGGCAGGTGGCCACACGGA
71	TCCGCATTGTGAGAAAAACGAGC
72	GGCGGTTTCCGTAGCTATAGGTGC
73	GGTGAAAATTTCTAGCCACGGGC
74	CCGACGGAGGATGAAGACAATCAC
75	CCAGTTTGGCCCAATTCGCCAAAA
76	GGATCTATTAGGCCGTGCGCACAG
77	CGGATGTCACCGTTTGGACTTTCA
78	ATCGCAAATCCTGCTCGTCCCTAA
79	CAGGGCATGCAATAATCGAGGTTT
80	CATGCGTTGATATATGGGCCCAAG
81	CAGCTGCAGCTTGTGACCAACCAC
82	TTGTATGTCTGCCGACCGGCGACC
83	GATGGCGCCCGTTGATAGGTATGG
84	ATGAGAATCGCCGGCAATCTGCTA
85	ATTTGCACTGACCGCAGGCTCGTG
86	CAGGGAGAACGGTTAAGTTCCCGT
87	AGGCCGGCGATCGAGGAGTTTGGT
88	ACACGGTGGTCTCTGATAGCGACC
89	GTGCAACGCCGAGGACTTCCATCA
90	TCCGTGCCTGATAGCCATTCCGAT
91	TGAAATACCACACAGCCAATTGGC
92	GCATCGTGTACATGACTGCCGCGA
93	CAGTGTCTAACGGCGCGCGTGAA
94	CGCTTGCAACGTTGCACCTACTCT
95	CGAAAACTAGTGGGCTCGCCGCG
96	CTTTCAGGGGAACTGCCGGAGTCG

5

10

15

20

25

30

35

40

97	TTGTGGCCTTCTTGTAAGGCACG
98	TCCACGAACGGCGACCCGTTGTCT
99	CGACCTTGCACGAAACCTAACGAG
100	GTGCAGCTTCACGAGCCAGCCTGA
101	CGCTTTCGTGCGAATAGACGATGA
102	TGCGCTTACAGGCTCCTAGTGGTC
103	CACGCGCTTAGTCGCGATCGCATA
104	CGGAGGGAGGGAGCTAGCCTTCGA
105	GCATCCGGCCTGTTGATGACGCCT
106	AGGCCAATCGATCTTATTGCCGAG
107	CCTTCCAATGATTGCATACGCCCA
108	AACACTTGATCAGGCGGGTCGTCT
109	TGGAATCAAGGCCGTAAAGGACAG
110	GCTCCCGTAACCTGTCCACCAAGTG
111	AGTGGTGAATGGCCGCTACCCTGA
112	TGTTGAAGCGAGCTAAAACGGCCA
113	CAGCGCTCCAGAATTGACAGCAAT
114	AAGGTGGTGCCATTCAATTTGGCTA
115	CGTTAAACCGCAATCCGTTCCGGCT
116	TGTCTTCCACCTCGAAGGTTTCCA
117	CACGAGATACCGGCGTAAGGGTGG
118	CTACGGCAAACGTGTGGAATGGGT
119	GTAGGGCGATGACGGGCGAACTAC
120	AATCGACCTCCGCACACATTTCGA
121	GAGTCAGCATGGCGGCGGAGATTC
122	AGATAAAGACGCTGGCAACACGGG
123	GGTACCTCAACGCGAACCACCTTGT
124	AAGCGATGGCTACCCAAGAGCGAT
125	AGAGCTTATGCAGAACCAGGCGCC
126	ATCGGTCTCACGCAGGGTTGGATA
127	TAGGTTGCCCGCCAGAAGAAACAT
128	CGGTGCTGTTGCAAAAGCCTGTAG
129	TGATGAAAGTTTGCGGCAGGACAC
130	GTTGAGTGCAGGATGCAGCGATAG
131	AACATTGCGCGGTCCACCAGGGTT
132	GGGCAGTTAGAGAGGGCCAGAAGT
133	TCGAGCTGGTCCCCGTGAACGTGT
134	GTCTTGGGGGCCGCTTAGTGAAAA
135	ACTGTTGGCTTGCTCTCATGTCCA
136	AGGACCATTTCGGAAGGCGAAGATA
137	CTTGGGAGGCATCCGCTATAAGGA
138	AATAAACGGAACGCACCGCTACAG

5

10

15

20

25

30

35

40

139	TTGTACGTGCGGTCCCCATAAGCA
140	CGCACCAAAGTGAATTTCCAGAC
141	ACCTGATCGTTCCTTATTGGGAA
142	GGAACAGAGGCGAGGGGACTGAGC
143	CCCTGCCTTGGCGTGTGCGCTTAT
144	ACTCTGACACGCCAACTCCGGAAG
145	CTGACGGTTTTTCATTCGGCGTGCC
146	TGCGGTGGTTCATTGGAGCTGGCC
147	GCATGGCCAACTAGTGAATCGCAA
148	AGGCCGTAAAGCGAATCTCACCTG
149	CGAATATTATGCCGAGAATCCGCG
150	ACAGACGAGCTCCCAACCACATGA
151	GGACGGTTTGTGCTGGATTGTCTG
152	AAAGGCTATTGAGTTGGTTGGGCG
153	GATGGCCTATTCGGAGATCGGGCC
154	GATCCAGTAGGCAGCTTCATCCCA
155	AATAACTCGCGCGGGTATGCTTCT
156	GGAGGAGGTTTGTCTCGGAAAGCA
157	CTTTGGTATGGCACATGCTGCCCCG
158	AGAAAGGCTCGAGCAACGGGAACT
159	AATCTACCGCACTGGTCCGCAAGT
160	CGTGGCGGCCACAGTTTTTGAGG
161	TTGCAGTTCAATCCATACGCACGT
162	GGCCCAAAGCCCCAGACCATTTTA
163	CGCCTGTCTTTGTCTCCGGACAAT
164	TGAGGCAACAGGGGCCAAAACTA
165	AGCGGAAGTAGTCCTCGGCTCGTC
166	GGCCCAAAGGCTTAGAGATAGTGG
167	GCACGTGAAGTTTAACCGCGATTC
168	AGCGGCAGAAACGTTCTTGACGG
169	TCGTGAGCAGACGAGATTGCACG
170	TCTTTGCCGCGTAACTGACTGCTT
171	TTTATGTGCCAAGGGGTTAACCGA
172	TGTTACTGTGGTTCACGGCAGTCC
173	CGCGCCTCGCTAGACCTTTTATTG
174	ACAAATGCGTGAGAGCTCCCAACT
175	CGCGCAGATTATAGACCCGAATGT
176	CAAATAACGCCGCTGAATCGGCGT
177	CCTTCGTGCATCGGTGATGATGTT
178	TGAACACGAGCAAACTCCAACGC
179	CAGCAGATCCTTCGTAGCGGTCGT
180	GGAACCTGGTGAGTTGTGCCTCAT

5	181	TCATAAGCGACAATCGCGGGCTTA
	182	CCCAACGTCACTGAAGCTCACAGT
	183	TGTCAGAGCCCGCGACTCAGACGG
	184	TACACGAAGCCTCTCCGTGGTCCA
	185	CTCAGAAGTCCTCGGCGAACTGGG
	186	ATCCTTTTATCTACTCCGCGGCGA
	187	AGGCGTGCAGCAACAGGATAAACC
	188	ACTCTCGAGGGAGTCTCTGGCACA
10	189	TTGCCAGGTCCATCGAGACCTGTT
	190	TCCACTATAACTGCGGGTCCGTGT
	191	GCCCAGTCGGCTCTAACAAGTTCCG
	192	CGGAACGGATAATCGGCGTCAGGT
	193	TAAAATAAGCGCCTGGCGGGAGGA
15	194	GCGCACTCGTGAAACCTTTCTCGC
	195	AGTTTGCCAGGTACTGGCAAGTGC
	196	ACAACGAGGGATGTCCAGCGGCAT
	197	TTCGCAGCACCCGCTAGGTACAGT
	198	TAACCCGATTTTTCGACTCTGCC
20	199	CGTCGCATTGCAAGCGTAGGCTTG
	200	GAGCTGACGTCACCATCAGAGGAA
	201	GGAGGCTGGGGTTCGCGCTTAAGT
	202	TTGTGGGAACCGCACTAGCTGGCT
	203	CCCTCGCACTGTGTTCAACCTCTT
25	204	TCATTGACTCGAATCCGCACAACG
	205	ACAGGGGTTGGCCTTCGTACGTAC
	206	AGGCCGTGCAACATCACACAGGAT
	207	GGGCCGTGGTCACGTAATATTGGC
	208	GCGCGGACATGAAACGACAAGGCC
30	209	CTTATTGGGTGCCGGTGTTCGATT
	210	GGGGCGGTTACCAAAAAATCCGAT
	211	GCTAAAGCGTGCTCCGTAAGTACC
	212	ATCTCATGCATCTCGGTTTCGTCGT
	213	ACGAAAAAAGTGTGCGGATCCCCT
35	214	CCAAGTACACCGCACGCATGTTTA
	215	ATCGTGCGTGGAGTGTTCGCATCTA
	216	TCCAGATACCGCCCGAACTTTGA
	217	TCTGCTGGCAGCACGTGAAGTGGC
	218	TTGAAATTGCTCTGCCGTCAGTCA
40	219	AGTCAGGCGAGATGTTTCAGGCAGC
	220	ACAAGCCGACGTTAAGCCCGCCCA
	221	CCCTAATGAGGCCAGTAACCTGCA
	222	GTGAGACACACATCCCCTCCAATG

5

10

15

20

25

30

35

40

223	CGACGGATGCAGAGTTCAGTGGTC
224	CCCGCATGCCTGGCGGTATTACAA
225	TTAGCAAAGCGGCGCCGTTAGCAA
226	CCCGACACGGGTCAGCGTAATAAT
227	GCGACGGCCCTGAGGTATGTCGTC
228	CAAAAGTGTGTTCCCTTGCGCTTG
229	TCTCGAAGCACAGCCCGGTTATTG
230	ATGCTAACCGTTGGCCATGGAAC
231	CTTGCGGAGTGTTAGCCCAGCGGT
232	TGCTCCCTAGGCGCTCGGAGGAGT
233	CCAATGCCTTTGAGTAAGCGATGG
234	AGCAGATAACGTCCCAATGACGCC
235	TTGACCATTACGTGTTGCGCCCAT
236	TCGCGTATTTGCGGAATTCGTCTG
237	CTGCGTGTCACAATGTCCCGCAG
238	TCTGGTGCCACGCAAGGTCCACAG
239	CTCCGGGAGGTCACCTTAATTGCGG
240	TTTTCGTGATTGCCCGGAGGAGGC
241	TCGGGATGTAGCTGGGGCTACCGG
242	CGAGCCAACGCAAACACGTCCTTG
243	GCAAAGCCTTTGTGGGGCGGTAGT
244	ATTCGACCGGAAATGAGGTCTTCG
245	TTGCTTGCTGAGTTGCTCTGTTC
246	CGCGTGAAGACCCATTCCCGAGT
247	AACCGTATTCGCGGTCACTTGTGG
248	GGGGCCAACCGTTTCGAGGCGTAT
249	TTGCGCTGGCAGTCCAAACGGCTT
250	GGGTGTGGTTAGAATGCACGGTTC
251	GCGAGGACCGAACTAGACAAACGG
252	ACGCACGCGTGACCGAAGTTGCTG
253	TAAAAGGTCGCTTTGAAAGGGGGA
254	TGCGATCGCTAACTGCTGGGACAA
255	GGAGGTATAAGCGGAGCGGCCTCA
256	ATGCTGACATGTCGTGCACCTCGT
257	TGTGGTTAAAGCGTCCGTTCAACG
258	CGTTCACACCGCGTAAGCTGCGT
259	CCTATCCCGGCGAGAACTTCTGTG
260	GTCTGCACTCACGCAGCGGAGGGA
261	GCACGAGTTGGTGCTCGGCAGATT
262	AACGTCGCACGACACAGTTTCGTC
263	ATGCGCGCTTATCCTAGCATGGTC
264	TCACGTTTTCGTCTCGACATGAGG

	265	TGTGCCTCATCCTTAGGATACGGC
	266	AGGTGGTGTGGGTCAACCGCTTTA
	267	CTGGATCGAAGGGACTGCAAGCTC
5	268	TAGATCAACTCGCGTACGCATGGA
	269	GATCCTGCGGAGAAGAGAGTGCAG
	270	TACGTGTGGAGATGCCCCGAACCG
	271	GCGCTATGTCAATCGTGGGCGTAG
	272	AGCGAGGTTTCTAGCGTCGACACC
10	273	CGATGAAGACAGGTTTGCTGTTGC
	274	ACCCAGGTTTTGCCGTTGTGAAT
	275	CCCTGTTAACGGCTGCGTAGTCTC
	276	AGGCCGATTTACCCGCCAATTGC
	277	GAGCCCTCACTCCTTGCCCTTTGA
15	278	GGGTGGACATCCGCCTCGCAGTCA
	279	GATGGCTGAGAACCGTGCTACGAT
	280	TCGACGTTAGGAGTGCTGCCAGAA
	281	CGAATGGGTCTGGACCTTGCATAG
	282	GTGCACCAGACATTCGAACTCGGA
	283	AGAGGCCCGTATATCCCATCCAT
20	284	AACGCCTGTTCAAGCATCAGCGG
	285	AAGGCTCAACACGCCTATGTGCGC
	286	AGTCCGTGTTGCCAGATTGGCTCG
	287	ATGTCCCATGTAAAGACGCGTGTG
	288	ATGGAGTCTGCTCACGCCCAAAGG
25	289	CGGCCTCCAACAAGGAGCACTAAC
	290	CAGAGCCGTGGCAACATTGCGAGC
	291	TCATTTGAATGAGGTGCGCACCGG
	292	GACGTACCGGAAGCGCCGTATAAA
	293	ATGCGAGCAATGGGATCCGGATTG
30	294	AGAGTGAGGCCTCCCTGACCAAGT
	295	CGCACCGTAAGTAGATTGCCCCG
	296	AGGGTATCGGAGCCAGGGCTTACC
	297	TGAACCTTTGAGCACGTCGTGCGC
	298	TCCGCCTTTTTGGTTACCTCGAAG
35	299	GAACGCCAACGGCACTAACACATC
	300	CCGACAGCAGCCAAGACGTCCCAG
	301	TTGTACACCTGGGCCACGCACAGG
	302	CATAAAAAACCTGGGGCTCTGCG
	303	TGCCAACTGTGCAGACCGGACTTA
40	304	GGCGAAAGAGCGAAACCGGCTCGT
	305	GGGATGCGTATTTTAGCGAACACG
	306	TGGGATTCAGCGACCAAGTACGCGA

5

10

15

20

25

30

35

40

307	CCCGATATTCGCCCCGGCCTATTCCG
308	CGAGAAGATGCCTCACGCAACCAA
309	AACCTTGACCCGTGGATGACGCTA
310	GGCTAGACGATGGATACCCGTGCC
311	GCCTCTTCTCGACGATGCGATTTT
312	GCTTCCGGATGAACGGGATGGTTG
313	CCCTCCATGTTCTTCGAACGGTTT
314	TTGATGGGCGGCAATGCTCTTGCT
315	ATTGTGAGATGCGCCAAATTCCCC
316	TCAGCACAGCCAGACGGTCAACTT
317	ACTCCACTCCTCGGTGGCAAACATA
318	TCTGGGCATGCCTGGACGGAGACG
319	TCTCAACTCCGGTACGACGAAACA
320	TTGCGTGGTCAAAGGCGCAACGTG
321	AGACAGCGATCCGCGGCTCATGAT
322	CGCGTCTCTAACTGAGAGCAGCCA
323	AGGCGCACATGTACGGACATTCAG
324	GATGAGTGGCACGTCGGTGTGTAA
325	TGATCCATATTGTCGGACGTTGCG
326	ACCTGCCGGGAGTTCATAGGCTAG
327	AGCATTGGCGTTTTTCCGCAACGA
328	GGTAATATTCAGCGCGACCGCTCA
329	ATAGCGTACGACGAGGTGACGCGC
330	GGGTGAGGGAAAGAGCACCTGCCT
331	TAGGTACGATGCGTTTGACGCTA
332	ACTGCCCGTACCTCTGGTTCTGGC
333	CAAAAATCGGGTGAACATTGGCTG
334	CCTTTGGCCTGAAGTTGTCGTAGC
335	GTGCCCCACGAGCGTATCGTTGTA
336	AGGCGCTACGTGGGCCTGGAGCAA
337	GGGTGCTACCATTGCATTAGTCCG
338	ACCACGCGCGTACGTGTAACCGAG
339	CCATGATGCATTGGGTGCATTTAG
340	GGTCCGGCCCTACGAAACGTTCTGA
341	CCGTGTGGCTGGAGATTCGTGTGA
342	GTTAGGGCGACGCATATTGGCACA
343	GGGTCAGTCAGGTGCGTTAGGATC
344	GCCGTGAAGTCGAATGCAGATCGA
345	GCCACCACCCAGTGCATTGAGGTA
346	GAGCTTAGTTTGCGGTGATCGGGC
347	TGTTTGCCGCCATTAGGGAGTAAC
348	GCTCCGCTGGATGTGCCGTTTAG



5

10

15

20

25

30

35

40

349	CGGTAGCATGCGAGATCCCTGTTA
350	CTACGCTCTACCAGTTGCCTGCGA
351	GTGCCTCCTGCTGTATTTGCCAAG
352	TTGCGACTCGACTTGGACGAGTAG
353	TCTGGGAGCTGTTTACTCCAGCCA
354	TGCACGCGGAACTCCCTTTACCAT
355	TGGCAGCAAATGAATCGAAAGCAC
356	AACTGGTGACGCGGTACAGCGAAG
357	AGACGATTACGCTGGACGCCGTCG
358	ATGCCCTCCTTCATGGAAAGGGTT
359	ATTCTCGGAGCGTATGCGCCAGAA
360	ATAGCGGAGTTTGGGTACGCGAAC
361	ACCTACGCATACCGCTTGGCGAGG
362	GATTACCTGAATGGCCAAGCGAGC
363	CCTGTTAGCATCACGGCGCTTAGG
364	CGGAATGATGCGCTCGACAACGCT
365	TGAGAGAGGCGTTGGTTAAGGCAA
366	AAGCAGGCGAAGGGATACTCCTCG
367	TCACGACAGACGGGCCGAGATTAC
368	AAGCAATTTGGCCTCGTTTTGTGA
369	GCTGGTTGCGGTAGGATCGCATAT
370	TTGTGAATCCGTTCTGTCCCCGAC
371	CTCCGATGACAATTGTGGAGAGCA
372	TGGGCTCCTCTGAGGCGAGATGGC
373	GGATAGAGTGAATCGACCGGCAAC
374	TGCACCGAACGTGCACGAGTAATT
375	GCCAGTATTCTCGGGTGTGGACG
376	TCGCTACCTAAGACCGGGCCATAC
377	TGGCATTGACGAGCAGCAGTCAGT
378	CGCGTCCCAGCGCCCTTGGAGTAT
379	ATGAAGCCTACCGGGCGACTTCGT
380	CCAGACAGATGGCCTGGAACCATG
381	TGGCGTGGGACCATCTCAAAGCTA
382	CCGCATGGGAACACGTGTCAAGGT
383	GCCCACTCGTCAGCTGGACGTAAT
384	ATTACGGTCGTGATCCAGAAAGCG
385	TGCGAGGTGAGCACCTACGAGAGA
386	GGGCCGCATTCTTGATGTCCATTG
387	CCTCGGATGTGGGCTCTCGCCTAG
388	TAGGCATGTTGGCGTGAGCGCTAT
389	CGATACGAACGAGGATGTCCGCCT
390	TACGCCGGTTAGCACGGTGCGCTA

5

10

15

20

25

30

35

40

391	CATACGATGTCCGGGCCGTGTCGC
392	ATCCGCAGTTGTATGGCGCGTTAT
393	GGGTAAGGGACAAAGATGGGATGG
394	ATTGGAGTGTTTTGGTGAATCCGC
395	GAACCGAGCCAACGTATGGACACG
396	GCCGTCAAGCTTAAGTTTTGGGC
397	ACCTGCTTTTGGGTGGGTGATATG
398	AATCGTGGGCGCAGCAAACGTATA
399	GTCGCCGATTGCTCAGTATAAGC
400	ACCCGTCGATGCTTCCTCCTCAGA
401	ATCCGGGTGGGCGATACAAGAGAT
402	TTCCGCATGAGTCAGCTTTGAAAA
403	GCAAAGTCCCACTGGCAAGCCGAT
404	CGACCTCGGCTTCATCGTACACAT
405	CTCATGAGCGCAGTTGTGCGTGAG
406	CAGATGAAGGATCCACGGCCGGAG
407	TCAAAGGCTCTTGGATACAGCCGT
408	TCCGCTAATTCCAATCAGGGCTC
409	ACGCACGGCGCTTTTGCCTTAATG
410	TGACAACGTCACAAGGAGCAGGAC
411	CTTAGTTGGGGCGCGGTATCCAGA
412	GCTCTAATGCCGTGGAGTCGGAAC
413	CCGATTACAAATTGACTGACCGCA
414	AGACGTACGTGAGCCTCCCGTGTC
415	AATGGAGCGATACGATCCAACGCA
416	GGAGGCGCTGTACTGATAGGCGTA
417	TGTTTTGAATTGACCACACGGGA
418	CATGTCTGGATGCGCTCAATGAAG
419	GCCCGCTAATCCGACACCCAGTTT
420	CCATTGACAGGAGAGCCATGAGCC
421	GAATCACCGAATCACCGACTCGTT
422	AACCAGCCGCAGTAGCTTACGTCG
423	TTTTCTGAGGGACACGCGGGCGTT
424	GGTGCTCCGTTTGATCGATCCTCC
425	CCGCTTAGGCCATACTCTGAGCCA
426	TAAGACATACCGACGCCCTTGCCT
427	GTTCCCGACGCCAGTCATTGAGAC
428	TAAAAGTTTCGCGGAGGTCGGGCT
429	CGGTCCAGACGAGCTGAGTTCGGC
430	CGGCGTAGCGGCTACGGACTTAAA
431	GCTTGGATGCCCATGCGGCAAGGT
432	AGCGGGATCCCAGAGTTTCGAAAA

5

10

15

20

25

30

35

40

433	GAGCTTGAGAGCGAGGTCATCCTC
434	GCATCGGCCGTTTTGACCATATTC
435	CATAGCGCTGCACGTTTCGACCGC
436	ACCCGACAACCACCAATTCAAAAA
437	GCGAACACTCATAAGAGCGCCCTG
438	TTTTGGTGTGGCCGGTTGAAGCTC
439	CCGCCGAGTGTAGAGAGACTCCGA
440	GACATCGGGAGCCGGAACATGAG
441	TCGTGTAGACTCGGCGACAGGCGT
442	ATGCGCATATACTGACTGCGCAGG
443	ACAAGCGAACCCGAGTTTTGATGA
444	GCATGAGACTCCGCGAAGACATGT
445	TCCTACATGTGCGGTCACGATCAC
446	GACCGATCGCGAAGTCGTACACAT
447	GTCGCCAGGACTGGGCCGATGTGA
448	ACCGATAAGACTTGCATCCGAACG
449	TCCATAACCAGTCCGAAGTGCCGG
450	ACGCGCCCTGCATCTCGTATTTAA
451	AGACCGCATCAATTGGCGCGTACC
452	AGAGGCTTGGAAGTAGGGACCCT
453	GCAATGGACGCCAGACGATACCGG
454	GCTGGACTTAGTCGTGTTCCGGCGG
455	GGGGCTCATGAACGAAAGGCCTTT
456	AGGCATCGTGCCGGATTGCTCCCT
457	TGCGCATGTGACGTTGAACAAAG
458	ATTGCATTATGCGGTCCCTCAAAC
459	TTCGGGTCACATCCGATGCCATAC
460	ACCCATCGCCGGAAGCGATGTTG
461	AAGCGCTGACTCGGCTAAGAATCA
462	ACTTCCAAGTCCTTGACCGTCCGA
463	TCTCAATATTCCTGTAGTCGCCCA
464	AACAGTTCCTCTTTTCTGGCGC
465	CGTCCTCCATGTTGTCACGAACAG
466	TGCGCAGACCTACCTGTCTTTGCT
467	ATGGACGGCTTCGCAGTCCTCCTT
468	TGAACGCTTTCTATGGGCCACGTA
469	TGAACCCTGCCGCGAGCGATAACC
470	GTTCTTGCGCGATGAATCAGGACC
471	AGGGTACGTGTCGCAGCTTCGCGT
472	ACCCTTGCTCCGCCATGTCTCTCA
473	GGGACAAGGATTGAAGCTGGCGTC
474	TGTCGTTGCTCCCGAGTACCATTG

475	GTGGTTATCTGCGAGGGCTTTTGA
476	GTTGTCCGAGACGTTTGTGTCAGC
477	GCTGGTGAACACTCACGAACCGCT
478	GCAGACAGGGCAAATCGGTGCAAA
479	CCCATCACAACGAGTGGCGACTTT
480	GCTTCTACAGCTGGCGTGCTAGCG
481	GAATGTGTGCCGACCATTCTAGCC
482	CCAGCGGAAGTTAGAGCTCTGTGG
483	TTTTTACCGACCACTCCATGTCGG
484	GCGGCTATGTGATGACGGCCTAGC
485	AGTACACGGGCGTGTTAGCGCTCC
486	TCCTGTGTGGTGGCGCACTCCAC
487	CCAACTAACCAATCGCGCGGATGA
488	AGTGAGTGACCAAGGCAGGAGCAA
489	CATCTTTCGCGGAGTTTATTGCGG
490	CTTCGTCCGGTTAGTGCGACAGCA
491	CTCACGAAAACGTGGGCCCCGAAAT
492	CGCAGCAGCTGAACTCTAGCATTG
493	AGGAGACATACGCCCAAATGGTGC
494	ATTGAGAACTCGTGCGGGAGTTTG
495	CTCTTTGTAGGCCCAGGAGGAGCA
496	GCCGCAGGGTCGATAATTGGTCTA
497	AAACGCCGCCCTGAGACTATTGGG
498	CTGAGTTGCCTGGAACGTTGGACT
499	CGGATGGGTTGCAGAGTATGGGAT
500	CTGACCTTTGGGGGTTAGTGCGGT
501	GGAAATGAGAACCTTACCCCAGCG
502	AACGCATCGTCCGTCAACTCATCA
503	TGGAGAGAGACTTCGGCCATTGTT
504	ACGGAAGTCACGGCGTCGCTCGAA
505	TTGCGCTCATTGGATCTTGTCAGG
506	AGCGCGTTAAAGCACGGCAACATT
507	AGCCAGTAACTGTGGGCGGCTGT
508	CGACTGATGTGCAACCAGCAGCTG
509	GGTTGCTCATACGACGAGCGAGTG
510	GCGCAAATCCACGGAACCCGTACC
511	ACGCAGTTTATTCCCCTGGCTTCT
512	AGAACCTCCGCGCCTCCGTAGTAG
513	AAAGGAGCTTTCGCCCCAACGTACC
514	AGTGATTGTGCCACTCCACAGCTC
515	GCGATCGTCGAGGGTTGAGCTGAA
516	GGGAGACAGCCATTATGGTCCTCG

517	GAGACGCTGTCACTCCGGCAGAAC
518	CCACCGGTCGCTTAAGATGCACCT
519	CGGCATAACGTCCAGTCCTGGGAC
520	AAGCGGAACGGGTTATACCGAGGT
521	TGCACACTAGGTCCGTCGCTTGAT
522	AGGGAACCGCGTTCAAACCTCAGTT
523	GAATTACAACCACCCGCTCGTGTT
524	TTCAGTGCTACGAAGCATGGATT
525	TTAGTTTGGCGTTGGGACTTCACC
526	AATGCGACCTCGACGAGCCTCATA
527	CCGAAACCGTTAACGTGGCGCACA
528	TAAAGTAACAAGGCGACCTCCCGC
529	TAATGATTTTAGTCGCGGGGTGGG
530	GGCTACTCTAAGTGCCCGCTCAGG
531	TGGCGGACGACTCAATATCTCACG
532	GGGCGTTAGGCGTAATAGACCGTC
533	GCCACCTTTAGACGGCGGCTCTAG
534	GAGATGTGTAAACGTGCAGGCACC
535	CAACCTCGTTGTCGAGTTTCTCGG
536	TAGCTCGTGGCCCTCCAAGCGTGT
537	GTGTCGGCGCTATTTGGCCTTACC
538	CCAGGGAAGCAACTGGTTGCCATT
539	TTCCGAAACTAAGCCAGAACCGCT
540	GCAAACCCGGTAACCCGAGAGTTC
541	GCAAATGGCGTCATGCACGAACGT
542	AGTACTTTCGCGCCAGTTTAGGG
543	AAGATCTGCGAGGCATCCCGGCTT
544	GCAAGTGTATCGCACAGTGCGATT
545	CCGACAAGGCCTCAATTCATTCTG
546	GTCTCGTCTCAACTTTAAGGCGCG
547	ATCCAGAGATCCGTTTTGCAGCGT
548	GTCACCAGGAGGGAAGTTTCACCC
549	TATCTTACGCCCCACGGTCGAGCT
550	TTCCGTCAGGCGGATCAACGGAAT
551	ATGCCGGACACGCATTACACAGGC
552	TGGGCCGCTTGGCGCTTTCATAGA
553	CCTAGCGCGAGCTTTACTGACCAG
554	TTGGCCAGGAATATGGTCTCGAGA
555	GTCTGCGGCGACTTGCTATGCAT
556	AACTTGCTCATTCTCAAGCCGACG
557	ACGTCAGCGATTGTGGCGAAATAT
558	ACGGCCTGCGTCAGCACATGCATC

559	ATACCTCCGCAGAACCAATCCGTT
560	AGTTCGCGGTCCCACGATTCACTT
561	TGCTCAATTTGTGCAGAAAACGCC
562	TTATCGCGAGAGACGACCGTGTCC
563	GACGCGACGTGAGTAGTGGAAGCG
564	ATGGTAGGGGCATTGGGCTTTCCT
565	CCAAATATAGCCGCGCGGAGAÇAT
566	GCAAACCCTGATTGAATCGTGCCC
567	TAGCGTCTTGCGTGAAACCATGGG
568	CCACCCCGACAGCGCTGGACTCTT
569	ACGAGCACTGAAGGCTGCTTTACG
570	CATATCAGCGTCGTCTAGCTCGCG
571	TGATCCCGGACCGGCTAGACTAAT
572	GGCCCCGACACTACAGGGTAATCA
573	GGCTCCAGGGCGAGATTATGAATG
574	CAAAATCCGATGGGCGGAAAATTA
575	CACAGGCGCATAGGGAGCAAGCTA
576	TAGCTATTGCCCGATGGGCTACT
577	TGGTACGCGGTCCATAGCAAGTCG
578	GACGCTGTGGCTCGGAACTGTTC
579	CCTGGGTTTCGCCGCGTGGTAACTG
580	TTCCCGCGTAGCCCAACAGCTATA
581	TTCCGCGATTGCTGCCGCATAACA
582	AAAAATGGCACCGAAGTTGAGGCA
583	CATTCCGCGCGAGTTGAAATCCAG
584	ACGCACGTTTTTTGGCACGGTTAA
585	TGTCCATGACGTCGTTTCTCTGGT
586	TCTCAGTCGGACTCGTATGCCAGA
587	CTCCAAACGCACACATCAAGCATC
588	TTCAACCAAGCGGGGTGTTTCGTGA
589	GGTGTCCGAGGGTGGTGACCTCGA
590	AGCGCTTTTGGTCATGATTGCAA
591	CCGAGGACTTACGTCTGCCAGGA
592	GCCCAATCCAGTTCTTATGCCGCC
593	AAGCTTTGCGAAAGGTGTGTTGGC
594	CGGGTTAACCACGCAAGTTATGA
595	TGATTAGCGCTCAATACACGCGTG
596	AAGGGCAGACCTTTGGTTCGACTG
597	GCGCCACAAGATTCACATGTCATT
598	GCCATGTTCAAGGGCCTTTCGAAG
599	CGCGGTGTTTTGTCTAGGTGCCGG
600	CAACATTGTGGTGGCACTCCATCC

5

0

15

20

25

30

35

40

601	CGATACGCGCCGGTTTGTTAAATC
602	GGCTATAAACGTGCGGACTGCTCC
603	TGGGTAAATCACTATTGCGCGGTT
604	GTCTTCATCGGCCCGCGCAAGCTA
605	GCGACACACCCTGTACTCTGATGC
606	GTAGCAGGGTCCGCAAGACCAAGC
607	TCGCCAACGCAGGGTAACTGCCAT
608	ACTCCGAAGCTTCGAGCGGCACGA
609	TCCCGCCCACTAGACTGACTCGTA
610	ACCTTCTGGGGTCGCTACCAATA
611	ATCATCCCACGGCAGAGTGAAGAG
612	CGCTGGACTGGCCTATCCGAGTCG
613	CGGTCTCAGCAACACTGTCGAAA
614	CGAACGTTCTCCGATGTAATGGCC
615	ATACCGTGCGACAAGCCCCTCTGA
616	AGCTCATTCCCGAGACGGAACACC
617	TTTCATGCGGCCGTTGCAAATCAT
618	ACTCGAACGGACGTTCAATTCCCA
619	CTGCATGGTGTGGGTGAGACTCCC
620	CCGCGAGTGTGGATGGCGTGTTGA
621	AATGTGTCGGTCCTAAGCCGGGTG
622	TAAGACGAGCCTGCACAGCTTGCG
623	GGCGTGGGAGGATAAGACGATGTC
624	TGCTCCATGTTAGGAACGCACCAC
625	CGGTGTTGGTCGGACTGACGACTG
626	CCGCGCGTATCTATCAGATCTGGG
627	AAAGCATGCTCCACCTGGAGCGAG
628	ACTTGCATCGCTGGGTAGATCCGG
629	TGCTTACGCAGTGGATTGGTCAGA
630	ATGCAGATGAACAAATCGCCGAAT
631	GCAATTCTGGGCCATGTATTCGTC
632	AGGGTTCCTTACGCGTCGACATGG
633	GTGGAGCTAATCGCGAGCCTCAGA
634	TCGTAGTCTCACCGGCAATGATCC
635	TTATAGCAGTGCGCCAATGCTTCG
636	CGAACAGTGCTGTCCGTCGCTCAA
637	TCCGCGTGGACTGTTAGACGCTAT
638	CATTAGCCCGCTGTCGGTAACTGT
639	GGAAAGAACTCAGACGCGCAATG
640	CGACTCGCTGGACAGGAGAATCGT
641	CATGATCCTCTGTTTCACCCGCGG
642	GGCGTAGCGCTCTAAAAGCTTCGG

5

10

15

20

25

30

35

40

643	AGTGATGCCATCAGGCCCGTATAC
644	TATGGAAAGGGCAACAGCGCTATC
645	CTGTGGTTGATGGAGGATCCACAC
646	ACTCGCTGGAATTTGCGCTGACAC
647	CAGGCCCGAACCACGCGGTTACAG
648	GGCGCAATGGGCGCATAAATACTA
649	GGTCAATTCGCGCTACATGCCCTA
650	TGAGGGCTGTTTGGTATTTGACCC
651	GATGGTGACTGGAGCCCTTCCGC
652	CCGCGCATAGCGCAATAGGGGAGA
653	TCTTCTGGCTGTCCGGCACCCGAA
654	GCGTTCGCAATTCACGGGCCCTTA
655	TCGTTTCGGCCTTGGAGAGTATCG
656	AGGTGCAAGTGCAAGGCGAGAGGC
657	CGCCAGTTTCGATGGCTGACGTTT
658	GCTTTACCGCCGATCCCAGATATC
659	GTGCTTGACGAAGAGGCGAAATGT
660	CAGTCCGTGCGCTTCATGTCCTCA
661	TACGCGTAAGAGCCTACCCTCGCG
662	GGCGAGTCTTGTGGGGACATGTGT
663	CCAAAGCGAAGCGAGCGTGTCTAT
664	GCCGTAGGTTGCTCTTCACCGAAC
665	AAATCCGCGATGTGCCGTGAGGCT
666	GGCTTCGCACCCGTACCAATTTAG
667	TGTAGAGTCCCACGTAGCCGGCAT
668	CACTAGTCTGGGGCAAGGTGCATT
669	TGTA CTGGCAGGCGCAATAGATT
670	AACGGGTATCGGAAGCGTAAAAGC
671	CGGACTGCCC GTTTGCAAGTTGAG
672	ATCGTTCAGCACTGGAGCCCGTAA
673	ATGCATCGAACTAGTCGTGACGGC
674	TTCCAGGCATTAAGGAGAGGGAGC
675	GTGCGACATCTACTCCACGATCCC
676	CTCATCGTCCTAACACGAGAGCCC
677	AATGGCACTTCGGCGGTGATGCAA
678	CCGTGGGAGGGAATCCAACCGAGG
679	AAATTCTCGTTGGTGACGGCTCAT
680	TTGCTCTTATCCTTGTCTGGGCG
681	TTAAGGATCAGGCGGAGCTTGCA
682	CGCGACTAAGGTGCTGCAACTCGA
683	GCTCGATTCACGGCCCGTTGTTT
684	AGCAGAGTGCGTTGCAGAGGCTAA



5

0

5

20

25

30

35

40

685	TGGAGGTGAGGACGACGTGCACTA
686	AACCGTTTAGGGTACATTGCGGT
687	TATGATCGCTCGGCTCACAGTTTG
688	GACTTTTTGCGGAAACGTCATGGT
689	TGTCGGTTATTCCACCTGCAAGGA
690	CTATGGTTTGCACTGCGCCGTCGA
691	AGCAGGGAAATTCAATCGTTCGCA
692	CCTAACCGAGCGCTTAGCATTTC
693	CCCGACCCTAACTCGCATTGAATA
694	TTGCTTAATGGTGACGCCACGGAT
695	GATGCTCGCCGTGTTTAGTTCACG
696	TCGGATGACGAGTTTCCATGACGG
697	ATGCGGTCTACTTTCTCGATCGGG
698	TTGCGAGGCTAAGCACACGGTAAA
699	AACTTAATTACCGCCTCTGGCGCC
700	GTGACCGCGAACTTGTTCCGACAG
701	TGCGGATTACCGATTGCTCTTAA
702	TGATAGGGGGCCACGTTGATCAGA
703	TCGCTCCGTAGCGATTGATCGTAG
704	TGTCAGCTGGTAGCCTCCGTTTGA
705	AGCGTCGCATGACGCTTACGGCAC
706	TCACTCAGCGCTGTGACTGCCTGA
707	GTTTGCGCTATAGTGGGGACCGT
708	GTCGCATTCTGCACTGGCTTCGCC
709	TGATTAGGTGCGGTCCCGTAGTCC
710	AAGGGACCTTGGGTGACGGCGAGA
711	TCAAATGGCCACCGCGTGTCATT
712	CTCCGACGACCAATAAATAGCCGC
713	GGCTATTCCCGTAGAGAGCGTCCA
714	TGGATAACCTCTCGGTCCATCCAC
715	GACCGCTGTACGGGAGTGTGCCTT
716	GCCACAGAGTTTTAGCAGGGACCC
717	CCCACGCTTCCGACCACTGACCT
718	CATTGACACAATGCGGGGACTGAT
719	AGCCACTCGACAGGGTTCCAAAGC
720	CAGGATGAGCAAAGCGACTCTCCA
721	CAAGGTATGGTCTGGGGCCTAAGC
722	GGTGTTCCGCCTAACTCTTTCGG
723	TTTAGTCGGACCCTGTGGCAATTC
724	CACACGTTTCCGACCAGCCTGAAC
725	CTGGACGAACTGGCTTCCTCGTAC
726	TTCAACAATCCGCCGAAAACCTGACC

5

10

15

20

25

30

35

40

727	AACAGGATATCCGCGATCACGACA
728	TACGTCGGATCCATTGCGCCGAGT
729	CATGGATCTCTCGGTTTGATCGCC
730	AGCCAGGCGCGTATATACGCTCGG
731	ATTTGGCACGTGTCGTGCCATGTT
732	CCGCGTTGCACCACTTTGAGGTGC
733	TTGGACGTGACAAGCATGGCGCTC
734	CTGAATCGCGCAAGTAAATGGGGG
735	GATAAGGTCCACCAGATTGCGCGC
736	CTAACAATTGCCAACCGGGACGGC
737	GGTAACCTGGGTGCTTGCAAGTTA
738	ATCGGAGCCACCATTCGCATTGGG
739	GTGAACTGGCTTGCCCCAGGATTA
740	AGGCGATAGCATGGTCCCATATGA
741	AACGGTATCGTGGCTAATGCACGA
742	AGTAGTGGTCCTCCAGATCGGCAA
743	CCGTTGAATTGGACGGGAGGTTAG
744	GCATAAGTGCGGCATCGGAAGGG
745	CGACAAGATGCAGCTGCTACATGC
746	TCGCAGTGATTCCCGACCGATAAG
747	CAAGGCGAGTCCACTCGAGGGGAC
748	GCAACTTGCACGGCATAAGTGGCC
749	TCCGAGCTTGACGTTGCGGACGTC
750	AGCGCTGGGCTGTGCTGCCATCTC
751	TTCATGTCGCTGAGTAACCCTCGC
752	CGAACCGCTAATGCCCATTTGTCAG
753	CACGGAAGGTGGGACAAATCGCCG
754	CACAGATGGAGACAAACGCGCCTT
755	TTTTCGCAACTCGCTCCATAACCC
756	ACGTTACGTTTCCGGCGCCTCTAA
757	TATCGGATTGCGTGGGTTTCAATC
758	CTTCCACAATTGTCTGCGACGCAC
759	TGCACAAAGGTATGGCTGTCCGGC
760	ACCGTGGCCGGGCCATAAGCTACG
761	TCCGATGCCAGTCCCATCTTAAGA
762	CTGAAACCGTGCGAATCGAGGTGA
763	CGGTGTTCCGCGTGTGAAAAAAT
764	TCTAGCAGGCCTTTTGAATCGCCA
765	GAGTCACCTCTGAGACGGACGCCA
766	TCTTCTGTCATCCTGCAGCAGCAT
767	GCGGATGAAACCTGAAAGGGGCCT
768	GGGGCCCCAACTGGTATCAAGCC

5

10

15

20

25

30

35

40

769	GCATTGGCTTCGGATTCTCCTACA
770	AGGCGGCCCAACTGTGAGGTCTTG
771	ACACCATGTGCTCCGCGCTGCAGT
772	ACGATGAACATGAATCGGGAGTCG
773	CTGCATCCCTGTAGCAGCGCTCCG
774	GTGCCGTATTTGACCTGTGCGTT
775	GCAGTGCGCACTTCAGTTCAAAAG
776	GCGATTTTAAGCGATGCCTTGACG
777	TAGGTGACCTAGGCTTGCTTGCGG
778	CTGGATACCTTGCCTGTGCGGCGC
779	CCCCTTACGGCTCGTCGTCTATGC
780	GCGCTTGCCCGATGCGATGCATTA
781	TTTCTGTAAGCGGCCTGGGGTTCA
782	GGCTGAGGTGAGCGGTAAGGATGA
783	TCTTGGCCTCCCCGATCTAATTG
784	GGAGGTAACGCCGTGTACGTAGGA
785	GTAATCCATTTGTGGCTGCGTCAA
786	CAAACCCATTCCAGCAGACGCCTG
787	TAGGAGGAATTTGGCATGCGGGCG
788	ATAGGTAGGATGTGCCCGGCGTTG
789	GCAAGTGCTTAGCTCGTCAGCCTC
790	CTGGCTGTGTGCGCATCTCGTTAAC
791	CTAACGTCGTCTCGCGCAATCACT
792	TTTTCATAAACGTTGTCCCGAGC
793	AGCAGGAGGACGAACCTCCGCTCC
794	TTCAAGCACCATCGTGCAATCCAA
795	AGCGTCGCCAGTGATCGCTAGTGG
796	TACATTCCCTGCCTCCGTGGGCTT
797	CGCTTCGCGTATTAGTAGCGGTT
798	TCGGACGCGTCGACACTCATTATA
799	TCTGAGCAGGCCAGCGCTCCAGCT
800	TTGAATTGCCAAGCCCTGAAAGCC
801	AGTTTTCGCCTTGATGCGTCGGTG
802	GTTTCATAGGCCACGCGTGCTAAA
803	GGAGCGAAGACTTCGTCTGCCCAA
804	ATTGGCCGAGGGTGAATGCAGCCT
805	TGATCCATCCGAATGCTTTTCCAT
806	GCACACAGTTGTCTTGGCCCATGA
807	CTGGCGGGCAGTGGAACAAAC
808	ATCTCCATGCGTAAGACTGCTCCG
809	TCTCCTCTCGTCGCAGTTCGTGGA
810	TAGCGTATTCACTCTTGCCGAGCA

5

0

15

20

25

30

35

40

811	CAATCAAAGCCACGGCGCGATGG
812	AGCGTCACGGAATTCAGCAGATCT
813	GACTCCCTGTTAATGCGCCCAAGG
814	TAGGCACTGCCGGTTCAGATTCAA
815	AACAGGGTGATAACGGTGGCCAAT
816	CGTGCGTACCATGTGTAAGTGCGT
817	GACCAATTCTACTTCGGCAGCCCA
818	ATCGGACCGATTTGCTTTTGGCTG
819	TCCGCCGAAGCACACGCTTATTGG
820	AACGGTACGCATTGTGAGCAGTGT
821	TGGCGACTACTGTTCCCCTGAATC
822	CAGAGGGGACAGCCGTATGCCTTA
823	CGGTGGTTTTATCGGAATCTGCGA
824	TTGGCCTCCGACCTCACGACATAT
825	CGTTTCGCTAGCATCTGGCGCCGA
826	ACTAAGCGGTGGAGCCGGTGGATG
827	ATATTGGCTGCGTTTACGGGCCGC
828	CCGCTATGGTGGCAATCCCGATAC
829	GTTGCATGTGGCTCAGGCGGCATA
830	ATTCTGGGGAGTGACCCAGGGCTT
831	CTCTCCAAGGAGACGAGCCAATGT
832	GAAAGGACGGGATTTGGGGGCTAA
833	TATGTAGTACCTTGGCTCGCGCCA
834	TCCCTTTCGATGAGCGGCTGTACT
835	TAGATCGGGCAGAGCCCGTATCTT
836	GGAATGCTTTAGGCTGCCGAGCTG
837	ATGGTAGCAACATTCAACGCCAGG
838	CTATGAAACGTGTGGCCCAGCAAC
839	ATGTTGCTAGTGCCTTTCGGGCCT
840	CCAATGTGCGCAGACTCAGTCATT
841	GATAGTGCTCGCAAACGGGCCTTC
842	GCACCCTGTTGCCTCATTGAGCGT
843	GGCGTGAATAGAGTGACCAGGCGG
844	ACGTGCCAGCTGCGGGCACTTTAT
845	AGTGGAATAGTCGCGTCGTGCCGC
846	ACTCGCCTATTACCGCTGGATTGG
847	GAGACCGGATTGAGATGATCCCGT
848	AAAATGGCAGGCGGCAAGCAATTG
849	CTGGCAGTTTACCACCGAACCAGT
850	TTACATTGCCGATTTGCGATGTGA
851	TAAAACTGAAGGGTCGCCTCAGCA
852	GGCTTCGCATGCCTTTGCAACATT

5

0

5

20

25

30

35

40

853	AAGACCGAAGGTCTCTCTGAGGGC
854	GCCTATGGCTCCAGCTCAGCAGTA
855	CGTATCATAGCGTTCGGTGGACAA
856	CATGCGCTCGCACTCTGCCTGTCT
857	TGGGCAATTCGGAAACGTCGGTCT
858	TTGCGGAGATGCGACGGTACATTG
859	ACTTTCGCACGTCGATCTGGACTG
860	CTAACTGCCGCGGCAAACTGATTA
861	GGCCGCGGATTTTATTCTTGAT
862	GAATTTGGAACGGTGTTCCGATGA
863	GTCCATCCATCTACGGCATCAGGA
864	TAAACGACCTGGCACATGTGCGTA
865	CACCATCCAAGAGCCAATCCTAGG
866	ACTCATATACGATCAGTCCGCCGC
867	GTGCCAACCGACGATCAACCGAAC
868	TGGGGTTCGTACAGGTCGGTTCAT
869	AACAGTAGAGGCGAGGCCTGCGGG
870	TGCATCGAATCCGAGATGGATCTT
871	GCGTCACGTTATGTCCGCTCTGTC
872	GGGACATGCGTAGCGCAATATCAC
873	CACACGTCACACCATCCAAAGTGG
874	ATGCTCAGGTGCTAAATACGGCCA
875	AAAAATGTTTAGCGCGCTGACTGG
876	ATAGTCCGTTTCCGTTCCCAACGA
877	TCGATCTTCTGGGTTGCAGACCAG
878	GTCGCGCAGCCGATCCTCATGTC
879	GTTGCGGGGTGTCGAAAAGGATCT
880	ATCTCTTCTCGGGTGGATGCCAG
881	TGATGTGCGTTTCAGCTTTTCGCG
882	GTAAAGGGGTGAGAACATCCGGCC
883	AAGTCGTCTCCCTGCGTCTCGTCC
884	CCGACCTAATAAGGCGCAACAATG
885	CATCATTGGCACCGTACCAATGCC
886	TGGAGAAAGGGAAGTGCAGCAACG
887	TGGTACTCCTTGTCATGCCTGCCA
888	GGCACAGGTTCTCTTGACGCGCG
889	GAATCTGGGCATTGCTACGAGACC
890	CGAAATGGGAGCGTCCACTACCAC
891	ACATATGAGCTCGCGTGCTTGCA
892	TCGAGCACGGTCACTGATAAAGCC
893	GAGGGTCCCTGCTCAGAGTTGGTT
894	AAATGCGATCGCCCCTTATGGAAT

5

10

15

20

25

30

35

40

895	CTACCCGAATGGATTGCGGATGGC
896	AGGGACTGGCAGGTCTCTGCGCGT
897	TAACGATCCATTCCACGAATGCAG
898	GGCCGCACGTACGATTACGCCTTG
899	TGGGGAATGCATCAGTTGTTGGCT
900	TATCTGGGAGTAGCAGGCAGGGCC
901	CCGAAGGTTTCACGCTCAGGTCGC
902	GAACCCAGCTGGGACATCCTTCAG
903	TGCATGCGAGCAAATAACCCGGAC
904	AATTGTCCGCCAAACGCTTTTCAG
905	GTCGGCTTCGAGCGATCGAGTGTG
906	TCGCGTGCTCTACGTAGCCCATGA
907	GGCTTCCGCGATAACGTAATTCGC
908	TGTAGCCGACTAGGGCCGAAGCCC
909	AAGCGAACGCCCTGGCTGAATATT
910	TGTCACGCGACGTGCTGCAGATTT
911	CCGTGTCCGTGTTGTGACAGGCG
912	CCCCACACGTTGCGCCTATATGTG
913	GGCGGGCACAACCAACACAGATG
914	CGACTGCGGGATCACCGGTGATTA
915	TCGGGACATGACCGGTACGGAGTC
916	TACCTCGAGTGGCCGTTGATCGGG
917	TAATTCATGGGGCTAGCCGAACCA
918	ACACTCTAAGCCGATTCCGTTCTGA
919	GTGGGCGTGAGTGACACGCACAAA
920	ACGACTCCTCGGGCAAAGTACGTA
921	TGTGGTCATGGCGCTACTGTTTTC
922	CTTTCGCTAGCCAGAGCGGGTTCC
923	ACAGGGCGTGTTAGCGTGTGACAA
924	GGTACTTCCGGCGTATCGGGCCAC
925	GTGGGTTTTGTTCACCCTTCTGGG
926	ACGCAATTCGCGATTACTTACCCG
927	CGCCTCGACTGCGGTCAAGCACAA
928	GTGAAATGGATCCAGAGAGGGCCA
929	TATAAACGCTGCAGGGCTCCGTTA
930	GTTATTACAGGCGGCTTGTAACGGG
931	GGGTTCTAGCGTGCGCGTTCAGTT
932	TTGGGCTCGAGCGGTACACCACTA
933	CCGTCTTCAGGACAACGGTATGCG
934	GGACCCTTTGACAGATTGCGGCAC
935	TAAATTTTATCGCCAGGCGGCGCT
936	GCCGAACGCAAGATCGCTTGAAC

5

10

15

20

25

30

35

40

937	TAGGCCATTGGTGCCCTAAGACGG
938	CAAACCACAGCTTACAGGCTGCGT
939	TAAACGGAGACTGGCACGGTAGCA
940	TAGCGCGCATCACACTTGAATCG
941	TGCTGACACAAACGAGCCGTTTCG
942	CGCTTAACGGCATTGACTGTCCAC
943	TTCCACGGCCGTGTATTACGGATA
944	TTTATGCCGTTGCCGAGGAAGACT
945	AGTGCCGAGATAGGGGACTGGGCG
946	CTAGTCTCCACGCCCTCGGGACGA
947	CCGCCATTCCGAAGATGGATGATG
948	TGACGGTGAAAGTCGATTGCGAAG
949	ATATGCGTCACCACCCGGTTCCGA
950	CCATCAGTGAAGGGGTTGCTGCCA
951	CATATGTGCTTGGCTTGCGATGAC
952	TCTGCTTTGGAAGCCTGAACTGCT
953	CGATTTGGTCAAGAAGGCGGAAAT
954	ATCAGAGGCCTTCCCGCCTCGTTA
955	ATTGTTGTCGTTGCCACATCGCAG
956	TGAAATGTGTCTGGACGCGAGTCT
957	GCGGGCGATGCTCCTTAAAGGGTA
958	CCGCAATCTCCATGCGTCGACCGT
959	TGCCGCGTAATCACCTGGAAGTTG
960	TTCCAGTAGCCAGCGGTAGTGTGA
961	CTGAATTCCGCCTATTGTTGCGCA
962	GCTTGAACCTCGAGGCGATGTTCT
963	CAAGCGTGGAAGTACGACCCGCCA
964	GTGTGCACTGGATCCGAGCCCTAG
965	TCCCTGGGCTAGCATTGCGAGGTT
966	AGAACCAAAGACGCTTGTTTGCCG
967	CGTCACATGCAAACGTTCCCTCCC
968	TGACCGCATGTGTATTGAGTCGCT
969	GCGGGCCCAATGAGTATCCGTCAT
970	TAGTGACTGTGAACGCCCTGGTT
971	GGCACCGTCTGCCGCGCGTATATC
972	TCGATGCAGTCTTTTCCCGTCAA
973	ACCCCGTGGGGTTTCGCCATTTTT
974	CTACACGCGCAGTTGTGACTTGTG
975	CGCAGCGACCTCATCTCTGGAGCC
976	CGACCCAGCACTCCTAAAATCGGT
977	ACGCGCCGCTCATCACTACAATCT
978	CGCAACTTCCTGTGGCAAAGCCAG

5

10

15

20

25

30

35

40

979	TCGTTGGGCACATAAGGCAACTGA
980	CCGCTTGTAATTGCCATTCTCCGT
981	GTAACCAGGGAGTCCTGGGCTGTG
982	AGCGCAAGATCTGGGGGCAGTCAC
983	GCGTACATCTGCTCATCAGCATGG
984	CCTCTGTGGCAGGAAAGAAACCGT
985	CCTATGCAATGGACCTGCATCGGA
986	CTCGGTGGATGGCGAATAAGGATA
987	CCTCACTCGTGATGGCGTGACGCA
988	TACGCTCACAGAACGCCATACGCC
989	CCGGAGAAGTTACGCGGATCGGAC
990	GCGCCCTCACTGCATTTTTGGTAT
991	ACTTTCAGCACGCGAACAGCGCAA
992	CTAAACGCCCTTGATGCATGAGCA
993	GCTTGCCTTTTACGATCGTCGCTA
994	CAGACATCGTACGCACTCGGCATC
995	TAGCCGCGCGGCTCCTATGCTCTT
996	GATGCCCTTTTGGTCCCCATGCCA
997	TGAGCTGCCTTGCCACGATGCCTC
998	CCGCCGTATACGTGCCATAGTTTG
999	TAGTGCTCTCCGCGCTCATCCAAC
1000	CCCTAGATAAGTTGGGGTGGGACG
1001	TGAAGGGCCACCTGATATGGTTTC
1002	GCCGCCTCCGACTGGTTAACCCGA
1003	CGCACGGCTACTAACAGCGGATCA
1004	CCGGACCAATTCCAACGAGCATCG
1005	CATTGAGGTCCACCGTTCACATCC
1006	AGGACGCAGCATGTCCCAGCCGAG
1007	TAATCGCGGGCCATACTACCAACG
1008	CGCAAATTTCTCCGGTCGGCAAGC
1009	GTGGCTCGACTAATGCCTTGCGTG
1010	TGTGGGCGTGTTCCGGCTCACTGT
1011	GTTCTTCCTTTTCTGCGGTGGGAA
1012	ACCTCGAGTCAGATTGTGCGCCTT
1013	CAAGTGGACAGACGGTTTGTTCCG
1014	TCCAGTTGAGTCGCGCCGACGAGG
1015	CGCAACAGGTCAGCCCTTATTTGC
1016	GCCGTGACTCCTGCAATGTCGGTA
1017	ATCAGCGCAAGCTGGTCTGAAACA
1018	CCCTGGCCAGAACGAGAGGCCATG
1019	ACGATCAAGGACTCGTCAGGGTTG
1020	TTCATGGCACCAAGACCACCGTTA



1021	ACAGCAAGGAGATGGATTGCGACG
1022	CGTAAATATCTGCGGCGGTGTGAA
1023	GGAAACACGTGTTCTGTTGGC
1024	CGATGTTAGGATTGCGATAGGCCA
1025	ATCGGACAAGGACAAGTGGATGGT
1026	GCCCGGAGGACAAAGTTCGAGTTA
1027	AAATCCGACAAATGGGCACATGGA
1028	CAGTTAGGGGATGCGGATGAGTGA
1029	CGGCAGGTGGAGATTCCGACATTG
1030	TAGGGCAGCCAGGTTCACTCATCT
1031	GCACCGTATTAGCAGTAGGCACGC
1032	ACGCATTACAGGTGTGCGAAGGGA
1033	CGTGAAGTGCACGTGTTCCACAGGG
1034	GCTGAACTACCGCCTAAAATCGCG
1035	AGCACGCCAGGGAGGATCGAGTTA
1036	ATGAGGGCAAGGAATGGGTCATGC
1037	GGGTCTCTCGTAATCAAAGGCCGA
1038	TATCTTGCGCAACGCCTCCATTTA
1039	GGTTACACCTACGGAATCCAGCGG
1040	ACACCGAGTTGGTCCGGTCAATAG
1041	TCCCAGATTAAACGCTAGCCACCG
1042	TTGGTGAAACTGGCCCGTCGGAAG
1043	CCAGGGGAGTTGACAATGAGGCTG
1044	TCTGCGTTATTGGACCGTTTGTCTG
1045	TATGGGATGCTAAACGGCGTACA
1046	CACAGACGTCTGTGCGGCTTGTGT
1047	AGAATGCCGTTTCGCCTACTCCCGT
1048	CGACGGATAATGCAGGCCTCATGA
1049	ACCCTCTAAAGCAATAGGTGCGCG
1050	CACTCACGGCAGAAGCCTGCTTGT
1051	ATCAGCCCACATATTCTCGGCCGT
1052	CAAATCTGGGGTCGTCCTAAACGC
1053	TGTCGCCCATGGCAGGTTAAATAC
1054	GGGGGCCCATCAATTCATTATCGA
1055	GTCGAGCAGCTTTAGTATCGCGGG
1056	CCGCTAAGCACCGAAGGCTCACAA
1057	TAGAATTAGCGAACGGTGATCCCG
1058	CACATGACATTTGGCAAAGGTCCA
1059	TCAACGCACTGGCGATGACTAGAT
1060	CGGGAAATGTCTTTAGCCGTGCAA
1061	ATCAGAGCAAATCTGCAGCGGGGA
1062	GGCCTGTTTCTGTCCAAGTGGCT

5

10

15

20

25

30

35

40

1063	ATTTCACCTCGCTGATCGCTTCCG
1064	AGTGACGCCGAGTCGCGAGGGTTA
1065	AGTTGTCTCATCCTGTCCGGGACC
1066	CTTCTTTGTGCACACTTGCCAGGG
1067	CACCTCATCGGAGCATAGCAACCC
1068	ATGCGATCCATGACAAGGGTTGCT
1069	CCCGTGGAGATGATGTGCGGCTTA
1070	CCCAATAGACGCCACAGCCAGTGA
1071	AACGACCACGACCCTCGCCGAGTA
1072	GGTGCTTTGTCTGAGGCGAGTGAA
1073	CTGTCGGCGCTGCTCTCCGAATTT
1074	CTCGCCGGAGTGTTGTAAGCATTG
1075	AGCAATCATGAGAGGTGGCCGGTG
1076	ATTTGCCACCGGCGACAAAAAGAT
1077	CCGCCCGTGTTGGCATGTCTTTTG
1078	ATCGGAAGTGCTGACTGACACACG
1079	CCTCAGACCCTATCTGGGTTGACG
1080	CTGTGTGGTCTGGTCCGGCTGTTC
1081	GTCCCCATTATCGGTGAGTGCAAC
1082	ACAGGCACGTAAGTGCTCAATCGG
1083	AGCAAGATAGCGGGAGTGCCCTA
1084	GGTTTACGCCATGACATCCCGTCA
1085	GTGCAGGCCTTTGTGTGTGAATCG
1086	CTTCGAGGGTAGGGCTTCGAAACG
1087	AGTCGACACTTGGGTTTACCACGG
1088	ACATAAATCTCGCCCGCTGCACTC
1089	GTTTGGTTTTCCACGGAGGTTTGA
1090	GCAGGAACCAGATTAGTGTCCCGG
1091	TTTGCTAGAGCGCGGAGCTAAAGC
1092	CTATGTGGCATCGCTGACATGCTC
1093	CCTAAGTCGGTTTGCAGCTGCTCT
1094	GCGTTCGTCCACAGGAACGGAAGG
1095	TAACCCGCGCCCGAGAAATTGTCT
1096	TATGGTGCTCAGAGCTGTTGCCAA
1097	TCATCGACCCACTAACGTCAGGGC
1098	TGCTCAAGCTACGCGTCACTTCCC
1099	AGCGGGAAGGTCTGAGGAGGGAAA
1100	CCGATGTAGCACCACCGCAGTGGC
1101	AAGTTCTGGGAATCACACGGCGCG
1102	CACCAGCCTTACGTGCGGCGTTAA
1103	CGTTTCGCCTCCTCTTCCGAATGC
1104	GAGGAGGCCAATAGAGCAGCGCGC

5

10

15

20

25

30

35

40

1105	AGTAATCTTGCGGCACACAAGCGG
1106	TGAGGACAAACCGCGCTAGGATA
1107	TCGTAGAGACGCAGTGCCCATCTC
1108	CGAAGCTACACCCCGAGTGCGGTG
1109	ATGATGTGATCTTCCCATGGCTGG
1110	TGTACACGTATCGCGTTCGCCTAG
1111	GGTGTGCTTTTACGCATGTACGCA
1112	AGGCGGGATACGTGGATGCTAGCC
1113	AAATTAGGCACAGCCCTCCCACAG
1114	ATAAGTTTGGTGAGCCATTGCGCA
1115	CCTATTTGCGCGGACCTCGATGCC
1116	TTACCGGAATATGCACTTGGCCGC
1117	CCTCTCGGACGGTCCCTTTGATCG
1118	CAAGCGAATGCTGTATTACGGCCT
1119	GCATTTCCCATGCCAGAACGTTGA
1120	GTTTTGGCTAACCGTCCTGCCTTG
1121	AGGTTTTGTCCGGGCGAATGATGT
1122	ATGTCCACGAGTGCGTCCGATATC
1123	AGACGCGTACGAGGGTTCTGCGCC
1124	AATACCGTTCCCATCTGTGCGAGG
1125	ACACAAGGTGCCTCATCGAATGGT
1126	GCCGGCAAATCCTACAAATCCA
1127	CTTATCCCATGTGCCGGTCTGACT
1128	GCGGCCATAATGCATAGCACGGAA
1129	TACGGTGCATCGCAGTATGGGTAA
1130	CACCAGATGTCGAGGATCATCGCC
1131	GCTCCTACGCCCCAAGAGGTATGG
1132	AGAATATGGGCAGCAGCAGCACTC
1133	CTGCAGTCGCACGCAGTAGACCCG
1134	ATGTCCCTGACCGGAATCTTTCCA
1135	TTGCGCCACGAGGCATTAGTCCGAC
1136	ACGTCGTTCCCGAGAATACGGTCT
1137	ATCCGCTGGCGCTTTGACGAAGAA
1138	TGAACCAAATTCTTACCGCGTGGA
1139	CACGCGTAGGCTGGTGTGTCATTC
1140	TCGATCCCGCGATCTGGCCTATTG
1141	GGAACACTCAACCACCGTGGATCT
1142	TCACACACCAACTGGCCACAGATG
1143	TGTGCTTAGGACACCAGGCAACCC
1144	GACATTTAACCCGACCGATTGTGC
1145	GGCACCGAGCCAGTAGGCCTCTGA
1146	CTCAAGCGTGCATGTTGGTAACCA

5

10

15

20

25

30

35

40

1189	GGTCGAAATGAGCCAGCAGCAGAT
1190	CCATTGGAATACTGCGTGCGGCTT
1191	GGAAGACTTCGCGAGGGCACAATG
1192	AGGGTGACTTCGAAGGTCCGAAC
1193	TCGTCCCTCTGGTGGTCAATCAC
1194	TGTGCAAATTATGCTGGGCGTGAG
1195	GTCGCCAACTGTCATGTGTGCCA
1196	CCTCGAACCTCAAGACGAAACGA
1197	CTTCATCACGTGACCTTTGTTGCC
1198	CCTTCATTCCCAGCAGGATGGCTT
1199	CGGGGACCTCAATGGAGCGTCTTA
1200	CGCCTCTAGCGCTTGTTACGTGA
1201	CTGCCAGACTCAAAACAGGGACGG
1202	CTCCTTACACCGTGTGAGGGAACC
1203	TTTCATGCCATATCGCCTCGCGCA
1204	TCTGGCTTTTCCTCGATCAATCGT
1205	GTCTGACTGTCTGCCCTGTATGCG
1206	GGTTAATGGAACGGCGTTAACGCG
1207	CTTCGCACTGCGGAATCTCAAGCT
1208	TGCCAGAGGCGTAGGAGTCCTGGA
1209	GACGGGCGAGCCAGTATTAAC
1210	GACCTCCAAAGTCAGTCTTGGCGG
1211	CGTTAGAGCATGACCGAACACGTC
1212	GTGGGCTCAAAAATTGGGTACGCC
1213	GGGGCAGAGATCACGCGTTCCTCT
1214	TTTCGCCCTACGAAGCGAAGTTTC
1215	TACGGGGTGATGTTAAGCTACGCG
1216	CCTGTGAGTCTGAGATCGCCGTGT
1217	ACTGAAGCTGGAACAGGCCATTCTG
1218	AGCACTGGTTCACATGGGAGTCCA
1219	TAAGGAAGATCACACTCCCTGCGC
1220	CACCACACGCTAAAATTGAAGCCG
1221	GCTGTGCCAGGATCATGTATCGT
1222	TTCGTTCTGCACTGGATTCTTGA
1223	TCAGCTCTCCTTGTGCTTGCAGTG
1224	ACGACGAGGTGAACTTCGTGGGAA
1225	AGCATTGCCGCGGGCCTTGTTTA
1226	CAGAGGGCAGATGTGACTCCTCAA
1227	CGATATTTAGCCTCTCAAACGCG
1228	TGCCAGAAATGTTGCCGATTGAA
1229	TAGGCCACCCGGTGTTCACAATTC
1230	GAGAGTCAGACCGAGGGACACGAG

1147	AGGAAGGCCACCAICCAATATTCG
1148	TTGGAGCCCTGACTGAACCAAATC
1149	TACGAACGCCAAGGTTATGCCAAT
1150	CGCACCAGAGTTATGCAGGCTCAA
1151	CCAGCTTGGACGAGGAAGGATGTG
1152	GTCACGCCTTTCAAATGACCCACA
1153	TGCTAGACCCAGCCCGAGTCTCGG
1154	TATTGTGGCACTTGGGTCCAGTGC
1155	CACGTGTGAGACCGGAAGTGCATC
1156	AACCTCCAGCAAAACGTCGAGGTT
1157	GGCAGCCTGATGCTACAGACCGT
1158	CGGTCCGTCCATCCTTCAGAGTTA
1159	CTATTCGCGGACCCTACGCAGTTT
1160	ACCTGTGCAGTCAGCACGAGTGCG
1161	GAGAACCACAGGTGGTCCACCCTA
1162	CCTCGCTAGAGAAATCCACGGGAT
1163	TAACATCGGTGCAAACCGTGGCGC
1164	ACCCAGAAGACATGGCATTGCCT
1165	AAAAGCGCTGCTCTAACACCGCCG
1166	CAAGTCTGTCCATTTCCCAACGGT
1167	CCGACACATGGTGGGCTTTTTAAG
1168	ACAGACCAGCTTTTTGCGCAGATT
1169	CGGCGATCCATTTCACTTCAAAGT
1170	GACGTTATCATGACACAGGTCGCG
1171	GGCAGAGTTGGATCGGATCCTCAA
1172	TTGCTGGCAAACAGCTCCTGAAGA
1173	CCTCAATGCCACCGAATTCGGTAT
1174	GGAGTTAGCGTGATTAGTCGCCCA
1175	GAACTCGACGTGTCACGGAAGGGT
1176	CACAAGCGACATTTCTGGTGCACG
1177	CCAGAATGCGTGAATTCGCGTCCT
1178	CAAGGGAGCCCTGCGAATTAGAGT
1179	ATTCTTGCTTCGGACGACTAGCCG
1180	TGCCACTTTGATTTCCAGATTGCC
1181	GATGGTCGGCAGATAAGTGGTGGG
1182	G TTCACACGGGTTGACCAACATGT
1183	GATTCAATTGCCCCATTCTGTCAT
1184	TACCGGAAACTGAGCCTCGTGCTA
1185	GGATCTTTACTCAGGGGCAGAGCC
1186	CGCGAGTGCTTTGTTCTGTGTGGA
1187	GTCGTCCGATGGCGTACATCCTT
1188	ACGGGAATCTCCCGAAGTGCGAGC

5

10

15

20

25

30

35

40

1231	GAGGCGATCCTGGAACCACGCAAC
1232	CCAGAGAGGCGGGCTACTGACTCA
1233	CACACAGTCCCATCGTACGGCAGT
1234	TTACGTTGCGGAAGCGTGCCTCTA
1235	ATGTACACGCTGCAATCGTGTCCC
1236	ACTCGTCGTCGGAAGCGCCCAGGT
1237	ATGCGAGAGCAGAATTGAGCCGGT
1238	AAGTTGGTTCGTATTCACGCGTGC
1239	TGGGCTTATCGCCGAAGATTGCTA
1240	CAACGGCGAAGACCCAGAATTTTA
1241	AGCGTACGGCGAAAGTCTAGGGAC
1242	ATGCATCCAGCGTCCCCTTGATTA
1243	ACCGTCATCAGTCGCAGGCTTCTG
1244	TCTTGACGGCTGGGCATGATTGGA
1245	TTAACATTCCGACCCAGGACCTGG
1246	TGGTGTCGAACTCCCTTGCGTGTT
1247	TACTCCAGTCGCCTGCGCGCAAAC
1248	CGCAATGCCGTAAGCATGCCAAGC
1249	AGTCCGCGCGAAATACGAACAGTA
1250	ATGTTGCACGCGCACTGTATCACA
1251	GGGATCAGCATCATTGGAAGGAG
1252	ATCGCCTAACTACCCGCGGCGTGC
1253	TGGCCAGGGAACACAAGCTCGGTA
1254	AAACATGGGTGCGCTCTGAGATCA
1255	GCGAGAGCTGCGATTCCCTTTTAG
1256	CCGGCCAAACAAGAGACGAGCGGA
1257	AATGGGGCACAGTCTCGCTTGACA
1258	TGTCTCGGGCCTTCAGGACACACT
1259	TCCACCTTCATTAAGTGGTTTCGGC
1260	GCTTCGGAATCATCCACCTGTCAT
1261	GAGCCGATGGGCTATCGTCGTCCG
1262	CACGAATTACGCACGCACAGAGGA
1263	GCTGTGACGCTCCCCTCACTAGG
1264	CGCTCTGAAAACGCGGGCTACGTT
1265	GAGTGCTGGACACCGTAGCCAGGA
1266	CCAACCCCAAGTGTAGGCGCAAATG
1267	GAAGTAGGGGATGTTGGCCGGCGG
1268	CAACGTGGGCACCTGTTTTAGCAG
1269	CTAGCTGCGATCCGAACCTCTACG
1270	CATTGAACCATCAGCCAAGCTGCG
1271	AGACTGGCAATTTTTCGAGGCCAA
1272	CTGGCCGTCCATGAGTTGGTCCAG

1273	CATGCTGAAACACGGGATTGCCAT
1274	CGATATGTAAGACAGCCGTCGCAA
1275	AGCGTAACCTACTGGGAAGGCACC
1276	GTGCTCGTGGCACGTACAGGCCTT
1277	GTTCGAACCCCGCGATGTTAAATG
1278	GTTGTTAGGAGGCTCGAGGCTGCT
1279	ACTGGTGCTACGCGGGATATTTGA
1280	CTGGGAGCTATCCTCAGCCGAATC
1281	GAACTCGCCGCTGCCGAAGGGTAG
1282	TTCGATCGAGGAGCAAGGAGAGTC
1283	GGGGAAAATTGAGGCCTTAGCCAT
1284	CTAAGGTCAAAGCGCTGTCGCCAG
1285	GTGAGGCTTACCCCGTGCTCTTGG
1286	CCGTAGCGGTGCTCGACCAGGTTT
1287	TGGGGACGAATCCGAATGTAGTGA
1288	GTCATGTAATTGCATCCACGGGT
1289	CTTTGCGCGGTGGTCAATAAAAAAG
1290	CACTCGAGATTCAATGGGCATGGT
1291	CTCGGGGATGCCCTCTTGGCATT
1292	CGAAACGTGGTGCAGAAACCTGAA
1293	GGAGTTCACGAGTCGAGCAGTCGC
1294	AGCCGTTTTCAAAGATCTCGACGA
1295	TGGCTGGACATTGTCTGCAATGCA
1296	ATCGGCTGCCTCAGTCCCTAATTT
1297	CCAGCATGGAGTTAAGTGAGCGCG
1298	TTCATATTTACGAATGCCGGGTGC
1299	CGAAATCGCACAGGAATTCGCGTC
1300	GGCAATTCGGGACACTCGTTTCA
1301	TTTGTGATTGGGGGTATAACCCGA
1302	CCCAGCTAATCCAGCTTGGGCTGT
1303	AAAATCGTTTGGCTGTAACTCGC
1304	AGGAGATTCATCGACTTCCGGGAA
1305	GCACGGGGTCTCAATGCTTAGGGT
1306	GCGCAACAAGTAGCCTACCGAGGC
1307	TAGCAGGCTGATGCCGTCTACACA
1308	GCAAGCGGCGATCGTACAATTGT
1309	GCACCTCTGGTAAGCCTGAAAGGG
1310	CGAGGGCGGTGAGTGCATACCGTG
1311	GGATTAACCGGAACTGCCCTTCTG
1312	GATATTGGGTCCGGCGCGCATTAC
1313	GGCCTTTAATCTCCGGTCGCAATG
1314	AACCTTAGTGCGGCTAGGTGGGGT

5

10

15

20

25

30

35

40

1315	CACGCTGACGCCAGTGTGGTGAGG
1316	GGTTCCCTTGACCCACCGAATTGA
1317	TTCTGACAACATCGACCCTGGCTC
1318	GCGAGCGAAGATAATCCCCAACT
1319	GTACTCTGTGCAACGGTCCCGAGT
1320	ACACGCCAGGAACAGTGTCTGTGA
1321	AAGGGAATTTAGCGCGCGTGA
1322	TGACGTACGCGTTTTAAGTGGGGA
1323	CTTAGAGGGACGAGGCCATGAATG
1324	GGACGACTCCGCAAAAAGGTCGT
1325	TCAATCCCAACATCCAAAGCCTCA
1326	GCACTGGTCTACCAAGCTTGTC
1327	ACTTGTCGAAACGAGACCGAGCA
1328	TCAGGAAAGGCCTAAAGGCGAAAG
1329	GGAATGTAGTCAAGGAGGACGGGG
1330	GCACGTGGTAAATGAATTGGCGAG
1331	GATCATCAGGGGTTATGCGTCGCG
1332	CTCACTCATTCTGATTGCCGCGG
1333	GGGGTGATCTCTCGAACGTCACCC
1334	AAGGTTGCTGCTAGCGTACCTCGA
1335	TATAGATCGCCCAACAGGCAGGAG
1336	GTTTGGACCTGTTGGGAGTGGGCA
1337	ATTGGGGAAAACCCGGTCTCAAGG
1338	TCGACGATAAAGTGCTCACGGGAC
1339	CGATAGAATTCAATGCAGGGCGGA
1340	CGGTTGCTACGGCGGCTGGTTTC
1341	CCAGGTTTCGGTTAGTCGCGCTAG
1342	ACGACCTTACACTCGGATCCGACG
1343	TCGCGTTAAATGGACCAAGGGGCC
1344	CCAGAAAGAAAATGGCGCCCGGAT
1345	GATACATCGCCGCCTGCTAGGCAC
1346	GAGATCACACTCGGAAACCGGATG
1347	ACTTCGCGGAAAAAGGCTGGCATT
1348	CCGAGCTGCACGAGCACACAAAGT
1349	TTCCACAAGGCGGCATAGTGAGGC
1350	AGCAAACCTGGAATCCGGAAAAACC
1351	CGCTATGTCGCAGCATGCATTTAC
1352	AGTCACGCCCAACGTGGTTCTTT
1353	AGTGGGCGCACTTGGCCTTAAATA
1354	ACTTGCAACTTCGGCCGTTTGA
1355	CAAACATCAGGTTTATGCCGTACG
1356	AGCGTGACCACCCTACAATGGCAA



5

10

15

20

25

30

35

40

1357	GCAGGCATCCGGCAGAGATGTCTC
1358	GAGCGGCTAAGAGGCCAGACCAAA
1359	CACAGAACAGGGTGTTTCCCGCTA
1360	ACTTTGCAGAAGGCCCAACACAAG
1361	CCTTCCTGGTACTTTGTGGGCGAC
1362	CTACATGCTCACCCCACCAGAGTG
1363	ATTTTCAGAATAGCCCCGCCTCGA
1364	CAATTGCTACGTTGACGCCCTCTG
1365	CTGTGCGCTAATCCTCGGTGGCCG
1366	TTTGTGTTGGCTCCGTACATTGGA
1367	ACGTGACGGGAAGGTGGTTGAATC
1368	AGTTCTTGCGTTGCACGAAACAGA
1369	GCTCGCCGCGCGTCTTTATGTCTG
1370	ATGAACATCGCGAGGCAAGCCTTT
1371	CAACCGCGCCACCAACATTAAGG
1372	TGATCGAGGACGGCTTGGTAGCCT
1373	GGAGGCATGCCTTCCGAGAGCAAC
1374	CACCGATCCTCAACGCAATTGCTA
1375	GGCCATGAATTGGGAAATCCATGT
1376	CTGTTCCAGGCGTAACCAGCGGGC
1377	TATGTCTGGCTCGCCATCAGAAGA
1378	GGAGTGACCAGCACAAGCATCGAG
1379	TCGGACTGGAAGTAACTCGCATGA
1380	GTAGGGTCAAGCACGATTGAAGCC
1381	CACCGGCGGTTCTGACTAACGTGAC
1382	GAATGACGCGCAGTGCAATTTGAAC
1383	GTGCTCGTCTAACC GCGGATAGAG
1384	GCGGACCTGGGTTAATTGACGCGC
1385	TTTTTGATGTTGCGCACCGGGCTA
1386	TTGCGTCAGCGCATCTGCTCGATT
1387	ATGAGCACGCCAGTTCGTTCCCTT
1388	TCAACGGTAAAGAATCGCCCCGCA
1389	CGCGATTGACTGAACCACACCTCT
1390	GCGTGAAAGATGACGGCCGGTATA
1391	CATGATTCCACCTCGATCGGCTAG
1392	CTACGACAAAGCAACCGTGCAAAA
1393	ATGCCGTGTTTCATCTTGATGGTCC
1394	TTCGTGGAGGGACTTTGGAGATCC
1395	GAAGCGCCGTAACGTACACCGTCG
1396	AGCGTGCGCTTGGCTATAAGGCTA
1397	ACAGTCAGGAGTAACGCCGCTCAA
1398	TTTAGCCGCTGCGACTGTAGGAAA

5

10

15

20

25

30

35

40

1399	ACTGTGTCGCAATCAACCCGCAAA
1400	TGCAGCCAATGCGGAACCTTAGAGG
1401	CCCGCTATCCCGGTCTTGCAAGTC
1402	GAGGGCGCAACATATGCAGTGCTG
1403	CGTACGGACATCGATGACGCAACG
1404	AGTCTCCCGAGAAACGCATAAGGC
1405	AGGAAGTGGATGAACGCGGCTGCA
1406	GGGTTGCTCACCCTCGTCATCAGG
1407	TAGGAATGCGAGTTCGCGCGGTAA
1408	CTCCTCACTTCCAAGCTGCGGATA
1409	TCAATAGCACCTAGCATGCTCCCG
1410	TGATTCTGCGCTTTCACAGGTCTG
1411	GTATGTGCGGGATGGAAATCACGC
1412	TACGGCAACTGTCGATACGAGGGC
1413	GGTTCCTATCCAGCACTCCTCGC
1414	ATAAGCGCGCCACAGGTATGTACC
1415	GAAAGTCGCCAACAGACTCGAGCA
1416	CGCTAATGCCTCATAGGCGTGTGC
1417	ATCCCGCCGCGACGAAGTACCAAG
1418	GACGCTGCTGATGGCTTTATCGAT
1419	CTCTCCCGTCGCTTCAGAGATTA
1420	TCATGTGGGCGCTCGTATCAGTTT
1421	GGCCTGAAGGTGAATGGTTACGTG
1422	AGCCTCCAAAGCCGGTAGAGTTCC
1423	TTGTCTGAGGCGCTCACCTTAGGA
1424	GCCTGAGTCCGGGTCGGGAAAGAA
1425	GGCACTATACCGGTTCTGGACGCG
1426	CCGTGTATACGGAAGGTACGCCA
1427	CCCAAGGCAAGTGTGCATCAGTCC
1428	GGAGTGCATCATGGCCAAATCTGG
1429	CCATGTTACGTCTGCGCACCACAG
1430	GGCGTTGAGCTTAAAAGCAGCGAC
1431	TTGGCACTCTGCAAGATACGTGGG
1432	GATCTGCACTGCAAGGTCTTGGGG
1433	CGATCAACTTGCGGCCATTCTGCG
1434	CGGCTGGGGTCACAGAAACGAGTA
1435	GCGGCTAGTTGTACCTAGCGGCTG
1436	TCGTCACTGTTAGAGAGGCCTCCG
1437	AGTGTCGTGAGCCCTAGCGGCGCT
1438	AGGACGCAGGGATTCAAGTGCAAC
1439	ACCGATGCGCGGTGCGTCTCATAC
1440	GGCAGAGGGTTAGGGGGTTTTTTT

5

0

5

20

25

30

35

40

1441	GGCAAAGGGTGTATTATGGGAGACC
1442	ACAAGGCTTCGGCTGGCAGAATAC
1443	CATATCCGTTCTATCGCCAGACG
1444	AAGCCTTTGTGGCCAAGGCCGCGT
1445	CCGAACCATGGCTTTATCCAGTGT
1446	GTTCAGCAGTAGCTCCCTCCTCGA
1447	GCGCAGTGACACCATGATGCTTTC
1448	ACGATCCATTTTGCCAGCATGCAA
1449	TCCCTTCATTTGCGGTTTTTAGCC
1450	TCTTCTTGCCACATTCCCTTTTG
1451	TGCCTTTTGATTGGTGGTCACGGT
1452	GACCCTCACGGTCATCAGAGGGAG
1453	CCGTTCAACACAGTGATACACGCG
1454	CACCAGGGGATAGGTGCGGTACGC
1455	GGTCGGAACTGATCTGTGCGATCC
1456	TGCTCCTTCCTAGGGTCATCCGTG
1457	GTGGACTTTGACGCCGGCTACCGC
1458	CTGATCTGTGCGCGGTTACTTGCC
1459	AGAGGAGCGGAAAAAACCGGACGA
1460	GCGACGAAGAGATCCAGCAAGCTC
1461	GGGACTTCCAGCTGAGGGACGAAA
1462	GGCGCACTCCAATACCACTGTTT
1463	GCGCTTGGAGACTGTCAGGACGTG
1464	CAAACCGCTGGTTTCTCCACCTGT
1465	GCGATTGCTTGGGATCGGTGACTA
1466	CTCAGCGACATTTTTCTGGTGGCG
1467	CAGCGGCGTCGTTTACTCAGGACT
1468	GACAGCCGTGAACGCTCAGCCGTT
1469	GGGCCGTAGAGGCATCGGGTAAAG
1470	CGCCGCTCACCTGCTTAAAGCATT
1471	TGCCAAATCGCAACTCTTGAGACA
1472	CCCCGATCGGGTGTAATTCTCCCT
1473	CAAGGTCCAGGTGACGCAACCACT
1474	CGAGCCTTCAGTGGTATGCATGCG
1475	CAGCAGCGTGCCCATCTCGACTTA
1476	CGGACCAAGATGGCAGTAATCCAG
1477	CTACCACGCTCTGCGCGGGCTGTA
1478	ACGTGGTTAGGCATGAGCTGCGTC
1479	CGACATATCCGACATGACCGGATG
1480	GCGCCCAGGCTGTGTTAGAAAATA
1481	AGCTGGGACTCCGGACCTTGAGTG
1482	CGGTCGTAACCGCTGCTACAACCT

5

0

15

20

25

30

35

40

1483	TCGTTCTCTGGAACAATTCAGCA
1484	CGGCATCTCCGGACAAAGGTTAAC
1485	TATCTTGTGCGAGCGCCACTCGGAG
1486	TGCAAGGGAGAAAGCCCCATGAGC
1487	ACTGCATAGCCCAGATCCGCTTGC
1488	TGTGATTCAGTCGAAGCAAGGCCG
1489	CATCCATCTACAATTCGGGCCAGT
1490	ATGAGCCGTTTCAGAAAGCCAAAGA
1491	ACACTGGAATTGCTAGACCCCGCG
1492	CTGAGCTGCGTGGGACAACTCCGC
1493	CAGCTACTAGGGCGCGATGTACCC
1494	ATAATGATGGGACGAGAAGGCCCC
1495	CGACCGAGTGTTACGACATGGTGC
1496	TGCAGTACCCGCCGCTCCACTAGT
1497	ATGCTAGCGCGCCTGTCAACGTAC
1498	AGACTCACTGCCGGCTGATCAAAT
1499	GCCTGGTGCGAAGATAGGGATTCC
1500	GGAAAGTTGGCGGATCCGAGCACT
1501	GGCAGTGAGCAATGTGTGACGAGG
1502	TGAGGTCCTCCCGGCGGACTACGA
1503	CTCGCCTTAGATCGTGGTTCCGCA
1504	GTCGAGGAATATCATCGCAGCCAG
1505	GCGAATGCAACGAGACAAGAAGGA
1506	TTCGCCACCAAGTCGGCATTGT
1507	CGGTGGCTGACACTTGCCGGATTG
1508	CAAGGAGCAATCAGATGGTCGGAG
1509	GTGACCCGGTCCGTTCTAGCTGTG
1510	CTCTCGCCACATAACTGCACAAA
1511	AAACCTGCCTAAGCAAGCACTGGA
1512	TTCCATATTGTACCCCGCGCATGC
1513	TGCTTGCGATATCACGATACTGCG
1514	TTAGTGTTGAGCCTTGAGCCGGC
1515	CTTGTTGCGCGAGTCCGTCTGGGA
1516	GTCAGCTGCCTGCTGGTGCTCTTC
1517	CATCCCTCGAGGTGTAGGCAACAC
1518	CAGATGCACTCCGACGGGATTCAG
1519	CTGAGCCTCGCGAAGCTGTGGCAT
1520	GCTATGCCACGCCGAGATAGAGC
1521	AACACCAACCATAACCGTCCGTTCA
1522	GCCCAGAGCTAAAGCATGTCTGGG
1523	AATGCTGCAATGCTAGCGTCGCTA
1524	TCCGGACGCAGTATCCAATCCGGA

5

0

15

20

25

30

35

40

1525	TAAGACCATGTGGCACCAAGGTGC
1526	ACAGCCACACACACGCGCCCACTA
1527	TAGAACCGAGCACGGCGCCTTGTA
1528	TTCGAGTAAGCTGGCAGGACCACT
1529	CTTTCGCAGGTTTCGCAGACAATCC
1530	TACGTCCTGTGCTGTTGACACCGG
1531	GTTTCGGGTCAATGTTTCGGGGAGA
1532	CCCTGTTGTGAAGGGGTTTTGTGA
1533	GGCAGATTGGTGAACCCCAAGATAA
1534	CCCTCGGTGTGTTCAAGCCAAATC
1535	CCCGCGAACATTTGAACAGCTTAA
1536	CCGTGTCAGTTGCTCCCTGGCACG
1537	TCCGTCTCAGCCGCTCCCTATCC
1538	ATAGCTGGGTCACCACAGGCGGTC
1539	ATAGGCAAGCGGTGTAGCACAGCG
1540	TTAGAAGCCGGTCTGGATTTGCGT
1541	TGCCGACCTTTACCAGGATCCTCG
1542	GCCCACACTATAACCAAGCTGGCA
1543	TTGCGCCACTAGTACGGATCTCAA
1544	CTTGCAGTTTATGCTGACCCGTCC
1545	TGCCTCCAAATTACTTACCGCCGT
1546	CCCGTATGCGGAAGCTATGGGCTA
1547	TCGTTCAACCCACACTTCAGTTG
1548	CAATGTGGGGGACATTTCAAGGTT
1549	TAGCGTCGCACAAATGGCTGACCG
1550	GGTGGCTTCGTGACAATATCGGCC
1551	CAGCGGCGTCCGAAATTGGCTCTC
1552	GGCTTGCTCTCGTTTTTGATTGCA
1553	ATGCGAGGAGGACACGACCGTTCC
1554	CCTGTTCACTACGACCCACGGGAA
1555	GTGCCACGGAGTGCGACTGTTGCT
1556	ACACATCCAAGTCTGACGATGGCC
1557	CAGCCCGAAAGGAAAGCCTCCGTG
1558	AACTGAATGTAGGTGGGCCCCTGT
1559	ATTTTCGACGATAAGCTGGCCGGT
1560	TGAGGGAGAACCCGAAATCTGCTT
1561	GGCGACTACATCCCCAATTGCTTG
1562	GCAGACGCGGCCTTCCATACTTTT
1563	ACAACCACATGACGTGTAGCTGCA
1564	CTGCTGGGCGCGCAAAGCTTGTTG
1565	AAGCCTTCTTTGGCTTGCTCCGCT
1566	TACCTGCTGCCTGGAGCAAGGCAT

5

10

15

20

25

30

35

40

1567	GACGCCGCAGCCATGAGTGAGTGT
1568	AGTTGGCCGCTTATTTTGCTCACC
1569	AGGCGCACGGAGAACATTTGCCAA
1570	CCAGGCGCCTTCGACAGATCCTCA
1571	GTGTCCCCTCCAGCTAGCCAGTTT
1572	GACAACAAGCCAAGGTGACACGTC
1573	CTACACCGCTCGTGACTCGGCAAA
1574	TGGTGCCATCAAAGCACGTTGTAC
1575	ACAATGCGTGTTGCGAAACGCATA
1576	TTGTCCAGCCATTGTATTTTGCGC
1577	ACGAGAGATAGCGGACTCCTCCGA
1578	AGCTTTGTCGTCAGGCGAGCTCTT
1579	GACAGTCGGCGTGACGTTTGTTGT
1580	AGCTAGCGACGGCCAACACGTA
1581	CTCCTGTTGCGGGCCGTTACTGGT
1582	ACTGACCGACGCAGTGCCACATAG
1583	AGGTAGGGTCTGGTTTGA CTGCA
1584	CCTCCATTTAGCGCGTTGCCAAT
1585	TTCTTAGGATCCGCGCACTCTTGG
1586	GTCGAAGGTGTCTACCGTGCGCAG
1587	GTCACTCGGCGGCCCAATCACTCG
1588	TCTCGGTCACCCGTCTTGACCCTT
1589	GCCCTCGACGAACATCCTGAAC
1590	TCCGGCGTACTCTGACACGGCGAT
1591	AGCCAAATGCTTTCGTGGTTCCGA
1592	ACTCCACGCCGCATGTTGCTGTGA
1593	GCTTCGAGTCGGTGGCATCTGTAT
1594	GGTCTTGGGCCATCGACTTGCTGC
1595	GGTATCGGACTGCACTAAGGGCAA
1596	AGCCCATGCGTTCCGGATGATTTG
1597	GCCAGGGTTAAAAGTGATGGGCTC
1598	GACGACGTGCTGGCTACGAAGGGG
1599	TCCTATTGACCGTGATCGTGATC
1600	ACCCGCCTCGACTCCACAACATAA
1601	GATGTGGATCACGACCTGCCAGTA
1602	GTGCCATTGCCACCCATAATGCGT
1603	TTAGCCTGTGCACCCAGTCAGGAG
1604	TCCGATGGGAGAGGCTGATCTCAC
1605	CACTACTGAAGTGGCCTGGCGCTG
1606	TGCGGCCATAGCGATGTGATAGAT
1607	GATTGCGCTTAACGGAGATGCACG
1608	TCACGTTTGACAACGCCAAGCATT

5

10

15

20

25

30

35

40

1609	GCATTGTTTGCTAAAGGCGGCATT
1610	AGTCGCTCTACGCGTGCAACGCTG
1611	TAGCTCCATGGAGGTCCGAAAGGG
1612	GACCGGTTGGACCTCACTGGCTTC
1613	AAGCCGGACAGTCAATGTGCGTAT
1614	TGCCTCGCTGAGTTCTTCACCGTG
1615	TCGTAGACCTTGCTTTTGGGCTCA
1616	ACCGCTATGCGCCCTACAAAGCAT
1617	TAGCGTCACCGTAGCTTGGGGCAG
1618	CTCTCAGCAACTGATGGCACCGBA
1619	AAAGGAAATGTGGTGCTGGTCGGC
1620	CCGGCTTAGATGGAGAACAAAGTGC
1621	AAGTAAATCGCCTCGCCCAAACCG
1622	TGGGCTGTTACGCCTACCGGACGT
1623	GTTTCGGTTCAGCCATGGGCCTAC
1624	GGCCAACATTTCTAGGGGAGTGCC
1625	TTCTTCGTTGGGATTGTCCTCACC
1626	TGCACATTGGGGTACGGATCTGAC
1627	GGCAGTTAGACGGCAAACCTGCAGG
1628	CGCGTCAGGCTATGAATGGCTCTT
1629	GCTGAATGCAAACCTCGGAGCCAT
1630	CGCTCTGGCGGATTCATTGTTTTTC
1631	TTTTCAATCAACCCTCCGGACGTA
1632	GTGGTGGAGTCTGAAGCACGACAG
1633	AAACAGGTCCGGATGATGTCTGGA
1634	GTACCGCGTGTACGCCACCGTTAG
1635	TCCAACCTACATTTGCGGAAGGAA
1636	GACGTACCGTCGTCCCGTGAGTTG
1637	GGCAATCCTACAACCGACGCTGAT
1638	GGCGGCTGCAGGGTCTACATCGAG
1639	ATACTACGCTGCAGCTGCGCGGGC
1640	GGATCGCAATCCCTCCGATGACGA
1641	TGGCCTTGACGCGGAGCCGAATCT
1642	AGGTGCCGACGAAACGACGAATAT
1643	GCTGTTTCACCGTCGTCGTTGTTG
1644	CGGTCCCAATGTTACAACCCAGAC
1645	GCAATTCCAGCCACTTTTGACCAA
1646	ACGGGCGAAAGCTCGGTACGGATA
1647	CGACCCGACTTTTGCTTTTCGAGTG
1648	AATTCAGTGTTTGCGTCATGGTCG
1649	CCTGTATGAGGTTCTGGGTCCGGCT
1650	TGGCATACTTGGTGCAAACGCCGT

5

10

15

20

25

30

35

40

1651	TCGCCAGTACAGAAACATGCGGGC
1652	CCCGCTGTTGCTCTCATCGTGGAG
1653	GCCACAATCTGACCCTGGGAATCA
1654	GCTCAGTCTCGGAAGTTTCGGCTA
1655	CTTCACGGGCCAACGACGGTCGAG
1656	CGACAGTTCCGTCCGTCTTGAGGA
1657	ACGGAGACGCAGTCGAAACGTCCC
1658	CATGCATCCGATTAAGGGGATCAC
1659	ATTGCGGGAGTCCCTAGCTTTCTG
1660	GTGTGGAAGATGCAATTGGAACGG
1661	ATACAACGGTAGGTGACAGGGGCG
1662	GCCGTGGGAGTAAGGGTACAAAGG
1663	GCACGTAGGTTCGGCTACTACTCGG
1664	ACTGTGATCTCTTGGGCAAAGGGC
1665	CATGCCTGAACAATCTCGCATCCC
1666	GAGCCTGGCTCCACAGCTGTGCTC
1667	CTTTCGATACCATCGTTGGCGATC
1668	CCCGGAGGTGAGGCATTGAATATG
1669	CTCATTCAGCTAAAAGCGGCTGGA
1670	GAAATGCCCTGGGGACTTTTTGCC
1671	TTTGCCTTCACAACAGACGCAGCA
1672	AAATCCCAAGACGTCGGGGCGTAT
1673	CAACGGGCGGTAGCTAAACCGTAA
1674	GGCCAACGACAATGCGAAACCTTC
1675	GACATCACGCAAAATCTCAGCGCA
1676	ACGTTCCGTCCACAACCGTATGTT
1677	GCTCATAGGTCTTCCGTAGCCCGT
1678	GAAACGAGTCTCTCGCGCCCTAGA
1679	CGGGACAGAAGCAAGTTACATCGG
1680	TGACCGCTCGATACCAGGAGGGTG
1681	CTGGCAATAAAGACCTTCCGACCA
1682	TGCGCGACGTCATGTTGGTGATTA
1683	GTTGGTTGTGGGAACACACCCGCT
1684	TGTGGGTTGGAACACAGGAAGT
1685	GGAAAAACGGCAATTAGCCGAGT
1686	TGGTGCGGAGTGCCCTCTATTGGG
1687	AACCAACAGGCTGCAGCCCAGACT
1688	AAACAGATCCATCTGCACGCCAGG
1689	GGAATACCGCGGCGATTATGGCTT
1690	TACTGTTGCGGGCAAACCGTCACT
1691	GATCTCTCGTGGAGCACGTTTTCC
1692	GGCATAGCAAACCTTGACCTCCAA



5

10

15

20

25

30

35

40

1693	ATCTGGGATTCGCGAGCCAATATC
1694	CGATCAGGATATCATTTACGCCCG
1695	ACGGTACCGAAACGGTCTCAGCGT
1696	CTCCCATACCTGCGTTCTTACCGA
1697	GCACGAGAACCTAATTGTCGCACA
1698	GCCACACGATCAAGACAGCGCATG
1699	CCCGTTAACTCACGAGCGGTCAAT
1700	AGAGAAGGTCATTGCCTGTCGGTG
1701	CGGGCCCTCTTAAAGTAGAGCAGG
1702	ACATCGCGTCCGAGGGAGTTAGCG
1703	AATGCCTAATCGAGCCAGCGGATC
1704	CTCGATCTTTTAAACCGGCGCTT
1705	CGTTCCTGGAAGGCAGGGTCTCAC
1706	CCTGTGCTTACTATCGGCGATCCA
1707	GTTAGTCGCCCTATTGGCCTGGTT
1708	CCGGTGAGATGACTGTAAATGCCA
1709	CGTGGTTTTAAACATCGCGCTTCG
1710	TAAGACGCAGAAGATGGGGTCCAC
1711	CACCACAGCTTCTTTGTTGACCC
1712	TCGGGTCCGTACCACCACTTTTGC
1713	CCAAGCCCCGAGTACCGAAGATTT
1714	TCCGTGATATGGTCGTGGCGCGGT
1715	TGTCTGTGTCATGGCACCTCGCAT
1716	AGGACTGCACTGTGCACGTCTGAT
1717	CCATCCTCATGTACAGCGCCGCTG
1718	GTACCCGCGCCTTCCTCGACACAG
1719	ACGGGTCTGGTCGACTAAGGCTT
1720	CGTATCGAAGGCGTGTACAACCGG
1721	TGCCCCGCCCTTTATGCAACGCTCA
1722	AACTTACGAGACGGCGGCTGCCA
1723	AAGTCTGACAAACGGAACGGGTGT
1724	TAAGCGCAGACCAAAGTATGCGGC
1725	GCAGTTTTTCAGATCCTCCGCAA
1726	TCGGAAGCATTTACGCGATCTCAG
1727	CACAGAAACGGTTGAACGAACGCC
1728	GCATGCTCAGATGGTCGTGCTCAC
1729	AAGGATTCTCGCTTCCGGCATGAT
1730	GGTGGGGTAGCGCTGGTATGAAAA
1731	ATTATTACGGGACCGAACCAACGG
1732	GCGCGAGTGTCATGATGTTACGT
1733	GACATTCGTGACTTGGTCGTCCGC
1734	TCATTAGTGCAGGCACCGATCAAG

5

10

15

20

25

30

35

40

1735	GAGTTGTGCGGAGTCATCGGAGTC
1736	GCCTTTACAGATTTGGCGGGCTAT
1737	ATGGCGTTTGCGAAGTCGATACAG
1738	TGCATCGGCCTCAATCAGAGAACT
1739	ACAATCATGGCAATCTGGCAAATG
1740	GACGTGGAAGAGTGCAGATCAGCA
1741	AGGGCAGGGGACGGACAGTAAGTC
1742	GCATAGGGCGAATCTAGTACGGGC
1743	TCCGGCGCATCCTCATTAGCAACT
1744	TGGCCGCTTCCACTAATATTGGAC
1745	CCGGCGGACGGCTCTTGTCATGA
1746	CGAGCAACCCAAAAGGAAGCAGTA
1747	GCGTATGATTTCGGCAATCCGCCAG
1748	AGTACCGCTACAACGCTGGTTTCGC
1749	GGGCAGGCCAGGTCCACCTGAGAA
1750	CCACTTCTGTGACCGAACCGTGCT
1751	CCTGGTACCAGGCAGCAGTTGATT
1752	TTAGGGTACCGTCGAGAGACGCCA
1753	GTTGCTTGTGCGCGTGAGGTAGT
1754	TGCTTCGACCGATGAAACTCGAAG
1755	TGCCACCCATACTATGCCAGTGG
1756	TGTGCGGCAACGCGTGAAGACGTT
1757	TGAGAGAAGCTGGCCTCGGATCAG
1758	TATTGCGAATTTCGAGTACGTGCCC
1759	CGAGAGGGGTCCCCAGTGATCGA
1760	TGCCTGGGGTGTCGTTCTAATTCT
1761	GTGCGTCATTGTGGGTCATCCCAA
1762	AGGGCTCCCAGCATACCAACGTTG
1763	AACTAGCCGCACCTTTGTGCAGAG
1764	TTAGCCCAGCCCTTCAATGGGAAC
1765	CGGCCTCGGTTGTACGGGTAGTCT
1766	TCTTTGAGGCGCGGACCCGCATAT
1767	GATGGTTCGCCCTTGTGTGCGCAGC
1768	GAGATTCAATACAGGCCGCGGGTC
1769	AGGGCGAAGGAAGGTTCCGTTTTT
1770	CTCGACCCCTGCCACTACTGGTTC
1771	TGTTCCGCGGTCTACGCATTACTG
1772	GAGACGACGTCCTACACCCGCTAA
1773	AGATTGCGACAGCGACACGTGATT
1774	GATACCGTTGGGCATTTCTCGGTA
1775	GATTGGGAGGCATTTCAGCGACGGA
1776	AGGAGGAAACGAGGGCGTAGGTTT

5

10

15

20

25

30

35

40

1777	GCCAAACAACGTCTGACGCCTAGC
1778	TTAATGCGGAAAGGATGCACGCG
1779	TTATCGGCCGTTAAAATGGGATGG
1780	CCTTGGATTTCGTTTCATCGCTAGCA
1781	AAGTGAACGTGCAGTGGTCTTCGA
1782	TCCTTACCCCTCGTTCAAACGCCT
1783	ATTCCTGAACCATGCATGGCCTGT
1784	AGCGAGACGCTCGATCACGAATA
1785	GCTGGTCTGGCTCGCTGTTTAGAA
1786	CGTGCGCGGCATAAAGATAGGTCT
1787	TCTGGCACTCACATCGGACAGTCT
1788	ACCATTGGAGGACCACAGAGCTCC
1789	TCCAGGGTCGGAGTACATGGCGGG
1790	ATATGCCGTCGGATCGTACACGCA
1791	TGCTGGCGTCAACACTTCCCGATT
1792	CAGGGCGGTGCGGTGAACTAGCCA
1793	CATGGAAGTCCGTACATCAGCTGG
1794	CCGGCCATACGCTGGCAAGATTAC
1795	AGCGGACACCTGTACTCTCCTCCA
1796	GGAGCCACACCAGTCGAAGATGGT
1797	CGCCACCGGAAATTGAAAAGACTG
1798	TGAAACGGATGTTGCTTCTTGACG
1799	TTGAAGCGGTGAAGAGCCTGTCCT
1800	CGAACCAAGCTGCATTGTCAGTGG
1801	GAGTCTGCGCTTGCAATCTTTGCG
1802	GCTGGGTATAGTTGCCTGGCAATG
1803	GCAGGCGTTCCATATTCGCAACCC
1804	GCGCCAACTAATACCTCCACCGCG
1805	TGGCGTTCAGTGCAACGCTGGTTA
1806	CAAACTGACGGGTATGGGAGCGC
1807	AGGTGTCGCTGGAACCCGACTTGT
1808	CTTCCAAAAGCGCAATTGGCTTTG
1809	TCGGGCTTCTCGCAATTCTGTCAG
1810	GCCAAAAGAATGCGCTGGGTAGGT
1811	TGGTGCCCGCACCGAGAGACTGTA
1812	CGAGGCCGTAGTGGGGACTGCTCT
1813	CGATCTGCGCATAGAGGGGACTTT
1814	TGTGCAATCGGCCTTCTCAGAGCC
1815	GATCACCTGGACCGCTACCGTTTT
1816	ATGGGGAGTTAAGGACCCTGCACC
1817	CATTGTGGACAGCCAATGGTGGCT
1818	CCATCACCATGCCACGGTAAGATC

	1819	GCACCCGTGTCGTTGGTTAGCAAG
	1820	GGAGTGGGTTCCGCGAATTCAGT
	1821	GGGGATTTCCTTTCGCAGGCTCGA
5	1822	CATTGATCATGTGCACTTGCACCA
	1823	AGCAGCGCTGCGCTTGTTCGGAT
	1824	CGAGTAACGCGGTTGCTTTCGAA
	1825	TGGCCTGGAACATAGGTGGAATC
	1826	CGCACACCAAGCGTTTATTGAGAA
10	1827	TCACCTTCACAGTGGGCATACAGC
	1828	CAAATATCCCTGAGCCCTCGAGCT
	1829	GGGAGCTGGTGAGCAGATGTAACG
	1830	AGGATTGCTTTTGCCTTATGCGGA
	1831	ATCGTTTGGGCGCTACGCAATTGT
	1832	CCGATTGTCCCAAATGCAACGTT
15	1833	AAGGGTCAAGCTCATGGAGCGGAA
	1834	TCTGACGTCGTTCAAGGGCTCGCT
	1835	CGCACCACTCCGAGGTATTTGTCT
	1836	AAGGGGTGAAAAAGGAGAAGCCGA
	1837	AAACCACGCAAATGGCGATACCAT
20	1838	CAGAAAGGATGACGCCTTAAGTCG
	1839	CATGACGAGAGCGGACCTGAAGTG
	1840	CTGGACATGTTTGTTCGCCACTG
	1841	AAGACCGACTCTCGTCGTTTGCAC
	1842	GCGCGATTACATACCGTTTCCGTA
25	1843	CACTGACCGGACCCAACCTAACAT
	1844	AGTGCAAGTCTAGACACGCCCGAG
	1845	GGTTGGTGCGAGATCCTGGACTGT
	1846	GGTCGTCCCGAAACGTAAACGAGG
	1847	GA CTAGTACGATCACGGGGCGGGT
30	1848	CCGACCTGACCCTGTGTACAGGTT
	1849	TGCTCACTGCCACACTGTTATGG
	1850	CGAGGAAACACATTTCTTCGGGCC
	1851	TGGCACCGGGTGGATTCTTGTCTA
	1852	GAGGCACGGTGATAGTGTTGTGC
35	1853	ATGCAGATGGATCTTTTCGACGC
	1854	TGCGATAGCCAAAGAGTCGAGGAC
	1855	ATGGCGTGTGAGCGAACTGCCTGG
	1856	CAATGCAGCTCGGAAGTCAGGTCTG
	1857	AGGATCAGTGACATGTCCCCTCA
40	1858	CACATCTTGGCTGTCACCCGAGAA
	1859	CGCATTATCACCTCAATGCCAGTG
	1860	ACATCCGCAGACTCCCTATAGCCC

5

0

15

20

25

30

35

40

1861	GTGAACCCGAACGAGGGGAGTCTC
1862	GCGTAGGGAATTTGCCTCACGACT
1863	TTTACGCGTCGCTCGGTTGTAGTG
1864	GAGAGGCGTCTAGGCGGTTCTAGC
1865	GCATGCTGATAACGAATGCTTCCC
1866	CTGAAGCTCGTGTGCGATGAGGGA
1867	ACAACGGCATGAGGAGGCTTTTTTC
1868	TTTGGAGACGCCAGTACGCGTGGT
1869	GCTATCATTTGGTGTAAGCCCGCC
1870	TCAACATCCAGGGCGGTGCTTGGT
1871	TTGATGTAATCCCCAAAGATGCC
1872	GGACCTTCGGCAGGTTATCGCCGT
1873	AGTAAGAAGAGGCAGGCCCCACCT
1874	AACGGCTCCCCGTCGTAAGCTTA
1875	CCTATACCGTCGTGGTTCCACGTT
1876	CCGCGCAGGCGCTAATACTCAAGG
1877	AAATGGGCCAGTGAAATCCTTGGT
1878	ACGGTTTCGAATACTGCTGGGCAG
1879	CCGCTTGAGGTTTCAAGTCAGAGCT
1880	ATCGTGCCCGAAGACACTTAAACG
1881	ACCTGAACCAGGGCGATTGCTTTA
1882	ACCCTATACGCTGGGCTAAGCGGG
1883	TGTTTCGCGACTAGAAGCCTTTGC
1884	GAAGTTGGCGGCTCACCCGTATTA
1885	TGGCTACACCGCTTAGGAGGAACC
1886	CCACAGTTGCGTGACTTACATCGC
1887	ACTGCCACTGCGTCTGAAGAGTGG
1888	GCGCCAGCAAATTTGCTGTGGTGT
1889	TGCCTCCGTGAGCCGAATAGCCA
1890	GTACAAACGGGCGCTATTTGCTCC
1891	GCTTCCCTGGCTCTGAACGGAAAC
1892	CGGCTACCCAGGCAGATAAGCTGA
1893	GGTTGGACCCGACAGGGAATTTCC
1894	GGGGAATACCCGGCGTTTGTAATA
1895	TGGTTGCGTGAGGTTATGTTGCGT
1896	TCGGTAGGGTTCAGTCGCTGAGGA
1897	TTCGGAGTGTGCCGGTGCTAGTAC
1898	TCGTAAGGAATGATGGCCGGGCC
1899	TCCGTCGACCGTCCAGCGAAGTTT
1900	AGGGAATATAACAACACCGCGCAC
1901	ATGTCCCGGAAACCAGCTACCTCA
1902	ACCAGCGACTTAGATAGCCGTCCG

5

0

5

20

25

30

35

40

1903	GGAAAACCTCCTTTGCGTCAACCA
1904	ACGTGCGTGCATACCCAAGAGGAC
1905	ACGCCACTTTCCTAGAACCAACG
1906	CGAAGTACGCAATAGTGCCACCCT
1907	GATCCCGCGGATCACCTATCAAT
1908	AGAAAGCGACCGTTTCAGGCTAGC
1909	CGCTCCCTTTCATAGTCCTCTCCG
1910	GTGGGTGGTCATAACGACAGCAGA
1911	CTGGAGGCTGCATCGTTCGTAACA
1912	CACCATGAGTTTCGGAGCGAGGAT
1913	CAAGCTGCGTTCGATGAGAGATTG
1914	CCTGGGAGCAATGACCGCTCTGGT
1915	TCCGGCGCTCTACCAAGATGAGAC
1916	CGACCGCGTCGCGTATACTATCCG
1917	AACATTCGCTAGTGGGGTCCAACA
1918	TGTATGATCATCCGACCGAGCAGC
1919	AGTGCGCCGAGAGGGTGAATAGAC
1920	AGGCTTGTTCTGGACCAGCACCAT
1921	GGGGCCACATAAAGAATTCCGAAC
1922	TGGTGAAGATAAATCCGCATGGCA
1923	ATTTCCACCACGCTCTTGCCAAAT
1924	CGCGTAAAGCTGTCACCGATGACC
1925	TCCCCAACCGGTAACAACAGCGAC
1926	CCTCTGCTCGCCTTACACCCATGG
1927	CAAGCTGCTCCTGTGCTGAAGGGC
1928	AAACGAACGATGGTCGGTAGACCG
1929	TCAGTTCGATGGCTATTGCGCCTC
1930	GGCTCTCAACGGACGCAAATCATA
1931	AGTAGAGTGTTGCGGCTGCCGATC
1932	AGACACTAGACCGCCGTGACCTGA
1933	ACCGAGCACCGAATTCCTTGTCC
1934	CCGTGGCCAAGATACGAACGAATT
1935	CCTCCTACAGCATCCACATGAGGG
1936	CACTCGGCAAATACGTATGCGCAT
1937	ACCGAGTTGAAGCACGAATTTGGG
1938	GACCACCTCGGAAGATCGTTCTGC
1939	TCAACTGGGCAAACGAAGAGCACA
1940	GCTTAGCCTCACACGTGCATACCA
1941	CTGCGGTCTCCAAGTACCATTTCG
1942	GTTCCGTATTACGGCGGCCATAAG
1943	ATCGACGCAACCGGATAGTCTCTG
1944	CGCAGATAAACCGGCATCTTTCAG

5

0

15

20

25

30

35

40

1945	ACCTGCCAATACGGGTCTACGGTT
1946	ACACCTGTTGCCATGCTGATCCGT
1947	AAACTGTCTACTGCGCAATTCCGC
1948	GCAACTAGCCCGTGCTAGGATCGT
1949	TCGTAGTGGTGGATTGTTGTGCGT
1950	GGCTTACTCCTCAATTGCGACACG
1951	CACGACTCCCTGCCAGATTTGATT
1952	CTTAGACGTCGGCAATGTCACGTC
1953	CTCAGAGCACAATCTGCCCTGCCT
1954	GCTAGGAAAAGTCGGCATTGATGGG
1955	AAAGCCCCAAAATTCCGCCTAACC
1956	GCGCAACGCTAAGGGACTATCAAG
1957	CGTCCGCTGGGATGAGTCTCCTGC
1958	ACAGGCCTCGTGATTGGTGTGGGT
1959	CATTCTCCTTCCGGGACCACGCCT
1960	TCGGAGTTGACCAAGCTCAGTGCG
1961	ACGCGCCACTGCAATTGCAAACAC
1962	AGTTCATGGAGCCGGCGTATTGTT
1963	ACGTTTAATGCGGGGCCCCGCCTAC
1964	TGAGGCTTTAGCCTACGCGCAGGT
1965	CAGCGTTATGAGCGCGGAGTTTAT
1966	GTCCACGTGACCACGGATAGTTGG
1967	GATTATGCTCCTACGCCTGCTCCG
1968	TCGTCAAGGGCATGATGTGTGGGA
1969	GATGGACCGCCAAAGACACCTTGA
1970	TACACGAGGATGGGGTCAAGCTTT
1971	ACACGCACAAAACGTTTGAAAGGC
1972	GTTATCGTGGGCCGATGGTACTGA
1973	ACATGACCGTATCCGCCTGCTTCG
1974	GAAGGCGAACCCTGAACTACGC
1975	TGACTTTTGCAACGGGTGGAACCA
1976	TGAATTCGTAGGTTTTGGGTGCGG
1977	AGCATTTATGAAGCGGCCATTGCG
1978	TGCTCCTCGCGTTGGTACCGTGAG
1979	CGCAGCAAGAAACAGCAACTGTTG
1980	AGACGCTTGGAGTGAAAACCTCGGA
1981	CATTCGTAGAATGCCCCAAATGGA
1982	CCAGAAGGTTCCGGGACCCGTCGTG
1983	GAGAAGCCGTTCTCAGAGCACAT
1984	TTGCGTTGCAAGATATCTGGCCCG
1985	GGGTTGCATGTTTCAGGCAAGACGA
1986	CTCACGAAGGTGACATATCACGCC

5

10

15

20

25

30

35

40

1987	GCCCGAGATACGGGTTCAAAAAGA
1988	CATCTTCGCGCTTCTTCACTCCGC
1989	TTACACGGTAAGCGTACGGCCGCC
1990	ACCTTCGGACAATGTGGCGTTCGC
1991	TGAATGGTTCTGCTAGGCCACAC
1992	CACGCCTGTCTGACATATGGATGC
1993	CGCCTCAACCCAATCTGAGAACGT
1994	TTACGCTTACTGCGAGCTGGGTCC
1995	GGCTTGTGGGGCAATACGCATCTT
1996	CACTCTCCTTTGGATGCGGAACAA
1997	CTTCGAAGCACTTCAGACTTGGGC
1998	GACCAGCCATCACGTAACGGCCCT
1999	AGGAACCGGATGTGGTTATGGAGC
2000	ATCCATGGGCAACTGAGCCTATGC
2001	GGAACAGCACTTGTTACCGCCAC
2002	TGGCTCGCTTCAAGCCTGTTTGCT
2003	CAAACGTGAGGTCATGACCACCAT
2004	ACCGATGTCTTGAAGTCCGGAGGT
2005	CGAAAATGCATGATGATCTCCCCT
2006	TTTGGTATTCTCGCTGCACCGTTG
2007	GCGTACTCAACCACATTCCCGACC
2008	AGCAAACAACAGCGGTCCGAGCAT
2009	GGACTAGGAGCGGGGATAGCTGAG
2010	CCTTAACGAAAACCTGTGACCGC
2011	CTCGATCGCATAAGCAAGAAACCG
2012	CCCGTTGTTTGGGCGACAAAAAGT
2013	CGGCGGCTCTCGCATGATCTCGTT
2014	CGGATGGAGAGGAGTCTACGTCCC
2015	ACCAAATCAGACTAGCGACTGCGG
2016	CAGAACAATATCGTGCGTCAACCG
2017	CCTTTGCGCGCTCCGAGTAAGGTA
2018	GGAAACGGCACCTATCTGTCGTGA
2019	CGACCGACAAAACCAAATGCCGCC
2020	CCAAGGGTGTGGGAGCTGAAGAGA
2021	TTAAGTGCGCATAGTCCTCGTGGG
2022	GCCTGGTGGGGTAAGTCATGATGC
2023	GAGCAGCAGATTGATGCGCTTATG
2024	TGCGCCAACCTCCGGAATATTTGC
2025	AACCCCATCATGAAATGCTCTCCG
2026	GTCCAACGGTACTGGCGTGATGTT
2027	ACTCGGCTGATCGTGAGATGGTGA
2028	ATTCGTGGGCGCATCTCGGAATGT



5

0

5

20

25

30

35

40

2029	TCCCGTCCTGTAATCCAGGGAACA
2030	CTTCGCTGCACCTACATTGCGCCA
2031	GCGTGTAGATGACTGTGCTTTGGG
2032	CTATGGTATCGAGACATCGGCGGA
2033	CCTCGTACTCCGTCGTATGCACAA
2034	TGGTGCGTCCGTAGTGCCTGCACT
2035	CGCGATCCTAGTTGAAAGCTTTGC
2036	ACGATCCAGGTGTTGGGCACTAAG
2037	CCAATCTAGGATACACCACGCCCG
2038	GATACGTGGGGTATAGGCGGGCCC
2039	CATGGAACAAACCGTCGTAGGGGA
2040	ACACTCGCGCAGTATTCGAGTCGT
2041	CTCAGTCTCGAAGGTGATCCGACC
2042	TCCCAATCCCCGTGGTATCGTCGT
2043	AATCAACGTAGTTCCGGTGGTCCG
2044	CTTAACAACCCAGGGGTTTGGGCT
2045	CCATCCTGAGAGTGACGGAGGTGC
2046	CTACCGCTGCATGGCGTTAGATTG
2047	TTATTGGTGGCGGACGGAGTGAGT
2048	TTAAGGGTGAACCTCAACCGCGTGA
2049	TTGATTGAAACGCTGCGCACTAC
2050	TCATGTGTAGGTGCGGCGCCGTAC
2051	CTCCGAACCTTCTGGGCCTCTTTT
2052	CTGTTGCCCATTTGGCCCGACACTC
2053	CACGATCGCTGAGCAACACATCAC
2054	CGGATCATAAGCGTCCGCCTTCGT
2055	AGGTAAACGCAACATGTGATCCGC
2056	GGGAAAACAGCTAAGCCTTGCGA
2057	ACTTATTGCCGGGATCCGTACACA
2058	TGCGGTCTGGAAGGAAGGGAGGG
2059	GCTGCCACCTGGACATCGCATACA
2060	GCAGGCATGACAGTGGCGTAGTAC
2061	GCGGCCCTGATGGTTTGGCTGAGC
2062	TCCCCATTTAGTCCCCTCCATCAC
2063	GCAACACAAATGCGAGCGTAGGAG
2064	GGCGTTTGTATTGAGCCACGTAG
2065	GGTAACGTCGCACGTGGAATTCCG
2066	ACTTCACAACGCTCCGTTGGACAC
2067	CCGAATTATAAAGCGCAAGGCACA
2068	GGACCCGATAAGACTCTGACGCCG
2069	ACCCGTTTCTCGTAGGAACCTGCT
2070	CACGTTGCACTGTATCTGGTTGCC

5

0

15

20

25

30

35

40

2071	CCTCGGATGGGCCCATGACCTTGA
2072	GGACGCCTGCTGTAGGGGTTTGAT
2073	CTCGAGCGTGGGCTAAAAGAGCAT
2074	TTTACTTCTTAGGGCGCGTTTGGG
2075	ACCACCAACATAGCGCGCACTAGT
2076	TGGTTACACGGCAGCCCGCGTAAG
2077	TTATGGTACGTTGCTGCGTGCGGG
2078	ACCGCGGATCTAACGAATCCCATT
2079	CATGATCCCGCCCTTAGGTTAAGC
2080	TACCGCTTCAAAGGGTTGCCGAAT
2081	GCACCGCGTCAATATTACCGAGGA
2082	GTGTCGCGGCTTTACAGAAGGAGA
2083	GCAAGCCATACCGCAATAAACTCG
2084	ATGAGGTCGTGCTGCGTTCACGAG
2085	CGAGACTAGTGCCGATGCAGGGTA
2086	GCCTCATCATAGACGCTGGATGCA
2087	GACAGGCGTCGGTAAGCTCTCAAG
2088	GCTACGAATCTTCCCTGTCGCCAC
2089	TTTGGCAGAACGTACCAGTGGGGT
2090	GGACAATAAGCACCGGAGAATGCG
2091	TCATGAACCTTCTGATGCCGCGAA
2092	CGCCGCATTACCTTAAAAACGTGC
2093	ACGAGTCCAACCGCCTCATTGATT
2094	GCGAAGAGTTGCTACTCTTCCGCC
2095	CGTCGGCAACAATCTTTTTCGTGA
2096	AATCCTGTGCACCCGTGAGACGCG
2097	AACCTATATGCATCAACGCGAGCC
2098	GAAC TTGGCAAAACAGCCCGGAAA
2099	CTCTATGGCCGTTTGCCGTCTGCA
2100	AGTGCACCGGGTTGTGGACACAAT
2101	CCTGGCTTTTCACACGCCAAGAAA
2102	CACTCAGCGTAGCCTGAAGCCTGG
2103	GAATTATCGACCGCAGCGGTGTCTG
2104	GTGACATCACATGGTGGCCGAGCG
2105	AGCACCTTGCCGAGTCACCAAGTGA
2106	TAGGTTGCAGGAATGGTGGGCACC
2107	GTCCCATACGTGTGGTACGCGGAT
2108	TCGGATACTCTCGCGTGCCACGGG
2109	CAACGTTGCCCCCTAAGCCCAAAT
2110	GTTAGGTCACCGCGGCATATCCTA
2111	GTTACCGGCCTCTACTTGGGTTT
2112	AATCCGCGTCTAGGTCATGTGGTC

5

10

15

20

25

30

35

40

2113	GCTACGCCTCTGGAGGTGGTACCC
2114	CAGGGAATGCTACAAAGGGTCCAA
2115	AAGGGTTAGCTGCCCCGGTTAACAG
2116	CCTCGCAAGCGCGATATTTATGCC
2117	GCCTCCCGGTCATGGTCAAGGGAA
2118	GCTGTTGAGCGGCGACCTGTGCAC
2119	CGCTGACTTAGCTCTGATGTGCCG
2120	TTCATGGCATTTCATCACGAAGGAA
2121	TAGTGTTATGCCCCGCGTGTGAATG
2122	CATGTAAGGGCACGGTCGTGGGCA
2123	CAGGAAGCTCGCTCCGTGATGCAC
2124	CCTGCTGATAGCAACCTCACTGCA
2125	ACTACGAGGGGCAGGGTCTAGGCG
2126	CATAATGTGGGTGCTGACGCCGAT
2127	TAGCGAATCCACACAGAGCCGCTC
2128	TCGCGAAATCCCTAAATCCTGTGC
2129	TGGCACGAATCAAGCCACCAACTC
2130	GCGGACCGTCTTTGCTATCTGACG
2131	AGGCCCCGCCTTGTAATTGGTCAT
2132	CTGGTCCCATACGCCGCTGACTAG
2133	TGCTAACTGCGGCCCTACAGAGTC
2134	TGGTTTTATGTTCCGTAGCGTCCG
2135	AGCTCAAATTCTCCACGGGATG
2136	CGCGAAGATAGTGAAATCCGCATC
2137	GAGTGAAACCTCTCGCGGGTTGCA
2138	TCGAATGCTCTGCAGTGACGTCAA
2139	AGGTGGCAATGATCGACGACCCTG
2140	ACCTTAACACAGCCGACCAGGTGA
2141	GTCCGGAGCCGTGCAAAGCAATAA
2142	TCTGCCTGACTGCTACATGCTCCC
2143	CTTTTGGGGATTAGAGGCCGACAA
2144	GGCATAAAGGCTTCGTTCTGTCTC
2145	GCGGACCGTAAAGCGGGCAGATAG
2146	TTTCAAGAGTGCATCGAATCCACG
2147	CCGGCATCCCTTCTCGCTGTTGCC
2148	ACACAGAGACGCGAACGGAGTGCA
2149	AGCGGCATTCTCCCACTCGTTACT
2150	GGAGCGTACTGCGCCTCGCAAGTC
2151	AAACCCGAATGACACGGCAGATAA
2152	GGTCGGGTCCATATCCAAGTAGGG
2153	AACCAGCGGATCGATAAACGACA
2154	GGTGTCCACCCGTTAACGCCGGTA

2155	AGCGCGACGTTGGCTTGGCTTAA
2156	TCCCACGGCTATAGGTCCAACGAC
2157	ATCAACGAACGATGCCGTTAGGTG
2158	GAGGCTAAGCCGTATGGCCGAGGC
2159	ACGGTCCGAAATGGTTAGAGGCAC
2160	ACGCAAACCATTCCTCGAGTAGGC
2161	TTACACGCTCGCTATTGGGCCATA
2162	CTCGGCACGGGTTTAGAACGCCGG
2163	ATTCGGTAAGGTATCGGGCTAGCG
2164	AGCACACCGTTATACATGACGGCG
2165	AGTCCCTGCCGTTCTGCTCATGGAA
2166	GGGCTTATGACCAGTCAGGTTGGA
2167	GGTACCACACGAGTGCCTGGTCT
2168	TTGATCGTGTCTCCCGAAACCCTC
2169	ATTGTCGCGATCGGCATTTCTTAA
2170	GGGTCCAACGACTTCTCGCTGCTG
2171	CAAATTCCTTGGGGGCCATAGTGG
2172	CCAGAGTATCCGCCGTTAGACGGT
2173	TCCTGCAGATCATCTCGTGTCTGG
2174	TGCGGGAGATTTGAACAAGCTGTA
2175	TTAGACGCCGAGCTAGGCAACGTC
2176	TTTCGGCAGAATCTCCGATTCAAC
2177	TGGCGAGCAGACCTACAAGACAGA
2178	GGCGACAGACCGGTACATCGGCCA
2179	TCTAGACCTGCGTTTCGTGGGACC
2180	GCCGAGCGTGGTACCATACGTTCA
2181	TAATCACACCCGCTTTCTGTGGCT
2182	GGCCGGAGCCATTGGACACTTCTT
2183	CCTGTAGACCTGCATGGATCGCTG
2184	GTGTGTGTGTCTGCGTTGGGGCAC
2185	ATCGCCGTTCCCGCAAAATAAGCA
2186	TGATCAACGGGGTAGTGAAAACG
2187	AAGCGACGATGCTTTCTTGAGCTG
2188	CACGGGCACGTGTTCTACGCTTGC
2189	ACGGGCTGGGACAAGAGCTAGAAA
2190	GGTAACTGGCTCCGCTCTCACATC
2191	ACTCTGGCTGTTGGCGAACGTGAC
2192	GACCGAGGACCAGTCCTTGCTCTC
2193	AGTAGCTCTTGCGGCCTAACGGCA
2194	TTCTTGTCTGGGGGAGAGCAGTG
2195	TTAGCAGGGAGGTTGTGGGCTCAT
2196	TCGGGAGAGGGCCTTACCAAAGC

5

0

15

20

25

30

35

40

2197	AGAACGTGGATTGTACGCTCCGCC
2198	CTTCACAGCCTGGAGCCACCAATG
2199	GAGATCGATGAAACGCACCAGCGG
2200	GGGTCCAGAGTTGGTGTGGGATAA
2201	CCGTCCACCCCAGATAGGAATCAC
2202	TGCCTCGCTTCTGTGAATCTACGA
2203	GATCACAGCGTCCGCGCATAACGG
2204	ATGACGCCTTACATGACGCACCTT
2205	GCGTGGAATAACGCCCTTAGTTCA
2206	GGTCTACCATTCTCGCCCCGACCG
2207	ACACCTCTCTGGCGTAGACGCTCA
2208	GTAGAGGTGCTCAGGACTCGTCGC
2209	GTAAGCAGGAGGCGAAGGCGCGAA
2210	TCTAAGGGCCGTTTCAATCGACCT
2211	AACCTGATTTCAAGGTCAGCCCGA
2212	GTCACGCGATTGGCCACCTATTA
2213	ACGATGCCGCGCATGTAACCTAGT
2214	TGAGAGATGTCTCGTCAACGCCTG
2215	GCATATCTCGCGGTGACAGACGAA
2216	TATCCTGGACCCAGCCTTGGAGGA
2217	GACCCAACGTCGAAATTGTGCGAT
2218	TGAAAATCGGGGCATCTAGTTTGG
2219	CCGCGAAAAGGATTTGTGTACGCA
2220	CATTCCATTTATCCGCAGTTCGCT
2221	CCTGTCTGTGCGAGCCAGCGTCTAT
2222	TCAGCGCGGCTAAACAAGTTATGC
2223	ACGCCTACGAACGACCCAAGAGAG
2224	TGCGCATCTACCATTGTGTGGATC
2225	AAGTCCGCGCTCGCTCCTGTAATA
2226	GCTGGGTCATTGCTCGAGTAACCA
2227	TGGAGCGTTCTGGCAATGACCGAC
2228	CAAGTCAATTCTTGGCCAATTCCG
2229	CGTTCATGCAAGGATCCCAGGTTA
2230	ATGCCAATAGAAGCTGGGGATGCT
2231	CCTAACTCTCCCTTGAGGCCGTTT
2232	ATCTCGGCGAAGGTTCCAAACATT
2233	GCGACAGATTACGCTGCGGTTTTT
2234	AAGCCCAGACGGCCAACACGTTAC
2235	TCAAGTTCAAATCACATCCCGTGG
2236	GATTGTCGTTCTGTCTGTGAGGCG
2237	ACCGAACTATGTTCCGGCATGGCA
2238	CGTCATCGGGTGTGCAATGCCGTT

5

10

15

20

25

30

35

40

2239	CGGACGGAGTCACGTTTGTGCACT
2240	TAAACAAGTCGTGTGCCTTTGCCG
2241	TAATTACTGGCCTGTGGAGCAGGC
2242	GGAGCGGCCCGAATGGTGCTCTTA
2243	ACTAAGCAAGGCTTGGATGTGCGT
2244	GGCAGCTCAGCGGCAGTACGCTAC
2245	GCGAGGCGAATTATCCGCGGATTT
2246	CATACGACACACCTTGGGGTGCTA
2247	TGCTTGGGCTTTAAACCCCGTTTT
2248	CCGTTTGGAAAACGCAAATATCGG
2249	AAACTAGCTAGCCGCACCCGCAAG
2250	GTTGTTCCACCAGTGATCACGCAG
2251	GCCGCTGACAAGATGATCATCGTT
2252	CTTTCATAAAGCCAACCGATGCC
2253	CTGACTGCATCTCGAAAGCGGGTG
2254	ATTTCTTCGGAGAATCGGCCACGT
2255	CATTTCTGGGCCCTAGCTACTGCGC
2256	CCGATCCCGCACATCCGTATCCTG
2257	TATCACCGGGAGCGTCTTATCGTG
2258	TAGGGCTCGTGCACCGATTAGAGG
2259	GCGTGGCACTCGCTTGTCTAGGTA
2260	CTCAACGAACTCAAGGGCCGCTAC
2261	AGCCTGGTATCGACCAATCCTGCA
2262	TACGCGTTCTAGTTGGCCGGATCC
2263	TTTATGGGTTTGTGCCTGATGGGT
2264	GGGACCCCTAGCAACGTCACCTTA
2265	CTGCCTCCCCAGGAGTCATTGGAT
2266	AACCCCGCAAGACCAGTACCAATC
2267	GGTCACATACGCGCTAAAAAGCGC
2268	AAATGGCTCCGACCAGTTAGGGAC
2269	AACGCGGCACGCTTAAAGGTGCAT
2270	GATCGCACGCCGATTAACTTACA
2271	CCTCCTGATTGGGAGTGCGGAATT
2272	CGGAGGGTAATAGGCTCCTCTGCG
2273	ACAAGAACTGGACATTACCGCGGG
2274	TGTCGTCTTAAAGGCCTTTGTGCG
2275	GGTGACCATGTGGCGTTTATAGCTT
2276	CACGGTTGCGCACGGTACCAGAAC
2277	CCTTTATTGTTTGGTCCCCTGCCC
2278	GTGCGCCTGCATTCTACCGTCAAT
2279	GTTTACGTTGATGGCTTGCCGCCG
2280	CCGTCGGTGGTAGGACGTGAATGT

5	2281	TGATCGCCCCAGAATCCCTGTGCT
	2282	AAGCAGCCAAAAATCGGTTGCTTT
	2283	CGACGGGACTTAGTAGCAGGGCCT
	2284	CCGATTGCGGAAACGACCAAGTAG
	2285	CCACCCCAACTCCAATCTTTCTCA
	2286	GTGCAGTAGACGACTACCGGCGTC
	2287	TCGCCCATCGTATCAAGCAATTC
	2288	GAATCGCGACTACCCGTCGGGTCA
	2289	CCAGCACTCGCCATCGGTTATAAT
10	2290	CGAACCGTAGAACTCCGGTCGGTG
	2291	GCACCATGACAGAGCCCCAGGATG
	2292	TGGGCTACCGCAGAATAAGGGTGA
	2293	TGGCCTGTGCTGTCGAAGGAAACA
	2294	GCCTCACCGATAGCGAGCGTTTGC
15	2295	GTGCGCGCCGGCTAAAACGAGACA
	2296	CCGCAGACGAGTTTCTTGTGACAG
	2297	GTTGCAATCGCGTGCTAGGAAGC
	2298	TGTTGTACACATGCATCCGGTGAA
	2299	CACTGAACACGATATAAGGGCGCG
20	2300	CGCGATGGTTCTTAGCAAGACGAT
	2301	TACACCAAGGAAGAAATGGGGACG
	2302	CGTGCCTTGCGTTTTAGGTGCAGC
	2303	GTCGTTTGTCTGGGCATTAACGGC
	2304	CAGGCTCTCGTTCGGTACAAACGT
25	2305	CGGACACTGTTTCACCAGAACCCA
	2306	TACCCATGATGCGGAAGAAGCGTA
	2307	CTGTCCTTAAGCGGATGAGAACCG
	2308	CGGGAGATGAGAACGGTTTTGTGC
	2309	TAGATCGCGACTGTACTCAGGCCG
30	2310	TAAACAGTTCGCGCGACTGTCGT
	2311	CGAGGAGCTCCACATAAGCCCAAT
	2312	TGGCTAGGGATGGGGAATCATCTT
	2313	AGGATTGGGTGCCTGGATGCATTG
	2314	TGTATCTACCGGCCTGAAGCAGGT
35	2315	TCCCTACGCGCATGACTCGCTTAC
	2316	TGGTCGATCACCTGTGACAGACGC
	2317	TGGGGGTAGTCCATGCATCAATTG
	2318	CCCTGCCAGGATTACTATTCCGGA
	2319	TCCCGCACGGGGAATTTAAGTAGA
40	2320	GTGATGTGCAGGAACTTCTGTCGC
	2321	ATTTAGGCATGCATGCGCTTCTCA
	2322	TCGGCGCTAGTGGACGCCGTCAA

	2323	GAGCTTCATCTCATCAGTTCCGCG
	2324	GACAACTCCACTGCTCCAATCGCA
	2325	GGCCAAGGATGGACCTTACGATGG
5	2326	GGTTCCGGAATTTGTCACCGCTTC
	2327	GCGCTGGATAGTCTGCGAGAAGCC
	2328	TGAGTCCAGTGCTGCCACCATGAA
	2329	TTGAATTGGGTGTCGGAGCGTTCT
	2330	CGGCGGGCAGACAATGCTTTGAAC
10	2331	GGGTCTGTCAAAGAGGGTGTCTGG
	2332	CTTTGTGCAAGACGAAGCACCTT
	2333	ATCGAATTCCGAGGAGGTCTCCAT
	2334	TCCGACCCTCAGAGTCGACTCATT
	2335	ATCAACGGCCACCTCCTCGCCGAG
	2336	AGCCACGGAATAATTCCGTCCACC
15	2337	GATCGCTTGCGTATCGCAAAGACT
	2338	TCCACGCCTTACCATCAACTGCAA
	2339	GCCAAGCGATAGGCCAGAACTCAG
	2340	AGCGTGTGGGTCATTTTAGCACGA
	2341	GTTATGCGCGGCTTACGAGTTCGA
20	2342	TCTGTCCACGTAACCTGCCTGCAG
	2343	TCGGCAGCCAATGATCATACCTCT
	2344	TAAGCCCGATCCGGTCCTGTGTTT
	2345	ACATGGCAGACTAACAGGCCTCGC
	2346	CATGGCTGCACTCTAAGTCGAACG
25	2347	TCTTCAACCCACGCGGAACGATTG
	2348	CTCGTGTCTCCAGAGGATTGTCCC
	2349	TGAAGGCATCAACCCAGAGGATTT
	2350	ACAGCTCGAAGGCAGCCACATTGG
	2351	ACAACGAGTACCGCGACAGAAGGG
30	2352	ATAACCGAAAAACCAGCCTGCGAT
	2353	ACAACCTCAGCACTTTCGACGTCCA
	2354	CGGGTACTGGGTATCACCAATGC
	2355	CATCGGTTATCGCTGCACGCGCGT
	2356	GAAGGAATCCCGGATAGTCCGTGG
35	2357	GCATGGTCTCAGCCAAAGAACCTG
	2358	AGCCTGCGACGTTTCCCGACAGAC
	2359	AAGAAAGGCGCACGGGATCGATAT
	2360	TGTCGCGAAGCCAACTTTCAGTAA
	2361	GCGGCATGCAAGGTAGGTCTGGAT
40	2362	GGTGGCCATCTCCTCGAATTGCAT
	2363	GCGTGCATAAGTTGCACATTGTGC
	2364	TTGAGGTAGCGTTTTTCGCGCATAT



	2365	ATCCCACTTGTGAGAGGGCGCATT
	2366	CGGTCAGCGAGCAGACATCAACCT
	2367	GCGTATCTTCGGGTCTGAACACTTG
5	2368	ATGCCATTGAACTCGCACTTTGCG
	2369	CGATTCCCATCATAATGTGGGTCC
	2370	CAATTTGGATAATCCAGCCACGCC
	2371	CGGCTTACCCTATGATTCCGTGCA
	2372	GGTGGACCATGCGCTGTGGTATGA
10	2373	TATTTGTCTGAAGATCGCAAGCGCC
	2374	GTCAGTGGGTTTTGAGAGCCCGCA
	2375	AGGGGGTCTGGGAAATCTGACAAAA
	2376	TGCTTGCTATCCGAAAAAGCAGG
	2377	TTATCGGATCAAATTCGGCTTCGG
15	2378	TGCAGCAACGAGTTACCCGGACTT
	2379	TATACATGTCCGGAGGGGCACCCA
	2380	TGCAAAACCGGAGGATGAACCCTT
	2381	TCGGTCTAATGTCCACGCAGACAC
	2382	ATGTGTTTGCCACGCGCTCCTATT
	2383	TGGCGAGGCACGGCTCTAATTCGG
20	2384	GCGACGACCCGAGCGACTTTTACA
	2385	CTCAGAGAGTCTATCCGGCGCCCT
	2386	GGAACATCTCCTGGGTCCCTCAGA
	2387	GCAACGCAGGGAAGTACTTAGCGA
	2388	TGACTTGGGCGGACAAAGAAACGC
25	2389	AGATCATCGGGACGCTTCATGCTA
	2390	CCCTTCTGACCGCTAAGGCCATAA
	2391	CGTGAGCCGTGGGGTGTCTCTGTA
	2392	TACCTTGGTCGTCTCCGCTTTTGT
	2393	TCGCCGCAAATGCTACGTGAAAA
30	2394	GAGTGACCTAATGGCTGCCCGACT
	2395	AAAGGAACTTGGCCAACCCTATGG
	2396	TGTTTTCGCACTCCACCTAATCGC
	2397	CAATGGGTTTCATAAGGGCAGGCA
	2398	GCCTAACACACAAGGGTCCCTCTG
35	2399	CGTCATGCGGTCCGAGGATCGATC
	2400	CCACACGGGCACGGAGTAATATCT
	2401	CATCAGACATAGGTGCGGTGCCGA
	2402	AGATGAAACCAAGGGAGGACGCAG
	2403	GGCTACCCATAGGCTCAGCAGCAC
40	2404	GGCTTGTGAGGGTGTGTTCTCGAC
	2405	TGTGTTACGGCGAATGCAACAGTC
	2406	CGATAACAGGTCTGCGCCGTTACTA

	2407	TGATAAAGTGAGGCTCCAGCGCGA
	2408	AATTGTGCACGGATCTGCACGGCG
	2409	GCCGATACTGAGCATTTCAGTGCC
	2410	GCAATGTACTGTCACCAAGTGGCGA
5	2411	GGCATATCGGTAACACTTGGTCGG
	2412	GGGTCTCAAACCAGCGTGGCCGCT
	2413	GTCTCCGGGACCATTGAGCTGGAG
	2414	GGCCTTCGGCATTTCAGACGGGTTG
	2415	CGTGATAGGCCACAGCGCTCAATT
10	2416	GGCAGGCCCGCGAGGATGATTAAC
	2417	CGGGTATGGTTGATAACAGCGTGG
	2418	ACGACGTCCTTGGGACCGTATTGT
	2419	CTGATATCGAGCCTGAGCCTTTCG
	2420	TCCCATTGGCCTGTATGCTGGCCT
15	2421	GTGTCGTCGATTGTTTCATCGACG
	2422	CGAAAGCCAGTAGCCGATTGCGTG
	2423	GGTTCGGCTTATTCCACTGCGACA
	2424	AGCGAGGGCTAACTTTTTAACGCG
	2425	CGGCGCTGATGACGGGACTCGATT
20	2426	TCACAGTGCTCGGCGTAAGGACTA
	2427	CCCATTACGAGCACACACCATGGC
	2428	GGCCGCTAATCTTTACGCATCACG
	2429	ACGGCTTCCTAGTGTCCAGCCCTT
	2430	CTGTCAGGTCCTACCCAATGGCTC
25	2431	CACAGCCCATCCCAGTGAAGTCT
	2432	ACAAACGATACACGCAACGCTGTG
	2433	TGGCGGCCAGCTAGCAGGCGAAGT
	2434	ATCTCGAAACGATGCGTGCCTAAA
	2435	ATCTCGAGAACAGCGTGCCTGCGG
30	2436	GAAGAAATCCGCCGACATCTACGG
	2437	GCGGAGCAACCTTGGCTGTTTCTA
	2438	CGCGTTCCGAAGACTTGTTGTTG
	2439	TGACCTGAAGCCCATCCATAAGCA
	2440	TGGTATTCATTCCGGATAAGCGGG
35	2441	GCGTTGCGGGTCATTGATGCAAAC
	2442	ACCGCTTTCTGTGTAGAGCCCTGA
	2443	CAAATAGACAATCGCAGCTTCGGG
	2444	TGTCCTGACAAATCAAGGTGCAGG
	2445	AAATTGCACTCGCGGAGATTTCT
40	2446	TGACGCCCATTTCTATATGGTGCA
	2447	TGTTCCGACAGGGCACTGCTAGAC
	2448	TCGCTGGCTTGGGAAGGCCTTCGT

5

10

15

20

25

30

35

40

2449	GTGCACCTCCGTTGGCGTAGAATG
2450	CTCATTTGGGACCGATCGGGTTGC
2451	GCCAGTGTCTGTCAATGGATGGGA
2452	TTGCCCGGCAGGTTCTGTGTAATG
2453	ACCCGCGAACCGAGACGCACTTCT
2454	TCCGTGCGATTGGTCAAGGTTGAT
2455	AGGGCGTCTCGGTTGAACCTCGGT
2456	TGACCGTTCAAAGAGCAAGCCAAC
2457	ACACTCACCTGCTGTCCCTGCTGA
2458	GCGTTTAACTCCTTGGGTGGTGGT
2459	CGCCTGCGCAGGTAAGTCTCCGCA
2460	AATCGAATTTCCAGCGGCTGTTT
2461	AAGCAGGTGGGATCCTGGGGATCA
2462	AATCCCAGACTCGCTCTTCGTGCT
2463	ACGGTTATAAGGGCCGGCTGCGAC
2464	TACGAGAGCGGGCTTAGACGTCGC
2465	GCGATTTTGACCCACGGTTATCGA
2466	AGCTGTATAATTTGGATGGCGCGA
2467	TCCGCGAGTCTTAGCCGATTGAAC
2468	GGCATCAGCTCCGTAAGCCGATAG
2469	TGTTATTGGCAGTTCGAGCGACAG
2470	GCGAGCCTTTTTGCTTGGGAAGAG
2471	AGAAGAAAAGGTCAGCGTCGACGA
2472	CGGGTCGACCCTTGAAGCATAACC
2473	CTCGGTTTTACAAACTTACCGCG
2474	GCAGTCCTATCCGGAGCCTGACAA
2475	AAGGTGCGCTATTTGTTGTCGGTC
2476	AGTGAATCCATGCCGACACCTGA
2477	TACAGGCGTAATTCCTGCGAGGGA
2478	CCGAAGTGCGAGAAGCACGTTGTT
2479	AAGGACTGGTATGGCCGAGCTTT
2480	GGACACCGCCAACCTCATAGTTGC
2481	AATGGTGTTTCGCCTGGACTACCAC
2482	TAGGAAAGCGTACACGGGAATCCG
2483	TCTACCCCAATGATGAGGACGTC
2484	CGTGTCCGTGTGACACTGTCCATG
2485	TCCAGGCTGTTGCGGATACGGTAG
2486	GTAGGCAAAATGGTCGCGATCAAT
2487	ATCTCCGTGGACCCGATTGTGACA
2488	GAATATGCCGTCAACGCTATGGGC
2489	TTCCGGAAGCGTTTGGTAACTTG
2490	TTCGATAGGAATACCAGGGCCTGG

	2491	GGCCATTTGAGGAGGATTATGCAA
	2492	ACCTTCTGACCTGGACTTTTGCGG
	2493	GACCAATCCGCAGTTGAGCAACAG
	2494	TCGGCCACTCACCATGAGTGTAGG
5	2495	AGCGCTCACATGTTGAAAAACGGG
	2496	TAACGCAAAGGCGCGATCCTCGCT
	2497	TGGGTGGGCCAAATATTACTGCAA
	2498	GTCCTCGAAAGGGGCATCCAAACA
	2499	CCCATCTGGTGGGAGGCGTTATCA
10	2500	GTGCGCGGTCTGCAAACCTCGCCAT
	2501	TGTGTTGCCAACCTAGGTCATCA
	2502	CTGATGCTGTTCTCGTCGGTTGAC
	2503	AAGCTGCAAAGGTGAGCGTGGCA
	2504	TCTGACGCGTGCTTGGGAGTCTAT
15	2505	GAATTACTTGGAGGCGCCGTGCAA
	2506	GATTCTTCCCGACCTAGGTTGGCC
	2507	CGCAGCGTATCCCATGTTGCTTGA
	2508	GAGATGGAATTGTTGCCCCAAAGA
	2509	GATGCCTGGATCGGTCTAGCGTCA
20	2510	GCAGCGACTGCTAAGCTATCTCGG
	2511	AGGGCTAATTTACATCGCCTTGCC
	2512	AAGTGACATCCTCACGAAGCGAT
	2513	TCAGGCAGCCGTAATTAAATGCGC
	2514	CCACTGGGGAAATCGCACTGTTGG
25	2515	TTGTCCAAAGCCACCTACGACAGA
	2516	TGGGCGGAATAGATTGGGTGTCTT
	2517	TAGAATTCGCCTCTTCTAGCCGCC
	2518	CATTACTTCTGCAGATGCGATGC
	2519	GGAAATGCTAGCTGGGGTAATCGC
30	2520	GCCGCCACTTGCGAATCTACATCT
	2521	ACAATAGCGGACAGCTCGCCAGAT
	2522	AGTTAGGCTCTCGGTGCGGTCCAT
	2523	TGGGCCTGAGAAGCGGTTAATAGG
	2524	ACGCTCTGAGCGACGCCTATCGTA
35	2525	CCTGGTGATCGTGTCCCAGACTCA
	2526	GCGTGTCCATTTCGCTTGAGGTTTC
	2527	ATCCTGAACGGCGATGACCACCAC
	2528	TTACGTTTCTCACCGATCAACGCC
	2529	GCCGTCTTGAGTGGCTAAAAGGCA
40	2530	ATCTACGATGCGGCTCGAAGTGTT
	2531	AACCAAGACTCGTCCCCAAACGAA
	2532	AACTGCGGTGGTGGAGGCAGGTGC

5

10

15

20

25

30

35

40

2533	CCTGAGTGGTCGGGCTGGAAAAAT
2534	TGCGATCTTCTCCACCTACAGCGC
2535	AGGCGCTTAGAACCGTGAAGGCAG
2536	TGGAAAATTTGGGAAACGCTGGA
2537	CCAGCGCCGCACCTTCTCCAATAG
2538	TAGACGGCTGGCGAATCTTACGGT
2539	TACCATAACAAGAGAACGAGCCGCA
2540	GTAGCCGAGAGCAATTTTCACCGC
2541	GCAAACCTCCCCTGCCCTTTAGCCT
2542	ATCCCGCTGATAACCGCCAGGATA
2543	AGTCTCAGTTCGGCGCAACGGTAG
2544	AACCTACAGTCGCCGCAATGCATT
2545	ATACACGTTTCAGCCGGCAACAAT
2546	ACGACGGGACGTGCCCTCGTTGAT
2547	AAGTCCAAACTCGAATGGGGCAGT
2548	GATTTATTGGCGCGGTAACGACCT
2549	TGTTTTCAGAGGCTACCCTGCCAT
2550	ACGGTCTCAGGGAAATGCGATCTC
2551	GACTTGAAACCGCCTATGCCCACA
2552	CGATCGGTTGTGTGCTGTCTTACC
2553	AGTAGCACAAATGCCTCATTTCCGC
2554	CTCGCTATCTACGCGTCTCCGAAA
2555	AGCCCGTTACGGCATCTAGGATTC
2556	TCGCGATGGCGAGAGTTCAGAATA
2557	TTACAGGATTCCAAAACCCGCAAA
2558	CGGTACCAACGCGCGGGCATATGA
2559	TGCCAGTATTATCCGTGCCAGCCG
2560	ATTTCAGACCTCGGGACAACCTGG
2561	GAAGTGCGCGTAACTTAGGGAGCC
2562	TTGGCCAGGTCATCACTCTGCCAT
2563	ATCGGCCGGTATTAGCTGCCCTCC
2564	CGCAGGTAAGGCCGAGCAATGTTT
2565	TTGGGAACGTGCTAGGCGGCCCTC
2566	CCGCAAAAGTAGAACAGCCTGGGT
2567	CATCTCGGCACACTGGTGCTGTAT
2568	ACGCGTAAATCAACGACGTGGTCG
2569	CGTAGGTGGTAAATGTTGGCCCAG
2570	GTTGGGATGCTGCTTCACTTTGGG
2571	TTCGAGCCAGAATAAAACGTTTGG
2572	AGAGATATTCGGCCTCGGTCGAGA
2573	CGACAAAGTTTCTCGCGAGCAACT
2574	ATTGCCGCGTCTCGTATCAAAAGA

	2575	CGGAGAATGGATGCAGGTTCTTCG
	2576	TATAATCATTTGCGACTCGCCCCA
	2577	AATTTTCCCCGATTTGAAGAAGCG
	2578	TCGCATACTTCGTGCGCGAGTATT
5	2579	CGTGAGCCGTTCTCATCCAAGCGG
	2580	GCAGAATCGAATTGGGGTGGGTTT
	2581	CTCTCGGTTTCTCAACCGAGCTCG
	2582	GACCAGTTAGTGCAATGGTTGGCG
	2583	TTCTCGCACAGCTAGTCAGCCGAT
10	2584	CCAAGTCTTGCGTGAGCGATCCTG
	2585	GCGAAAGTGGCTCGTATTTCTCCA
	2586	CCTCGGGACTGTCCGACTGAAAAA
	2587	AGGCGAGTGACGGCTCATCCATG
	2588	GCGGCTCTGCCTACGATATTCAACA
15	2589	TGCACCTGTCTGTAGATTTGCGGT
	2590	CATAAAGCACGGACGCGACTTGAT
	2591	CCCTCAACGTAGGGCGTGACTTTC
	2592	GGGTCATCGTGCAATTATGCCGTA
	2593	CCCGGATAATCCTTTGTCCAGCCG
20	2594	TCCGATAAGCGAACTCACATGGGT
	2595	CCTGCTGGTTCGGTCGTAAGCGAA
	2596	GAGGCACCAATCGGTCTGAAAATG
	2597	TACGAAAATGGTTGCGCCGGGTCT
	2598	CCCAAAGATCGTATCACCACCCAA
25	2599	AATTGCCGGAAGCAGTCAGAATCG
	2600	CCGAATCAGCCGTATTTGCTGGAA
	2601	CCCGCTTATCTGTACTCGATCGCA
	2602	TTTTGGGGATCCCTATTAGGCGCA
	2603	AGTGACAGCGCTCACCACGGTCCC
30	2604	CCATGAGTGTTTCGGGACATCGTA
	2605	GCCACATTCTGCTACCTCCGTGTT
	2606	TCCTGTGCTTTGTGACGTGCTAGG
	2607	GACCGCATATACACCTGATGGGCC
	2608	GTAGGCCCGTCGTTAACCATCTCA
35	2609	CGGCTCGCGAAATGGAGTTTAGCG
	2610	GCTGATCGGCTTTTCACCGCTATA
	2611	TATCAAATCGTTGGCACGCGACTA
	2612	TTGGCGAGGATCCCTAGGCGTACT
	2613	AAGTCCTGAGGCCGTTTCGGTTTCT
40	2614	ACTCCGGACATCTCGGCCAGAGAT
	2615	CCAAGGGGAACACAGGATCGTAGA
	2616	GTGGCCTAAATCCGCCTTCTCAAC

5

10

15

20

25

30

35

40

2617	CACTCCGTCTCGTCCATTAATGCG
2618	TCAAGAACCCAGTGCCGGTCAGCA
2619	GAATCAATTTTCCAGGGACGGGAC
2620	GAGAGCATACGCAATGTTCCCTCC
2621	ATCGGTGTGCTGGAGCGCCAGAGT
2622	GCCTCTCCTATGACGATGACCCAC
2623	TGGGCGCGCTTTTAAGACTACATC
2624	CGTTGGGTACCGTTCTATCAACCG
2625	GCAGTGAGCTGGGTTCAATGCTTC
2626	CATCATCCACACAGGCAGGTGTGT
2627	AGACAAAGGTCCCCATTGCGAAAT
2628	ATACTCGTCGACGAGAAGCGGAAA
2629	GCAGAATGTGTTGTCTTCGCAGCC
2630	CACCATGCCTTCATCTTGGCCTAG
2631	ACTCTTCAACGCCAGGTTAAGCCA
2632	GCGACCTGCGGCGTGTGTATTCTC
2633	TCGGTGTATGCACCCTTTCTCCAT
2634	ACCGTCGAATCTTGCGGCCAATGT
2635	TAATGCATGCTCCCGGCTCACGTT
2636	TCTGTACACACCACGTCGTGCACA
2637	CATGGGGTTGTCAGACGACACCTA
2638	AATCTGATGCTCGCTGTAGGACGG
2639	TCGAAACCGCGGGAAAGGGTAAAA
2640	CGCTAGGGCCTAGGGGCACAGACA
2641	TGGGGGACGGGCGTCTAATCCTCC
2642	AGGCATGCACCCATGCTGCCAGAG
2643	TCCCAATGGCCTGTCAAGCATAAA
2644	GAACCTGAGCCTTTGCTAGCACGA
2645	CGAATTGATAGCGTTACGGGCGAA
2646	TTGCACGCGCGCGAACGACTATTC
2647	TGCGGTGAAGCAGTCCAAGGTCAG
2648	TGAGGACCATCCAATGGATCGGTT
2649	TCGGTGATTGGTAATTTGGATCCG
2650	GCGGGCAGGTAGTTTGAAGGATG
2651	CAAGCACAAGCCCATGAAATTTCA
2652	CGGTACAGCGGATAGCCAAGGATA
2653	CCATGCTCTTCGCTGCAGCATACT
2654	CGCGGCAAAGATTAATTCCCGGCG
2655	GAAGACCCGTCCGGGTTTCCATAC
2656	CTGGCAAGGAGGATGTGGCTCGTG
2657	CTGTGCAGGGGGTGGCTCTGTTGA
2658	TTCAATAATGATCACGAGGCCCCA

5

10

15

20

25

30

35

40

2659	TGGTGATGCGAAGCCTTACCTTTG
2660	CTGCCACCATCTACGGCGCAGTCT
2661	TTTGCCAGCTCTCGCAGAAGTTA
2662	AATTCAGACGCCACATCGACGGTC
2663	CCGTGGTCTGCCTCGATTACCTAC
2664	GGCGAGGAATTTGGAACCTTATG
2665	ATCCGATGATCAGATACCGGCTGG
2666	CCATAGACTAGCGCCAGAGTGCCC
2667	TGTGGACCTAGAAAATTGCCAGCC
2668	GAATAATCATCGCGGTCCTCATGG
2669	GGGATTGGCTCTTGGTTGGAAGAA
2670	ATTGTGCTTCCTCGAACTGGGAAA
2671	TGCCCCACCCCGTAAGTCAATAAT
2672	TCAGGACCGACGGTGCACTTAGTG
2673	CCAGCCGTACAGTGCAATTTCCG
2674	CTTAAAGAGGCGCGAAGCACAAACA
2675	TACCGCTCGTCGCGATCACAATGA
2676	CCGAGTGCGCGAAGTGTCTATGTG
2677	GCACCAGTGCCCGATCAAAACGTA
2678	TGCAGGCTTCTCAACGGCTGGGAG
2679	CTCCGTACGTATCCCGCGTGATAC
2680	GGAAGTGCAACTTAAAGCCCCGCC
2681	CGAACC GG CAGTCGATCGTTGCAT
2682	CCGTTAGTGGTCGACAGTTCGGTT
2683	TCAGGCTACGCCCTCAGCACTACA
2684	TATACGGGCCGAGGTCCGTATTG
2685	CCAACGTGTGACGAAGGGCCATTG
2686	CTGCTCAGCGGTGCTTGAAAGACA
2687	GGAGATTGACTTCGCGTTTTACCA
2688	ATGGTTCAGAAGGTTCTCGGGTT
2689	GAGTGGAGCATTCTCGGCCCTCAA
2690	TGGATTGGAACCAATCCCGCACAA
2691	TGCTCTTGTGGTCACTCGAGAGGA
2692	TTGGGAGCACGGTTACCGCCTGTG
2693	CAACGCGAGCTAACGGTAGTTTCG
2694	AACGCTGAGCGCTCACCTTCACCT
2695	CCGTCGTAGATCTGGAGGCTTCAA
2696	GGATGGCATGGGCACACTGTAACC
2697	TCGCTCGTAGATATCCTTCACGCC
2698	GGAGCAATACCGCGTCCAAAACAC
2699	CGGTGTGCTTCAAATGCCAAAGGA
2700	TTGTT CAGACTTAGGCGCTGCCCA



5

10

15

20

25

30

35

40

2701	CGGCGGTACTCTTTCCACTGTCCT
2702	AAGACGATTGCCACGTGCCAGAG
2703	AGGTGAGCGCAGGCATATTGCAGT
2704	CTCGGGCCTGTACAGCAAAGCCGT
2705	TGCGCGCTAGTGCTGCCTATGATC
2706	CCATCCTTTGCCTTGAGGGTAAGG
2707	AACAACAGCGTAAGACGGACAGGG
2708	GAGGCGGTGAGGCTCACAATATT
2709	CGAGGTTAGACGCCTATGACCCAC
2710	AACTTGCTATACCGGGCGCAGCAA
2711	CGCGGTGAATCGCATACACAGCGC
2712	CACCGAATCAAGCCATATGGCTCT
2713	TTACAGCTATCCTAGGCGCTGCC
2714	AGAAGCGCGAAGTGTAACCCCGCAT
2715	TGCATGGTATTTGCGTGCGATAGG
2716	GGCCGGACCTATGTGAGATGGAAA
2717	TCAACCTGAGTCCTGATCCCAAGC
2718	TGCTTACCGTTCAGGGAGGCGTGT
2719	GGAGAGTTACGCGATGAGCCACCT
2720	CGGTATGCGGTGTACAGCTTTCGT
2721	GTAAGCCGGGTCTCGTGTCGCCGT
2722	GCGTAGTGCGAACGCCCCGACCTA
2723	TCCTCGCGGCTTACGTCAAATTCG
2724	CGACGTTCAAAGCGGGAGAGGAGG
2725	CGAGGCACCCCGACATGTTGAGAT
2726	CTATTTCTGTGCCGCGTCGGACAAG
2727	GGCTGCTCAGTGACGTGTCAACTG
2728	ATCACTCGTGCGTACCCGACCGTC
2729	CGAGATGTCCTATACCGTGCGGAA
2730	TCACACCGAGCCCCATAAATGAAA
2731	AGCTACGTGTCTCGAGCAAAAAGCG
2732	TCAGGGCGAGTTTTTTTCAGCGGCG
2733	TTCTGTTCTGTCTATTTTTGCCCGG
2734	TGGTATGCCCAGGATCCAGCCTAC
2735	TCTCAGTCGTTAGGCCAATGGCGG
2736	AAAGATCACCGTGAGCGATCGGC
2737	TAGCAGGACTTGCACTCGTGATGC
2738	TGCCCACGGTACCGTTCAAGGCTG
2739	TGAGGTGCGTCGCCCTAAGTAATG
2740	AGCAAGGGTTACAACCCGCAACCC
2741	CACAACAGCCAGTATTGCCCACAA
2742	GGCAACACCATACTCGACGAGCTC

5

10

15

20

25

30

35

40

2743	GGCTGGATTGACAATTTAGCCCCT
2744	CGTGAGAAATGCTACACGCGTCAG
2745	CGCATCTGCCCCATTTTGTCCTT
2746	GTCGGCCTAGTCGGCAGAACGGTG
2747	TCGACACGCGTAGCAGCGTGGACA
2748	TCCCTCACCTTCCAAAAATGTGCT
2749	GGGCAAGAACATGAGAACAGACCG
2750	TCGTCCTGGTACGACTTGCGTAGA
2751	TGGCGGTTGCATGTGATGATCAAG
2752	CCTCGCGTGAGTAAAAACCGTCCG
2753	ACTTCGCCACAGAATGCGGCCAG
2754	GTGTAGAGCTTGGGTAGCCCCGTT
2755	CGCAGCATCCGAGTTAACACACAT
2756	ATGAGCCTGGGATGATCCGCTGGT
2757	CCTGGCATAAGTGCCGACATGCTT
2758	GCGCATGAAAACTACGACGGACG
2759	AAAGATGGGTGATGGGAGCGTCT
2760	ATCCTGGGCACGAGCGGATTTATC
2761	TCACCGCATTTGATAGTTACGCGA
2762	TGGTGGAGCGGACTCTGGTGTTAT
2763	CACAATGAAAAACAATGGCCCCA
2764	CCTTGCCGCGCTTGTGGTACCAAC
2765	CCGAGACCTTTGCCACACGAAAGA
2766	ACCGCGGTGTACACCTGAGCAGGC
2767	GTCGTACGCTTACCGCAGCGGAGA
2768	TCGTAATTTGACCGACACACGCAG
2769	CCTAGACGGATACCCTGAGCGGAA
2770	AAGCGACAGCAGAGGTTCAATCGC
2771	GCGTGGACGATATCACCTGGGCGT
2772	GTCGGAGAGCCAGTGGTACGGCTT
2773	TACCCTCCGGACCAGCTGTAATGA
2774	TATCCGCACGGTATAGCAGTTGCA
2775	CATCAGTCGGGCTACCTTCAGCCT
2776	CGGATTAATGCCTTTCTCGGAAT
2777	TTCGTGCTGCCAAGCTAATGCAAG
2778	CCACTACGGATCAGCACAGGTGTC
2779	GGCCGAGACCACAGTAACAGGTT
2780	CGCGCGGAAGCATTGAAGTTACTA
2781	TCGGCTTACCGCTTCGTCTGACTT
2782	GACTGACGTCAAGGCAAGCAACAC
2783	AGAGGAAGGAGGGGCTGTGACAGA
2784	TTCCAATGCGAGAGATGGCAGGCT

	2785	AAATGGGGTGCTTCGAATATGTCG
	2786	GCTGTCGGATTATTGCACGCCTGT
	2787	CCGACTTTGTTTATGTTGCTGGCG
5	2788	GCTGCGATATAACCCGTCCCAGAA
	2789	TGAGCTGGGCGTCAACTCCGAAGA
	2790	CCCAAGCATCCTAAATCTCCCTCG
	2791	CGACAGCAATCCACATGCATTCTT
	2792	TGAATGGTCGGGAAACCAATGCAT
10	2793	CTTTGCATCGAGATGCGGGGTAGC
	2794	TCCATTTCTCCGCAACTCTCAGG
	2795	CCACTACGCCATCCTGACAACGAG
	2796	TAGTAAGGCCAATGTACGCCGTCC
	2797	GTCATGCATATGGGGCCTGTTTC
15	2798	ACCGGTAGACGTTAGCGGGTCAA
	2799	TTGGTTCAAACGGCCACACGTCTC
	2800	GACACAACTGCAAGGGAGGCATG
	2801	CTCGAGCGCTGTCATCATATCGGC
	2802	GCGGCTAAGGCACAAGTAGACGTG
	2803	ACAGCCTAAATGGCGCAAGACCGA
20	2804	GCCAAATGCTTGAATTTGCTTCG
	2805	CCGATGATGTAAGCCGTCCGCCCT
	2806	AGGAGCAAACAAACGCCAGTGACA
	2807	ACGAATTGGGTAGCCGGACTGAGA
	2808	CTGTTCCAGTTCGGCAAGTGCGGC
25	2809	AGACAAGTCAGGAACGCGTTTCCG
	2810	AGACGACGGCCAGATACGCTGCCA
	2811	AGGAAGCGCTTCTCCGGTTCTTC
	2812	GATGGACGCAAACACAAGGCGATC
	2813	CGCATAGCAGTCTCCGCATCTTGG
30	2814	TGGTTCGGGTGTGCAACAGATAAA
	2815	CCGTATGCCACCTCCAGAACTCAA
	2816	GTAAAGGAACCCCTCGGGAATCCT
	2817	GCCTGATGCTCGTTAAAATTGCGT
	2818	TCGCACTTGGACCATGAGATCTGA
35	2819	TTCTCAGGCTGGGCAAGAGTCTGT
	2820	CGGACCTGGGGATGCTGGGATTAC
	2821	TCGAGCCGATAGGGTTGGCATTGC
	2822	TACGTGTGTCCACACACGTCGTA
	2823	TGTGAAATTCGCGTTTCGCATCTT
40	2824	TTGCAATGCTCCAAAAAACTGCC
	2825	TCTCATCATGGCTGTGGCTTTGAC
	2826	ATTACACCGCTTGGTTTGGAGTGG

5

10

15

20

25

30

35

40

2827	GCCGTGCAATGCACAGAGTTCAAG
2828	GAGATCAGACCGTGTCCGATGCTG
2829	CCACCTATCTTGATGCGACCTGGA
2830	CCGATCGCCGTTTATGTCTACGGC
2831	GAAAATCACGGTAAGGCACGTTTCG
2832	GATTCTCGCTTCCCAACGAGCATA
2833	CCAGAGCAGCATTCCACAATGGTG
2834	TGTGAAATGTGGCAGTCTCAGGGA
2835	CGATCCTGCGTGCCTCATCCAGGC
2836	CCCTCAAGTGGGCGAGGGTTTTCA
2837	TCGCCTCCGCCTCGTGTGTAGAAG
2838	TTCGCTTTCAGCTCATTGGAACGA
2839	TGTAATCTGAACAAGCGGACCCCT
2840	TGGAATCTTCTTGAGCGCCGTGA
2841	GGCTTTCATCTTTAACCGCTCGGT
2842	TGATCCGAGCCATTCTAATCACC
2843	TGGTAGGCGTGATGTCCTACGCAA
2844	AGGCATCGGTAAGAAGGCCCTATG
2845	CGCCGCGAGACGATCCTTATTATT
2846	ACATGGACGAAATTACGCCCGTCA
2847	ACAGAAAGGTGGGGAGCCTAGCGT
2848	AGGCTTGCGAACATGGGTAGTGAC
2849	GCGTGGGCCTTGCTCCTGTTTAAC
2850	GAATACAGAGCGTCCGATGTGCCC
2851	GCGACTCTGTAGGGAGCGCGATAT
2852	GGTGCACTCATATGCGTCGCATCG
2853	CTGTCCACGGGGAAACCTTACTT
2854	TGGCTTACTGTCGCAATCTAGGCC
2855	GCACTCAGTTTCCGGTATCCCATG
2856	GTGAGGTTACGTAAGGCACAGCG
2857	GTAACGCCTTTGTCCCCAGCGTAT
2858	GCATTGATATGGTCGGTCTCGCCT
2859	GTGGGTTTAAAGTGACAACGGACGC
2860	CAAAACCCTGCCGAAGATGTTGGT
2861	TCCGAGGAGACTGAACCTGCTACC
2862	CGGGGAAGAACGATTTCGCTAAAT
2863	TGGTTAGCTTATGTCGGAGCCACC
2864	ACGCGTCGATGAACTAAGGCTCGC
2865	TTCTCCTGACGAGTACGCAGTGGG
2866	TCCGCGGTTGCCGTTTGTTAGGA
2867	TGCGCATCTTTCAGGGGATGATG
2868	TCTTTGGTCCTTGGTGTTTACGCG

5

10

15

20

25

30

35

40

2869	GAGAACTCCCGCTACAAAGGAGCC
2870	TTAACGTGGGAACCGTTGGTGAAT
2871	GGGACACCATCCTTGGGTTTGTTA
2872	CAACAAACCGCCTTGGGAAGTGAC
2873	TTGAAGGCCACCGATACTGATCGC
2874	TCGTAATAGAACTGCGCCCAATGC
2875	GGCACGTTGCCCAAGTTGGATCCA
2876	ACATAGCTTGGCCGGACACCCACC
2877	CTTGCCGCCTTGCGAGTGGCTAAA
2878	AGTTCCGCGTCCTACTTCAACGCT
2879	AATGGCTCGCCAGATACCGCAGCC
2880	CAAAAGGCGTGTCCGAACTTTTCA
2881	CGTCCACTTAGGTGGAGATACGCC
2882	GAGCCTCTTCGTCCTGAAGACCGA
2883	AACATCAAGCGGCAATCTCCCTTC
2884	CGTCCTGACATTATTAGCGCGTGC
2885	TGTGCAGACCCTAACGACCTACGG
2886	TTAGGTCGGCCTAGACCCCTCCGTA
2887	TCACATCGCTTAACTGAGCGCATT
2888	AGACCTTCCCACGCGAGATGCTAC
2889	TTCTTGCCAAAATGTGTCCAACCA
2890	CAGTTTTCAATTGCAGCGAAAGCAA
2891	GTGCCGATCCCGAGACAAGTTCCG
2892	CATCCGGCCTCAGTGATTCTTACC
2893	TGCTGGAAGCCACAAACGTTACGT
2894	GAACGGCCAGGGGACAACCTATCGT
2895	TCATCTAGGTCTGAAGCGCAAGACA
2896	TTTGGTTACCAGCACCCATGTTCC
2897	GACAACAGTCTGTCCGCCACATCC
2898	GCCAACAGGAGATGCTTGCACCAT
2899	CTAAGGACGCATTGACCCCTGAAC
2900	GGTCGCGTAGTGAGTCAGAGGCGT
2901	TTACCTCATGAACCCTTCGCGGCG
2902	TATACAGCATCGTCGCCGGGCATA
2903	GCTTAGTGGCGTCTTCGTCGTAGG
2904	TGCACTCCGCAACCTTGTGAAATC
2905	AACCCGTCATGCCGACTCCATCTA
2906	AGCACTAGTGGCGTGCGACTTTGC
2907	TAAAAAGTGCCGCTAACCACGGAG
2908	CGCGGAATATTTGTCGTCCGATTC
2909	TTCTGCTATGCGTATGGGGGCCCG
2910	CGAACTACTGCGTCAGCCTCTCCC

5

10

15

20

25

30

35

40

2911	AGATGACGAATTAGCGGGGTTGGG
2912	AATAACAGTGGCAATGAGCGGGAA
2913	ATATGTTGATTCCCGTGCTGCACA
2914	AGAGTGGGCACCACCAGGCAGACA
2915	AGGCCTGGGTTTCTGCGTCTTAGT
2916	ATGACTTCAGGCACCTCAGCACCT
2917	CGGACGTGACAAACGGACATACCC
2918	CAAGTGTTTCGGCCCAACTCTCGA
2919	GAACCCTTATCGGGATAGGCCCAA
2920	CAGGACGATACCAAGCAGAACGCC
2921	GCGTCTTGTGATTCTGCCCTAACC
2922	AAACAACCATCAATGTCGGGTCCA
2923	TGTAAAGACCAGTTGGCGGCTCTC
2924	GCGTTTTGACTCGGTGGTCAGTCC
2925	TGTATGGAGGCACGGCAAAGTCTT
2926	TTACCTAGGTTCCCGCTGACACGC
2927	CGGCTCGTGGGAATCCTCTGAAGA
2928	CCGGCTCGGGCATTCTTGACCT
2929	CAACGATGGAATTGTCTCCTTGGG
2930	CGGGCTATTATCGGGATTATGGGG
2931	ACGTACCTGAAGATGCAACGGCGG
2932	CATGGTGCAGCACGCACAAGTAAC
2933	CGTCGATATGTCGGGCTATTGCCT
2934	AAATGCAGGGTTAAGAGGAGGCC
2935	TGCAAGGACTGATTCTCCCGCTGT
2936	GTTTTCGGAACGCCGCAGAGTTCA
2937	CCCTCGATGGTTCATTGGGAAGAC
2938	CCTGTTGCTCATAATGGTGGGGT
2939	GAAAGAACGATCGCGGAATAGCTG
2940	TCCACCTGTGTGCCTTTATCCTCA
2941	TCCTCCGTGAACCGCTGTAGCGCA
2942	GCCCCAGAGAGTCCCTGCTCCCTA
2943	TTGAGATTTTTACGGTTTCCCCGC
2944	CGATAGGACGTGGGCATGTCCCAG
2945	CCCGAACTTTGAGATCCGAGAACA
2946	TCACGCAGCTAGAGTCGCGTTACC
2947	AGATAACGCCCACTGACGACATGC
2948	ACGCTTAGAGCTCCGATGCCGAAT
2949	GGGCGATAACTTAAATTGTGCCGC
2950	AGGACGTTTCATGCGTCTCTTGCA
2951	CGGCTGGTAGAACTGTGCATCGTA
2952	TTCGAAATGTACTTCCCACGCGGA

5

10

15

20

25

30

35

40

2953	GCAGGTTGGCTGTCTTGTGGAGTC
2954	CGTTTGGTTGCTTCAAGAACCGGT
2955	CATACTTGGTTGTTGTGCCACGC
2956	GGGGTCGGCTGAAGTGTATCC
2957	GTGACGTTGATTAACGACCGTGG
2958	CTTATGGCAGCGCCAGGGGCACTC
2959	GTTAGGGGACCCACCTCGTTTGAT
2960	CAATATAAATGCCGCGCATCGAGT
2961	TTCTTCATCAGCAGTCCCCGAGAA
2962	AGTTGCGTCCCTTGATGGCATTIT
2963	CCGACTTTCGTCCACGATTCCTCT
2964	ACTTGGCCGGACGACAGCAAAGAC
2965	CACCGCGGTAGATGTATCCCTTCC
2966	GTTAGCTTTAGCTCGGCACGCCTG
2967	GCGCATAAGAAGGTCCGCTAAAGC
2968	ACATCATCACGCCTGGCGTGACCA
2969	CCGGCGAAGTTTGGTGTGATTAGA
2970	TGGGAAGGCAACATGAAAGTCCTT
2971	TGCACCGCCAGATTGTGCTGAGTC
2972	ACATGTGAAGTGAGTGCCGTCCAA
2973	CCTCTGGAGGGGATTAGCCACGCT
2974	CAATAGCCATGTCACTGGCAACGG
2975	ACCCATGGTTCCAACGTTCTTTCG
2976	AATCTGGTCTTGGCATCCTCCAAA
2977	GTATACCGGTGCATGCTGAAGCAA
2978	AGTGTCTGTTTCGAGTCGACCCG
2979	CGGGTATTGACACACACGAGGAC
2980	AGTGCAACAGAGCGCTTGGTCACG
2981	TGCACCTATAGTTTGGTGCCGGTG
2982	TGCTCACGTACCAGGACACTCGAG
2983	AGTCCACACCTCGAACGACAGGCG
2984	CGCCGACCTGGTCAAAGAGCGCTA
2985	GCCTAAGGGCCTGTCGTTTTCCGA
2986	TGTGCGTGCTTATGTTCCGGTCTC
2987	CAACCGTTGGCCGTAACAAAATC
2988	CGAGAATCAAGGCGTACCATCTCG
2989	GCGTAGGCAGCCTCCAGGGAATGG
2990	GATGGTGTTCGCCAAGACCAAT
2991	CAAGCTAGGGACAGAATTGCCAC
2992	TAAATAGGCGAAACCGTTCGTGGC
2993	TCAAGACCCGCAATGTGTTCATGT
2994	GCGGCTGGTAGACTCTTGCACAA

5

10

15

20

25

30

35

40

2995	CAGGCGTAAACCTGAACCAAACGG
2996	GCCGATCTGTGCTGAGGTTTCATCA
2997	GATATCGCGTCGCAATATCACGCG
2998	CCCTGCACGATTAAGCCACCTGTA
2999	TGACATACAGATTTGTGTGGCCCC
3000	GTTTGC GGCCGGTATTACGATGT
3001	TTTTACCTGGCCATTGGTGAGCTC
3002	CTCTACTCAATCAGGGTGGGAGCG
3003	GGGTTGGAGGGAGTCTTGACCATT
3004	CGAGGTCGGTAAGGAAAAGCTTGC
3005	CTTTACGCAGGCACCTCCGAGCTG
3006	CATTGTATGGCCACGTGATTGACG
3007	GTACGGTGCGAGAGCGCCTAAGCG
3008	TTCCATATGCCGAAATGGACACAA
3009	TACGCCTTCCGCTATAGCTCGTGA
3010	CTGGCCGCTCGGCTAGCCATCAAT
3011	CTGTACGCCACGCATGAAGGGTGA
3012	CTTACGCGTCCAATGACTGCCACC
3013	CACATGGTAGAACTCGATCGGCAG
3014	CGCACCGGAAACTAGTGGATGTGT
3015	ACTATGGCAACCGACACTTGGTCC
3016	CTAGTTTGCGCTACCCACCTGCAA
3017	TAGTATCGCCGACAATAGCCTGG
3018	CCAATATTTACGGCCTGATCAGCG
3019	ATGGCTATCCCTTACTGGCTCGCC
3020	CAAAACTTGGCAGGCTTGGGACTT
3021	AATGACCGAGGCTGCAAGATTGAC
3022	ATCATCTTTTCGCCACCAGACATGG
3023	CGTTATTACCGATGCACACGTTGC
3024	CACACTGGCAATCGCCTCCCTCGT
3025	AGGTTGGTAGGAAATCGGAGCGCT
3026	GCTGAACCACTGTGGTCAAGATGC
3027	CGTTGAGTACGACACGGTCGAGGT
3028	TTTTTCCGCCGCAATGTGATCTAA
3029	ACAATACCTCGACCGCTCAGCATC
3030	AGTATCCCTGCTGGCATAACGCGG
3031	TCTTGGGCTCGGTAGTTCAGCACT
3032	CCCTATATCGAGCCCATAGGGCGA
3033	CACGAGTGGCATCAACGGCCTACT
3034	TGCAGGGTCCGATGTGTTCAAGTA
3035	GCTTGACCGCTGCTAACCTCGTAC
3036	TTTTGCATCTCTCCACCATCCAGA



5

10

15

20

25

30

35

40

3037	AGAATGTGCACCGGCTTCCATCTT
3038	TGTTATGACCCGCTCTGTGGCGTG
3039	GGAGCTCCTGTTTCATCGAGGCTA
3040	CATTTTGCTGTTTGGGGTCCCAT
3041	CCCGCTCCTTCACGTGAGACGAGA
3042	GCGCTCAAGTCGATTGCCACAACC
3043	CGGTTGACGGAGACCGCAGTACTT
3044	ACTCAAGACCGGTGCACCTCCAGC
3045	TGGATGTGAGCGTGTCTGAGTTT
3046	TTTCGTGTGCATGCAAGTAATGGC
3047	GCGGCGTTAGCTCGAGCTAACAAA
3048	GGGTATCCTGCCCAGCAGTAATT
3049	GGCTCCGAATCTCTTGTCCGGTCT
3050	AGGATGGCCACGCCGAATCAAAGT
3051	GTGCGGGGACGTTTACATAACGAG
3052	ACTTTTGACCTGAGGCCGCTTGCA
3053	ACTCCGCTTCAATGGAGACCGTTG
3054	GATCGGAATTCGCCGCCATATTGA
3055	ATGCGTGCCCATGGAATGACTTTT
3056	CCGCATCGCACGAAGGCAGGTCAT
3057	CACCCTATGCGTCTCCAATTCCTG
3058	TGATATGCATCGCTGAGCCTCTGT
3059	AGCTTCACACGCTCACTGAACCTG
3060	AACCCGGAACCTCCTCTCACTCGG
3061	CTCGTCAAACCTTGCCGAGGAGTC
3062	GTAGCTGGCAACAGGCAATCAGGA
3063	CTTGTCACGAATATTCGCCAAGCG
3064	CAGTATCTGAAACACGGGGTGCTG
3065	GGCTAAAATGGGCGCCACGTGTA
3066	ATGAGAGCCAAGCGCCTCAACTCC
3067	TATTGTTAGGCACCGCTTCGCGCT
3068	GGAAGTAGATTGCCAGTGCTCGCC
3069	AGTCGACCCCAAGGCAACTGGGTC
3070	GGTACTGTTAGCTCGACGATGGCC
3071	CCGCAATACTTGACGGTAACAGGG
3072	AATTCGGGTTTGAACGGTTGGAA
3073	GACACGCAATCGGGTCTATGCGAA
3074	GATTTTGGCGTCTCATTGCGTGAT
3075	TGCCATAGGGAGGAAACGCAATTA
3076	GAGGTGCCCATGTTAGTGGTGTCC
3077	GCTTTAGCGGTCATACGACCACCA
3078	CCGCTACCAACAATCCGATTAACG

5

10

15

20

25

30

35

40

3079	CATAGTGGGCTGAAACCCCAGGAA
3080	GAGGATCTGGCCACATCGAGAAAG
3081	CTCGTTTGGTACCACGTTTTGCCG
3082	AATACACGCGGCGTAAACAGACGA
3083	TGTCATGGGCCAAATGACAGTGGC
3084	ACAGCACTTCCGACCCGTGTACGA
3085	CTCCGTAAAGAGCACAGCTTTGCC
3086	ACGAACAGGTAGGGATCGGTCCTC
3087	TGGATCCACCTTACCGCGCCATCG
3088	AGTATCAAATAGCGGCGCGGCAAG
3089	GAATTACATTGTGGATGGAGGCGG
3090	CTCCTCGGGGAGTCGAGGAGTACG
3091	AGTGTCGAGCCAACTCCCACCAAT
3092	AAATGACATCCGTTTGGCCACAGC
3093	CGAATCATATCGCCATCGAACTGG
3094	TATAATGCACTCGCTTGGTGCGCA
3095	GCCAAGCAGATGGTAATTATGGCG
3096	CACGCGGGAAGAGCACGTAGAACT
3097	TACCCGAGAATTTGGAGAACAGCG
3098	TGACGGCAAACGTGGCATCTATC
3099	CACAGTGTTCCAGCCCTTGACGAT
3100	TACCCGCCCACACATGAAAGTTGG
3101	TGGCATATTTAAGATTCGGCGACG
3102	ACTGAAAAAAGAACGGGTAGCGGG
3103	TCTGACCGCAATAGGTGGTCATTG
3104	ACTTTTTGGCGGGCCCTCTCTCGT
3105	CTGCCCAGATCATTGCGCGATCCG
3106	CGGAGGTAAATGCTTTAACCGGC
3107	AGGCGTCTCCAAACGTCCTTCTGT
3108	AGATGCTATCCTGAGTGGGCCTGC
3109	ACAGGGTGAAGAGACCGTGGGATG
3110	GACTGTCTAACGGACGACACGACG
3111	AGCTGTTAGGACCCGACAACCGGT
3112	TTGCGTAGTGTGGGCATTTCTCT
3113	ATGCGCGCTTCTTTCCTTGATGTA
3114	TTAAGGGCGTCCGCGTCTATTAG
3115	ACCTTTAACTTGTACCGCGGCCC
3116	AGGGATGCAGAGGCACCACATGTT
3117	CGGTTGACGTATGAGCATCCGCA
3118	CAGGGCGATAGTCACATGGAGGTT
3119	GCTTGACTGCCCCGTTTCATATGT
3120	CGAAGGGGTTGTGCAATTACCCGA

	3121	AAAACGCACCGCAATGACAAAATT
	3122	ATTCCTGGACAAGACCCTCAACCG
	3123	CCTACCTGCCTGCTAGCGGTGAGG
5	3124	GCTCGTAAATGGGGAGGAATTGGA
	3125	ACATGAAAACAGGCTCAATTGGGG
	3126	GTTCCGCACATGGATTGAGGTCTC
	3127	GGCACCCAATACCACGAAGAAGAA
	3128	AGGGGCATTTCGAACTCCATCTTT
10	3129	CATCATCACAAGGAACGTCGGTG
	3130	TAAAGACCCACCGTCAGCAGCAGC
	3131	CCCCAGGCGTAATGCACCACATAG
	3132	GCAGGTCGAACGCTAGTGGTTGAA
	3133	GGAACCTAGGAGTTCACGTCGCCA
	3134	GCAGATACGGCTAGCTGAGGTGGC
15	3135	CACAGGCCTAGAGCCTCGGCGTTC
	3136	GTTTTGCGCGCATGAGGTTCTTA
	3137	TTGCGCCTGATGCCAGCAGTACTA
	3138	GATATCAGGCTTTCCCACTGCCGC
	3139	TGCGCGGAGACGGAGATCTATGAA
20	3140	CATTGGTGTTGGCTGAGAGTGGAC
	3141	GTCGGCACTTGGGCACCATTAATA
	3142	ATCGATCGGTGTCTACCACGGAG
	3143	CGTAGCCTTCCACCGTGTGATAG
	3144	CGCTCTCCGTCTGAGGAAAAGGGG
25	3145	TCGCCCCAGCCAAGGATATATTGC
	3146	TCTCTTGCAAGGAACTCTGCCGTC
	3147	GTCTTGACAGACGGAGGGTGTTA
	3148	GCCAAATTAAGCGGGCTCGTAATC
	3149	CCATTTGTTGACCGATGGGAGGGG
30	3150	TGGTCAAAAGAGCACGATCCAGGA
	3151	CGCTACTAAGACGCCCCTGTCCAC
	3152	CATACCTCCCGCTTGGATTCACTG
	3153	CCGCGGAAGGAATGTCATCTACAA
	3154	CACGGGACATTCATTCACAGGACG
35	3155	ACTAGTGAGGCGTGAGGCGGGCGT
	3156	AGGAGTCACCCACTCCGCACAAAA
	3157	TCATGACAGCGCACCCCATACCAT
	3158	GGTAGGGGACTATCGATCGTGCTG
	3159	ATGTCTCACTACCGCACGTAGCGG
40	3160	TACTGCTCCGGTCTTCCGCAGCTT
	3161	ACGGAGGAGCGACTCGTTCGCTGC
	3162	GAAGTCTGTCGCCGGTGGACGGAC

5

10

15

20

25

30

35

40

3163	CCGTAACGTGTATTCGGACGAGCG
3164	CGTGGAAGCGACTTAACCAATCGT
3165	GGCATGGGCTATGCCTCACACTAG
3166	GGGTCGTATTTTCAGCATCGTTCGT
3167	AATGGTCGCGCAAACCGTAAGAAT
3168	CTGGATTCGGTACGTCCAACGTTT
3169	CGCAAAAACACCCGTAGCCAAGAA
3170	TATGGATACGCTTTTGGACTGGGC
3171	GCTTCAAACGCGCTTCACGCTGGT
3172	TACAGCCCGCTCTACCTCGCCACC
3173	TCAACCGATGTCAAAATGCACGTT
3174	AGCTCTCTCCGAAGTAGGGCGGTA
3175	ACGCACACATGGAGACTTGGCTCC
3176	TTCTTGAAAGCTAGTGGGGCGCTA
3177	CAATCACGGCTGGGCTATTCTGTG
3178	GTGGCGACCCGTCGGTGAAAGAGT
3179	CGTCGAATGCCGAACCAGTTAAGT
3180	TGCGTATTTGCATGCTCACAGCTG
3181	CGCAGTTGGTTTGTGCACGGCTGC
3182	GTTTTTCCGTGAAAACCTGGCATCG
3183	ACAGGTTCTCCACCACGATTTGA
3184	CTAGCGCGCTTTTAGGTCCTTGCG
3185	CAAAATCAAAGGGATCAACCGGTG
3186	AACGTAACCCCAGTGAGTCAGGCA
3187	TCAACCGGTGCACTTTAGAACGCC
3188	ATCGCAAAGTTGCAGGCGAATACT
3189	ATATGTCCCTGGGTGCTGCACAAC
3190	TGGCACTTTGTAGTGCTGCGGTGG
3191	ACGCACGACGTCCTTCTAAGCTCG
3192	CCCACGTGCACTATAGGGATTTCG
3193	CCGCGCTTGGTCAGTCATCCTTGC
3194	AGCGGCTCAGGGAATAACAACAGG
3195	ACAACGCGATCGGAGGCAACCAGT
3196	AGCAATTGCCTCCGTAGAAACCCA
3197	GAGTCGTGGCATCGCCTGCTATCG
3198	TCTATGCAAATACTGCGCTTGCGA
3199	TCAGCTTAAGTTACGGTGTGGCCG
3200	TCCAAGGTCGAACAGGGATCAGAA
3201	GTTAGGCTGGCGTCAATAGCGCTT
3202	GGTGTATAAGGAAGAGGGCATCG
3203	CCGGCGGGCTAGATCAATATTTCT
3204	CTAACGTCAAGTTTTACGCCCCGA

	3205	GCAGCACAGTTTTCCGATTTGCGG
	3206	CGCACGCAAGGGGAGGGATGACTG
	3207	CGGGGCCGAAAAGGACGTCACAAG
	3208	TTCTCCAACACGGCTAACC GG TAG
5	3209	TTACAGCCTGGCCCGAGGTAGTTG
	3210	TTTCGGGCAGCATGAGTTATCGAA
	3211	CTACTGGACGCCCTGCTTCGAAGT
	3212	GGTCGTCCGACGTGAAAAGACCAA
	3213	GTTTTCGAGCTCTTTCTCCGCAGG
10	3214	GCGTGAAGGTACCCAGTGTCACAG
	3215	TTTCTGAACGCTTCGACGCAACAC
	3216	TGCTAATAAGCACGCCTAGCCCGT
	3217	AAATTAATTGTGGTGGCTCCGGCG
	3218	TTACAATCCTCGGGCTCACTGACA
15	3219	GCTGAAGGACAAGGCGTGGGCAAC
	3220	GGGATAGGAGACCCTCGCAATGGT
	3221	TTGCAGTACGTCCTTGCGCATGAA
	3222	TTGATCACTGGATTGGGTGCGAAC
	3223	TCTGCAGACGTTGCGAGAGATGAT
20	3224	AGTCTAGCAGGGATCGAAGCGGAT
	3225	GGGGTCCCGCAACAAC TAATGAAG
	3226	CAACCTCTTATGTGGTGTGCGCGA
	3227	CTCGCTGGGTTGCTGGAGTAGCAC
	3228	CGTTGTATTGTGCAACGCGAAGTT
25	3229	GGGCTCAAAGTGCCTGAGTCGAAA
	3230	CTGCTGTGCCCTCTCAGTGAGAGC
	3231	CGGACGTA CTGTTCCGAGTCCTCA
	3232	GTATACCACCATACCGGGACCGCA
	3233	CTGCTGCGAAGGGAGACACGTCCG
30	3234	AAAGAACGTGGAGGATCCATTGGG
	3235	TCGATTGGCTGATCTCCAGCCTAC
	3236	CTGCGAATTCGAAGGTTGTTACGG
	3237	GCAGGAGGGTCAGGAGTACGTGAG
	3238	ACCAACGGAAGGGA ACTTAAGGGC
35	3239	ATGATGGAGGCTGCGTTTTGGTCG
	3240	AAGCCCAATTTACCGCTCCGAATA
	3241	CTAGGCTGTGCGGACTAGAGGTG
	3242	TGCCATCTGACCTGGTGATTGCGT
	3243	GTCGTCAACTTTTATCGCGCACCT
40	3244	TTGAATGTAGGCTGCTGCAAGCGC
	3245	CACCTATCGTGGCCTCTGTCCCAG
	3246	GGAGCGCCCAGTATAATGAACGTG

5

10

15

20

25

30

35

40

3247	AATGGGGGTTCTTAGGGTGCCGTA
3248	GCCATGAGGAAAAGCACTGGGTCT
3249	TCCGGGTCGTACTGTGTATGATCG
3250	GGAGGTTATGTGCTGCTGATGACG
3251	CTTCAGCCGTGAATGGTGTGAAAG
3252	CTTCAAGGGCTTCGTCTGCTCGTG
3253	TCAGGGGTCACGCATTGGGTTTCA
3254	ACGGTCCTCGCATAATGGACCACT
3255	AGGCGTAAACGCCGGTCATAGTCT
3256	GATCTGGTCGGAAAACAGGAGCGC
3257	CCCATCGATGTTATTTCCGACGCA
3258	TGTTTCTCCGCATCAGTACCGCAT
3259	CGGACCCGGATCGACAAGTAGTCA
3260	AGCCAGAGCATGAACTGGAGCGTC
3261	TGGAGTTTACATCGGAACGCAGGG
3262	TCGACCACCGGTACGATACAATCA
3263	GCTTGTGGAATTCCGACGGTTCCA
3264	CACATCCACCCTACTGAGGCACAA
3265	GCCGGATGAATCTGCCTCGCTACA
3266	GGTTGCAATTACGCCGGGATTAAA
3267	ATTTCTCGCAAATCGTCTGGGTG
3268	GCTCCTACGCCATGTGCACGTTTA
3269	AGGGTTGTGAAACATGGGGGTGA
3270	ACGCGACCTGCTGTCAGCGTGGTG
3271	CGCCTAACTAGGGGAGTGAACGGA
3272	GTTGACCTCCGGATTTGCTCACGA
3273	TACCTCCGTCATTCACTTTCCCG
3274	GGCGTTCCACATGTAATTGGGTCT
3275	CGCATCACGATCGTTAGGAGGGAG
3276	GGGCATTAAGCACGCACTTCGTCA
3277	TTTCCATAATTGACACCACGCGG
3278	GACCATGAGATGCTTTTCTTGCGC
3279	CGCGGTCGTCCTCAGAGAATGTTG
3280	TGCTGTGACGATGGCTCCTACCCG
3281	GGCGAATGCTTCTTCGCATCAAGT
3282	AAATGCACAGCGGAACTGACCACA
3283	TATCGACCTGGAACACGATCGGTT
3284	CATTGAAGTCATGAAGCCTGGTGG
3285	CTTTCAACCGTAGTGGCTTGGGCA
3286	CCGGTAAGGTGCAATTGGAGCCTA
3287	GGATTGAAAAATCGCCGGAAGATC
3288	TGAAATTGTGAGGGAGCCTTAGCG

5

10

15

20

25

30

35

40

3289	AGCGGGATCCCAGAGTTTCGAAAA
3290	CGAGTGTCAGTGGTCGGTTGCTCA
3291	GCAGCATCCGTTCCCCTATAGTGG
3292	GTATTCCTGACCGGCTGAGTGTGG
3293	GCAGCGTATGGGGTTAGCCAATGA
3294	CGCCCTGGTGGAGTTGTATGATGA
3295	AGGTAGACTGCCCCGCGCAGAGCA
3296	ATGCGTGAGGAACTGACTTCGGAC
3297	ACGGGAGAGGACATGCATTTTCAA
3298	ATTCATGCAGGAAGTCCGAGGGAA
3299	AGCTCTCTCCGAAGTAGGGCGGTA
3300	TGGCCACATGATTGGAGCTCCAA
3301	GCCCTTTGCTTGCAATTGATTGATC
3302	AGGAGATTCTTCGGCTCATCTCGC
3303	GCAGCTCCGCCAACGAACTTATAG
3304	TGGGTCAGCTTCGGCCAGGCTGAT
3305	ACGCTCAGCGTGCGCTAGATACGA
3306	GCAACGAGAGCGAACGGTTAACTC
3307	GAACACAAACAGAGGTCGTCAGCG
3308	CGTGCGTTAGCGTCGGCGTATGTT
3309	GTGCTAGCCGAAAGTAGCGTGCGA
3310	CGCGGAGGTTTGCAAGTTGTTAAC
3311	TACTGCCCGGCCTGAAATGACTTA
3312	CATGCGCACATGAGGGTCACCTTT
3313	CTCGGGTTCTGAAAGCGATGCTTC
3314	GGCACACAACGAAGGCTGATGATA
3315	GGAGGCCGAGTAACCTTGAGGGTC
3316	ATTCCTATCGCGCGTGCTTCTAGC
3317	TTGCCGGTGTGTTCTGTGAGCTGTT
3318	TTATGGGAATCTACAAAGGGCCGG
3319	GGGTGATCCAAAATCCACGGAGGC
3320	GCGAGATGAGCAAATTGTATCCCG
3321	CCTGCACACATCATGTCTCAATGC
3322	GGCAGCGTAGGGATTTCTAGGGG
3323	AGAGATTGCTCCTATGTCGGCAGC
3324	CCAATACCCTGGTGACCACTCCAA
3325	GACGTCTGTTATGTCGTCGCAAGG
3326	CCACAACGTCGAAATGACCTACCA
3327	CTTGGTGGCATGCATGCCTTGCCC
3328	TACGTTGCCCCGACGTGGAATAAA
3329	GGAAGAGAAAACCGACAGTCGCGA
3330	GACGAACAAGAATTTGGGGCAACC

5

10

15

20

25

30

35

40

3331	CGTGCCCGCGAGTTCATGGTGCTA
3332	AAGAGAAACCCCTTCCGGAGCTCA
3333	TTTTAAATCTGCCGCCCTTCCATG
3334	TCTGAAGCAATTTGGCCTCCTCAA
3335	GATGCGCAAGAGGGTATTATGGGC
3336	GTGAAAATCTCGCAACTTCCTGGC
3337	ACGGGAAGCGGTGAATTGTTGGTA
3338	GCCCTACTATTGCCTTGGCAATGA
3339	GTAAATGGCAGGAAGCGGCTCTCG
3340	AGGTGCCAAATAGTGGACTGCGGT
3341	TCGGATGGTAGGAGGCGAGATCGG
3342	GAGGTGAAGGAACAGCGACGCTAA
3343	ACCGTCGTTACCGCTCTGGTGTCG
3344	TTCCAATGTCCGACATGCTATGCC
3345	CGGCTTTATAGGTCCAACATGGCG
3346	CCGGCCTGGAAGCAGAGTTATTG
3347	TTTATCGTTCAACGCTCACGTCCC
3348	AGACCCGCTGAACGGAGCTTGGAT
3349	ATCCATCAGGAGAAAGCTGGCTCA
3350	TTGCCAATGCGTAAATCGGTTCTC
3351	GCTTGGCAGAAGGCGTACACTAGG
3352	AGGCTCCAATGCTTTAGCCGCAA
3353	GATACTAGGAGCGAGCCCCTTTGG
3354	GTCGTGTGCAGCCGCATATGGAGG
3355	TACCCCTGTTGCGGATAGATGTCG
3356	TAGGGTAACAGAATGAGGGGCGCT
3357	ATCGTGTCGGGGATCGAATTTGAG
3358	ATCTCTCGTGCGGTCTTGCAAG
3359	AGAAGCCACATGTTAGTGCGGGAG
3360	ATCTGCGTTAACTGTCCCGACTGG
3361	CGCTCACAACGAGCTTACTCATGG
3362	TCTACGCTACGATCCGTTGCATCA
3363	TTTAACACCGAAATGGGAGCGTCC
3364	ACAGGGCGTAGTAGGCCGCTTTCC
3365	GTCGACCGTGTTTGTGGGGGATAT
3366	AGAAGACCTTGGCAATCCGAGTCA
3367	TTGGGTGCTTAAATGCGGTCTGA
3368	AGCGAAGTCGTATTGACGTGCGGT
3369	ACTTTCAGCTCCCAGTAGCACGCA
3370	GCGCATGGTGAGTCCGTATTGCCG
3371	GGGTCGTGTCAGAGGACAAACACC
3372	ACAAGAGGACCTCCGGGTGAAAAT



5

10

15

20

25

30

35

40

3373	TAGCGGGGACCTATCCGCCTCAGT
3374	GCTCTATGCCATGTCCGTGGATTG
3375	AGCTCATAATGCGCGTTGACCCCG
3376	ACAGTGGAACGTTTCATGCCGAG
3377	GGTTTCGACGAAAAGGATGGTCGT
3378	GCGGTACGTATTCTAACCCGACGG
3379	GGTATTCGCCATGCTTGGTCTCTG
3380	GAGCCTCTCCGATTCTGGCCGAGA
3381	TGGAACGTAATACGAACGCCGAAC
3382	GGCAGAAGTGGAAGTGAAGTCTGAT
3383	CGGGTAGGCCTTCAGGGTACAGGT
3384	AGCGATCTTGGACGCCGGCACGAT
3385	GACCAGGTTGGTACAACGCCTTGG
3386	GATGTGCTACAGGACCGCTACGC
3387	TGAGGCGCACTCATTAGGAGGTGT
3388	CACCTTACATCCCGAATCCGCGTA
3389	CCAAACATAAGGTGTGTCGGTCCA
3390	GCGTTTGCTAATGGTTGCGATTGC
3391	CCCTTGCCCTCAATCTGTATTGCA
3392	ATAGTCCCGTGGCGACTGTGATCC
3393	GAAGTTCGCGCCCGAGTAACATA
3394	GGGAGCCACGACAGAGCTCCTAGG
3395	CTGACTCTTACGAAGCGCACTCGC
3396	AGGTATAGCGGGGCGTCTAGCAAA
3397	TAAGACGCATTGCTTGGACCATCC
3398	GCCTAGTAGGCCACGGCTTCATGC
3399	CGTGCCCTAGCATACAACGTTGGG
3400	GGGAATGCGGCAGTCTGTCTACCT
3401	GTTGAAATACTGGCCCCGCGGGAC
3402	CGGACAGGTGAACCCAGTCACCTT
3403	CAACAGCCCGCTCCTTGGATATAA
3404	TTAAAGGAATCAGGGGGACCCGCC
3405	CGGGTTGTAACGCTGTTGGACGAA
3406	GGTACGCAGCGGGACCAATAGAAA
3407	ACTGCAAGCCTCTTAGTTCCTGCG
3408	TCAATACCACCCAGAACTGGGCG
3409	GGCAGTTGACACTCATCGACCATC
3410	TAGCACGGCCATAAGACGGTTGAA
3411	TCCACAATGTCAGCTCACTGCAAA
3412	CAGGCGGAGGGGTTTTACATCCTA
3413	AGGGCACTCGAAGATCCGACGGGC
3414	CGCAATGCCTTTTGCTGTGGTAAT

5

10

15

20

25

30

35

40

3415	AGAAACGCAGACGTGGCGTTTTGT
3416	TGAGCACGAATGTGGAACAGTCAA
3417	CTCGTTTCCATGGGGTAACCGACT
3418	CCTCATAGCTACGGGTGGACGACG
3419	GTACGCCGTGTATCACCCATTCA
3420	ACCCATAGTTCGTGATAGCGCGA
3421	TCTGCAGTGTTGCCCTCCGACGC
3422	TGCACATGCAACTAATAGGTGCGC
3423	CAGCGCAGTGCCTTACCAATATGA
3424	TTACGCGCCGAAAAACACCTGAACA
3425	CTCCCTCGCTTTATATAGGCGGCG
3426	GTCGGACCCCGAGAGTCCTGTAA
3427	ATCGACGAACAGGGCCTCCGGCTT
3428	TGGTTTTTCACCTCCGTCCTCAAG
3429	GGAGGGGGCCAACTCCTTGACTTG
3430	TCCTGTCTCGGCCTTTGGGAATT
3431	CAAGCCATTACCCGCTAGCTGAAA
3432	CGCAACCGACATTATATTTTCGGCC
3433	TTGAGGGCGACTGCAACACACAGG
3434	GCTCGAGTAACACGGTTGACCCGA
3435	CAGCCCTAGCGCCACGGTAAAATC
3436	GTCATTAGCGACTTACCCGCCGTA
3437	CCCAGTGGCCGGCCCTAGATAATA
3438	CATTCCGTATGCTACTCGCGAACA
3439	AAGTTTTAACGCTCAAGGGGGCCT
3440	TTGGCGGTTTCGGTACAGGATCCT
3441	TACTGCGATGATGGGGATTTGACA
3442	CGGTGAGCGAAGATCATCCCCTTA
3443	ATGCAAGTCACCGACCGGCACCTC
3444	CAAGTGCCGCAATTGGCCTTTTAT
3445	CCCGTGGTGGATACCTGGGTAAGC
3446	CCGTCAGGGTCTAAGGACCAGGGT
3447	CTTCCGTAGGCGGTGATTTCCAA
3448	GCTGAACTGAGATGGTATCCGGC
3449	CCAACGAGACAGCATGAAGCTCCT
3450	ATAAGTTCGTGGGCCGCAAGGTC
3451	GTGGCCAGGCCATAACTGGTCACT
3452	CGCTTAGCGCGAGACTCTGAGGGC
3453	AAGAGCGGCGCCCTAGAACCCAAC
3454	CCACGGGAACGTCTACGAAATGAT
3455	AGTCGTGTATCAGGTGCCGAGAGG
3456	TGAAGCGGCTGGCGATAAGTAGAT

	3457	CTGAGGACGTGCGGTTTCATGCTGA
	3458	GAAGGCGTTCGGAAAGTTTTTCGT
	3459	AAGAAAACACCGCTGAGACCTGA
	3460	TCAGCCGCTGTTGCAGGGAGAAAA
5	3461	TTCTGGAAATGGATCGGATAGGCA
	3462	GGGAAATGGTCTTGTGGCGACCA
	3463	GGTGTCGAAGCCACGATGTATCCC
	3464	CCCCGACTCCCTTCGGGCATAAGT
	3465	CCAAATGCGATAACGCAGCGTGAT
10	3466	GCTCGCCAACGTACGAGGCTCAGA
	3467	GGCTTATCAGTCGCCACCAGAGAC
	3468	GATGTGACCCATCCATTCCTGGGA
	3469	TCCTGGTTTGGTATCCCCGAATCA
	3470	CGCCCCGTATATAGCCGGTAAGAG
15	3471	GGTTCAGTGTAAACGATCGCGGCAC
	3472	CCGGTATAGAGGAAACCCGGACGT
	3473	CCTCCCAGGAGATCCTACGCAATT
	3474	TGAAACTCGTCACGCTCCTTGCA
	3475	TGTTGCGTAACCACCAACCCTCCT
20	3476	GCAGCGCAACCTTGTACTTCTTGC
	3477	CGCAAGTGGGAGCCCAAGAGTTTG
	3478	TGCAGGGTAACGAGGGTAAGTGGG
	3479	GAACTGTAGGGTCTCGCCGGTCAA
	3480	CGAGATGTCCAGCAGCGGTTGTTA
25	3481	TTGTGGTTGCTCCGGGTAAAAGGA
	3482	TCTACGCATCCCTGGGTAATTTGC
	3483	AGAAGCTGCGAGTCACCGTGACTC
	3484	GGGCGGTGTTGAAGGGCTCTATAC
	3485	TTCCACAACGGGTGAGTAGGACGG
30	3486	GCAGCCAGACTGGCCTACCGATCG
	3487	CCCGCCGAGTTGGTTGGCTAAACA
	3488	GCTAGGGTGGTCCTTTCAGTGGGT
	3489	CGTGACTCTCCTTCTTTTCGGCAG
	3490	ACTGCCCATGGGCCACTAGGCTTG
35	3491	GGCGTACGAAAAGGCCAATCACTT
	3492	ACTTGTGGTCGACAACGATGTGGC
	3493	CCACCACCCCTGACCCGAAAAAAT
	3494	TGTTGTGCATCACAACATCAGGCC
	3495	GACCACCCGGTAAAGAGGGATGGT
40	3496	GCCACCCCTGAAGCACTCGTTATG
	3497	GCTACCAGTTGGAAGACGGGTTGC
	3498	CAACGTTTCGCATCCCACAGTTGTA

	3499	TATCGGGTCGTAATGGGCAAAGAG
	3500	TCGGTGTGATTGATGGATAACGCC
	3501	AGAGGTCGAGAGCCCGATAACCTG
5	3502	GTAGTTAGGCGCGGCCCTGGCTCA
	3503	TGATTCTCGATGTCACGCCGAACA
	3504	GATGGTTCGCCCTTGTGTGCGCAGC
	3505	GCGCAGTTACGTCCATTGTCCAC
	3506	CCGCCTGATTTAACAAGCCAAGGT
10	3507	GACCAAGTGCAGGCGTCAGTCTGG
	3508	CAAAAAAGCAATTCGCCCTGGACG
	3509	ACTGACCTTCTCGCTCTCTCCGTG
	3510	CTCGCCGTGTATCGCTAACCCTCT
	3511	CGGCATTTTTCACATGCTGTGTTG
	3512	ACGTAACGCCTGATGGGGTACACC
15	3513	CCCTGTGACCGTGGGAGACACACA
	3514	GCGCATACTCTGGGTAGTCGGCAC
	3515	TCCCCTGCCCATCTCTGAGTTAGG
	3516	TGCAGCGCTAACATAGCGGGTGCA
	3517	GCAGCGTCCACAGGAAACCGCAGC
20	3518	AGCGTACCATCGATGGGGATTCTGA
	3519	TGGCCTCGCGATCACCACGATGTT
	3520	TTGGTAATCACTCGGCCAGCGCTA
	3521	CGTTAGTAACGATCGTCGGTGCAA
	3522	AATCGCAGATGGTTCGTGGCACAA
25	3523	TAAAGCGTCTAGAGGCCGGCTGTG
	3524	TGGCTAAACGAACTGGGAATCGG
	3525	CCTATGCAGCCACTGGTGTCTTC
	3526	ACGTGAGATCCAAGGGTGGCTCCT
	3527	TAAACGCCAAAAACCACGAGCAGG
30	3528	CCATGGAATGGAAAGCATTGGACG
	3529	ATGATCCCTGGGCTTAGTCGCCTT
	3530	ACCGTATGCCTCAACAGAGTGGCT
	3531	CCACCAAATCGCATAAGCTCCACC
	3532	TCTCAGTTTAATCCCGTGATCGGG
35	3533	AAAGGACTACGCCCATCGCTCACA
	3534	CGGGAAGAAAGGCCTAAAGCTTTG
	3535	TTTTGGACATTTTCTGCATCGGG
	3536	GCAGGGGTCCTTTTCCACGGTAAT
	3537	TCAAATAGGGCGTAGGCAAGCTTG
40	3538	ATGAAGTTCCATCCTGTCCGGGCC
	3539	AGAATGATTAAGCGCAAACGCAGC
	3540	GGCAGCAGAGAGTGGCCTAGTTCC

5

10

15

20

25

30

35

40

3541	GTGCAGAGCCGGCCTTATGTAAGA
3542	CATACGGGTATGGCGATGGTTACC
3543	AAGAACAGGAACCGCTGACAAGGA
3544	GATGTGTGTCGCGTCCTTAAGGGC
3545	TATCCATGTAAGGCTCCTGAGGCG
3546	AGTTTTTTCCTAAACGATCCGCGC
3547	CTGACCGGACGACCCAGAATGTAT
3548	GCATGTGGTCAAAGCTTGTCGATG
3549	CAGAAGTGCATGGGTTCGGATGAA
3550	ATAGCGTACCGGAGGGCTTACCAG
3551	AAGACTTGGCGCTTGTTGGGTAAGG
3552	TATTGTGGCGCCTCACGCGCAATC
3553	TCGGCCATGGGATTTCAAAAGTC
3554	TGGTCGGTGCCGTTTCACCTTTAC
3555	CATTTCCGCGGGCAGGAGAAAGAT
3556	CCTGAGTCGCGATACGACTCAACA
3557	AGGTGTACCGCCGTCGGGTTATAC
3558	TCCTTGTACGAGCCAAGCCTGGGT
3559	AGAAGCCCGAAGTCCCGTGTAGAC
3560	AGAGGGGCCCTTAGGCAAATACGT
3561	ATGCGGCAACATCCGATCGTAGAT
3562	CGCAGTGGGCAGTAAAGACAGAGG
3563	TCGGGTAGTGCAAACCTCAATCGT
3564	TCTTCACTGTGGTGGACTTGGGG
3565	GTCCCAGGGCGATTGGTACTAAGG
3566	GGTAGATCCAGCCATTGGGACCTC
3567	GGGGATTGTGCGCTCCAAGGACCC
3568	CTCTGTCCTAGACTGAGCCGTCGC
3569	CGATGAACAAATGAGTGCGTGTGA
3570	GAGGTCGAGCTGCCTGAGAGGAGT
3571	CAGTGGGACTGCTAACGTGGGTCA
3572	GAGTCGCTCGAGGAACTACGGCCG
3573	CGGCTACGGAATGATGCAGGATGG
3574	TCGCTCTCGCTATGGCAATTCTGG
3575	TGAATCACGGCCCTCTCTGGTACA
3576	CAGGTGCCATCGAGCGCTTTAGTG
3577	TGGGAAAATCGAAATCGTCAGGAA
3578	CGGGGAGGAAGATGTTCCAGCGGT
3579	TGTGGACCGGTGGTCACGTCTTTT
3580	GCACGTCTCGCAATCTGCGATCAG
3581	CCTAATGCCGTATCAGCGACCAGA
3582	ATAACGCGGGTGAAGGATTCTGTCT

5

10

15

20

25

30

35

40

3583	TTCAACCTTGTGGGGCGTCCCACT
3584	CTACTTCCAAATCTCCGCGTCGGT
3585	AGCGAACGCACTGCCAGTGGATAC
3586	GAAAGTGGCGGCGAGGAAAAACAC
3587	CAGGGGGCGCATATTTGACAGATT
3588	TAACTCGCTGCCCTCAACTCAGGG
3589	TCGATTGTTGGGTCTACCGTGGTT
3590	GCTGGGATTAGTGCCGGGTAACCG
3591	TGGTTGCAACATCGCGCTATTACG
3592	GGGCGTGCTTTGAGCTGAAGCGTG
3593	ATGTTGAGGTTAGTCCCCGACCGT
3594	GACCGCGTAGTTAGCAATGTTGCG
3595	CCAACCCACTGACATCGATGGAAA
3596	TGCTGCTATTGTGCGACCGATATG
3597	TACAAAGAATCGGGACCTGCGACT
3598	GCGCCTCATCCCGCATCGAATTAT
3599	CGAGGGATTTTGACCACTGGATGA
3600	TGATAGGCATACGCGGAGAAGTCC
3601	CGAGTTGTCAACGGCCATCGAATT
3602	CCCGCACCGGATTATTAACGAACC
3603	TCGTCCTTGGGTCCCATGTAGAAA
3604	TCACGAAGCATCTTTGCGACGTAA
3605	TGTAAGTTGCCAACTTTGCGGGTT
3606	GCACACCACCGGCAGATATCAAGA
3607	GTGTGGTTTGTGAATGCGTGGTGA
3608	CAGCTGCGGCCCCACCTTCGATAC
3609	CAGCGAAGGACGACTACTGTGCAC
3610	CAGCAGTTCGTTGCTTCCTGATTG
3611	AAACAATGGAGTGTACCTCCCGCA
3612	ACTATACGAGCATCATGAGCCGGC
3613	CTTGATAAGGTGGGATTCCGGGCA
3614	TTTAGTAGAACGCTGCGCGCGGTG
3615	AACTGACGTTGAATAAAACCGGCG
3616	GCTTTGTTCTACCGCGGATCATCA
3617	TGATATGCAGCGGCTCGGCCTTAT
3618	CGGGAGTGCGTTTATGTCCATGAT
3619	CAAATACCGGGAACGGATCGAAGC
3620	GATCAAGCCGAATGCTTTGCAAAG
3621	AGAGAGGATGCGCTCCGGTTAGAG
3622	CTTAGTCAGCATACCCGCGGGCAG
3623	GTGTCTCGGGGCGCAGGACCTGTA
3624	AACGCTCCACTGCCGTGATTCACT

5

10

15

20

25

30

35

40

3625	GATCGTTGAGTCATCCCGTGGAGT
3626	CCTGGCCGGGTGCAATACTACAGT
3627	CGTAGCCCGAACGTAAGGGTCAGC
3628	CTGTGGCTTCAAGAGGATCCGTTG
3629	CTTGGGTGCGGTGTAATGTCCTCGA
3630	GCCGTTGTGCGCTATTCTTACGGA
3631	TCGCACGATGGCTAGAACGAGTAA
3632	ATTTGTTGCAATGGGATGGCTCTG
3633	CGAATATCCGCTCGAACCTGACAA
3634	AAGTGGCGTGCGTCATAGCGCGAC
3635	TGATGTCCCTCCACACCGTGAAC
3636	CAAATGAAGTCGGGGCCAATATTG
3637	GATGCATAGCGTGATTCCGGTGTA
3638	GTGACCGTAGAAGCTCACCAGGGC
3639	ATAAGGACATATTCGGCCTGGGGA
3640	AGATCTCACAACCGGAACCGGACG
3641	GTTGCGTTTGGGGGCGTCATACAA
3642	TGTGAGGTTTTCTAAGGCGAACG
3643	CATCTTGGTTTGCGAACGAACTCA
3644	TTCCTGTCACAGATTCGTGGCCTT
3645	AACCTACCGATCCCTGAACGTGCA
3646	CCTATTCTGGACATGCGGCCACAT
3647	GTCGATGGGGAGCTCCAGTTGCAT
3648	CGACCGTGAGGGTCCATACGTAGA
3649	TCTCGTTTGCACGCAACTGGGCCA
3650	ACTCCGCCGAATGAAGGAATAGCT
3651	CCTCGACCTGGCGTGATGGAAGGC
3652	TAACAGCCGTTTTGCGGTTACAA
3653	GCCTCCTGCAGTACGGTGTCTGTT
3654	GGCAGTCGGTCCCCTTAGTTCTGA
3655	TAATCCACGGCTTTGGTGAAGTC
3656	CGGTGCAAGATCCTGGTTGTGTGA
3657	TTTCACCACTACCTTAGGTCGGCG
3658	CATCCCGTACCGGGAGGACAAGTC
3659	ACGAGGTAAAGGGATCCGTGCTGG
3660	CTAATAGTTTGGCAGAGGGGCGCT
3661	AGCATGGTAACCCTGAGCCAGCAG
3662	GGAATCCTTGTGGGAACAGCCGAT
3663	CTGATGTGGGAAAGAGGGTGGGAC
3664	ACTTTTGAATCCCGGCGTTGTA
3665	GCGATGACGTGACGAGTTCTCACC
3666	CCAGGTATTGAGCCCCGCCATATA

5

10

15

20

25

30

35

40

3667	TTGGACGTCCTCCGAATATTGGCA
3668	GGTAAGTGCGGGAAGTACGCTGAC
3669	CCGCCTGAACCGTCGTAGGGATTA
3670	CGTTTTTGAGTAAGGATTGGGCGA
3671	TGTGGTATTGAGGCATAGGTGGCA
3672	TCCGGAAGGAAGGCGCGATATGGC
3673	GTTGAGCGAATCGGACGGCTTTAC
3674	TGAGTCTCCGAACGACAAGCGATC
3675	AGTGAAGAGGGAGAGTCCAACCCG
3676	GTGAAGCCTGACGAATCCAACGTG
3677	GTGCAGGCCTGTATCCCCATGACT
3678	GTGGGTTTCCTACACACCGGATGA
3679	GCGCCGTCGACTCTCTTCAGCTGC
3680	CTAGGCCTGCCATCACTGAGCAAT
3681	TTGGTGATGACTCATGGCCAGACC
3682	TATCTCCCGCGGGGTATATTACCG
3683	CCGAGGGACACGTATCCCTGTTCCG
3684	TATCCCGCAGCACGCATTGATCT
3685	TGATGATAGAGCAGGGTGCCGTCA
3686	GTAGGAGCACACATTCGGATTCGG
3687	CCCTTACTACGCCCAGCCCTTTTG
3688	GTACCAGGGGGTGTGCTCCAAGGG
3689	TGACCAGGCGGACCAGACGGTTTT
3690	CGTAAGCGGCGGTAGGTGTGCTAC
3691	CGCGGGGAGGGATCAGCAGTTTTG
3692	AAAGCGTATCCAGAAAGGCCATGG
3693	AAGAAGAGACGCATGCTTGACGT
3694	TGGCCATTTGCGGGAGGTGGCTTA
3695	AACGCCGAATTGAGGAGGCGGTTA
3696	GCCTCATTACGACATTGGCAGCAT
3697	TCGAACGCGATTTTGAAATGCC
3698	AGGAATTCTAGCCGAAAGCCCTGC
3699	TCCGCTGGTTGGGTGCTCTGGTTG
3700	GTCCGCTCCGTCCGATAGTATGA
3701	TGTGCAAGGACGGATGATTGCACT
3702	GGACAAGCGGCAACCTGGGAGAAG
3703	ATGCGGTGGCTACGGACTAATCCA
3704	TGCACGCAGGTGGAAAGCAGGCTT
3705	AGATTGTGGGAGTTGTCACGCTCC
3706	AACAGCAGTGAGGGCTGAAGCTTG
3707	CTGCCTGTTTCCTTCACGCTCCAT
3708	CCAATCCACTTGAGTCAACTTGCG



5

10

15

20

25

30

35

40

3709	CATTCTACCGCCCAACTTTTGCAA
3710	CGGAGAACCATGCTGAGCAGTCCA
3711	GACTGTTCCCTCCAGAAAGGCGCAT
3712	AAATAATTGCTCCACGCGAAGCGC
3713	GGGCCTGGAAGACCAACCAAATAC
3714	ACGACGCGAGCACGTAGATATCAA
3715	TACGGGATCCTCGTGGCTACATCT
3716	CAAAGTCTCCCCGACCGAGTTGAC
3717	CCCGAGGCGAAGATCTCTAGGCAC
3718	CAAAATTCTCGCCACGAGACCCTA
3719	CTGTGCGCATTCCAAACACATCAC
3720	CATGGAAATGCCAGCTGCCTCCAT
3721	CGCGAAACCACAGTCCTCGTCGGG
3722	GTCCGCAGCTGTCCCGACATTGGT
3723	GTCTCATTGGGACGATCGTCTCGA
3724	AGAGCGTTGCATGCTTGGCTGCGG
3725	CTTCCGCCCTGTTCGCAATGAGG
3726	TTGCGGTTCATACCGAAGCCAACA
3727	TGCGCGAGAATCGTTCGTACGACG
3728	TGTATACCGTAGGCGTCCGTGGGG
3729	TGCGGGGTATAGGGCTTCCTTATG
3730	ATCCCAGCCCAAGCAGCAGACGCA
3731	GTTCTTGCCACAGGAATGGCCGT
3732	CACATGGGCATTAATTGCTACGGC
3733	ATAAGTCGGTCTGCCTGGCAATGA
3734	ACCTCGAGGCTGAGAACGTCAAAA
3735	GCGGAACGCTAGCCCCTTATGGTT
3736	TGCGAGGCTCCTGGAGCAATCCAA
3737	ACAGAAGGGCGATCGCTCTGGCTG
3738	GGTTGGCAAGGGGCCAGCTCCTAC
3739	ATCGCTTCGCTCTATGGAGTCCGA
3740	CGTCCCGATAGGCCGCCTTGATCT
3741	GAATTCTGAGGCGGCATTGTCCAC
3742	CAGCCCATCAGTATCGGCTGCGTA
3743	TGGAGAGTCGGATCCGTAGCGTCA
3744	TGGATCCAGTGCGAGTCTTGGCCG
3745	ATGCGGTCGTGCTTGAATCCTCT
3746	ATCGCACTGCCGCGTCATAACAGC
3747	CACGTCTCCGCCGGAACACAACCTG
3748	AAGACAGTGGGTGAACGCACGGTA
3749	ACGCGCATAGGTGGTCAAACATCG
3750	CCCGGCGGTAGAAATTGACAACCT

5

0

5

10

25

30

35

40

3751	AAGGGATACTCAGGCGCCTGTTTT
3752	CTTCTCTCTTGTGCGGGCTCCCGT
3753	TTGAAGGGACCTGCCAAATGGCGA
3754	ACGCATGACGACGTCCAGTACGGG
3755	AAATGGATGTTACGCCGGCAAGCT
3756	TCGTGCGAGGCCTCTTCGGCATACT
3757	TACATCGCGTCGAGTCATTCTTGG
3758	TCACACCACATAATGGCACCACGT
3759	CAGGTTACGGTTGAGGAGTGCGA
3760	GGTGTACACCGCTTCGTTGTCCT
3761	ACAATAATAAGGGAGCATCGGCCG
3762	TCGGGTCCTATGATCCAGTCCCAA
3763	ACCCATTCTCTCTGCGGCGATCAA
3764	TCGCAGGTGTAGACGGACGAAAAG
3765	CTCTTGCGTAGTAATCGGCCCGCA
3766	TTCCGTGTCACGCGAGCCTGCTTT
3767	ACTCTAAGTAGGGCTGGGTGCGGA
3768	TTGGTGGCTGTAAAGGTGCTTGGC
3769	CCGAATTACCCATTACATACGGCAC
3770	GATGGATAGGTTGCTTCCCGCAA
3771	ATGACGGAAAGAATGTGATTCGGC
3772	ACGGTTCGGCTTCTGTTAGTCACG
3773	GGATCCCGTAATTGAGGCGGCCAC
3774	ACCCGTAAAGTCGACGCCTGCGGG
3775	TTCGATGTGAACGGTTGGCCAACC
3776	TCGATCGGGAGTCTACCGCCATGT
3777	AGCAACGAGTTTATGAGCGCAGGA
3778	TGGGAAACGAATGGGTGGCGGTTG
3779	TCTGTGTTGCCCCACCTACAGCAA
3780	CCTGCATTGGATGTACCCGCGGGT
3781	GAACGAGGTCCGGGTTTGCATCTC
3782	GGCGCCGAAGCAGAACGACCATAT
3783	AGGCATCACGCATCAGGTACTTGG
3784	TTTACAAAAGCATCGGCCCTGGGA
3785	CCCAGGCGGTCAACCAATTGTAGA
3786	CTGCAGCACGTGCCTGAAATTCGT
3787	CCGTTTTGCTCCAGCTATGAGCGT
3788	ATTTGTGCCGATTGGGGTTATTC
3789	TAAGCAGAAAGCCGCAACTCCGGT
3790	GCGACTGATATAGTGCTCGGACCG
3791	AACTCTATTCTGACACCGCCCGAA
3792	GTGCGCTCCAAGAAGAAACACACC

5

0

15

20

25

30

35

40

3793	ACGACCAGCGGTCTGAGATCTAGG
3794	ATCCCCTCCTCAGGTCGACGCTGT
3795	TGACATACGCGTCACCCAGCACAG
3796	TAACCGCGACTCTGACTCCCTTGT
3797	AAGCGGTTTGATCTGTGCAATCGG
3798	CTGTCAACTCGGTCGTCCGCACAG
3799	AACTTTGCCGTTTAGGGCAGGTGA
3800	GCTGAAGAACTCCCAATTGCTGG
3801	AAGATGCGATGGGTCAGTCCTCGT
3802	ACCCACCTCTGAAGGTTGAGACGG
3803	AGGCTACGCACCCTCGAGAGTGAC
3804	CGGTCACGAACGTGGTCCAGTTTT
3805	CAAAGCAACGCGCGCCACTTAAAA
3806	ACGAGGAAGGAACTGATCCCCAGT
3807	TTCGCCACTATGGGCTCAGCATT
3808	CGCTCGGCAGAGGAGTCCACTCAC
3809	TGTTGGCACGACTCCGTCCATGAA
3810	TGCCTACCCGGTGATTGCGACATC
3811	CAACGGTCGGATCTGAGGAGATCT
3812	CGTTACGAAGCGAAGTTCCCGAGT
3813	AGTGACGGCCAAAGTCGCCATTCT
3814	ATTCAGCTGGGCATAGGCGATGGG
3815	TAGGACAGCGTGGCTGGCTACACA
3816	AATTTGTCCAGCTCTGCACGACCG
3817	TGAGTGGGCTGTGATCCGTTCCAC
3818	TGTGGTGACACGCCAGAGCTGGTT
3819	CCTCACAGGTGTGAGAGGAGCCGC
3820	AGTCCCGCTTCTGCAAATTCGAA
3821	TCTGCGCCTACCCGTAAGCTGAAC
3822	GCCTCCTGAGTTGATTGATGCATG
3823	CCTAACGGTTGGTTCCGCGTTTTT
3824	TCGCAAACCCACGAATGAGTCCCG
3825	AGTGCTAAGGTGGGCGAGCAGAGG
3826	CTGGAGACTGCGATGGCAGGGTTG
3827	AAGGGATAGTGATGGCGATGGACG
3828	CTATCCACGGTGATGTCCGCCATT
3829	CGGACTAGAACTTGCCAAGCACGA
3830	AGAGCCGGATGGCATTGCATGAAC
3831	AGTTGGCTAGCGGTCGAATGAGCA
3832	GCATGCGGTCACCGCTTCATCTAA
3833	GTGAGATTCCAAGCTCGCCGGTGA
3834	GCCATCCACCGCACCAATGAACGCT

5

0

15

20

25

30

35

40

3835	GGGTGGTCCTCACTGTGGTTGGCA
3836	AGGCGGCTACGACGAGCGTCGTTA
3837	GCCAAGTGATCGTGCTTCCGCGTA
3838	TAGCCGTTTATTCCCTTGATGCGC
3839	ACTATGTGGGACGAGCGTCTGCGA
3840	GCACCTTCGAGAACCCATCAGATG
3841	ATTTTCTGTACCGATGCTCACCGG
3842	CACTGGAGCAATAAATGGCCAGGC
3843	GGGTTACGTATCTCATGGATGCG
3844	GCACGCTCCCAGTATGCTCCTTCA
3845	GAAGGGACTTAGTCCGCGGCCCTC
3846	TTCGTTACCCTAAGGGCGTTTGCA
3847	GTTCCAGGTCACGACGAGCTGCGC
3848	TCGTACGTAGTCACACCGCGACTT
3849	GGGCTGGAGTAGCGGTCTGCTATG
3850	TAGCGGCACTCGTGTTGCGAGTGG
3851	ACGTTGGGTTCTGACACGGCGATT
3852	TGTTGCTGCGCCCCAAGTGATCTT
3853	CCCAGGTCGTTACGGTGCATCACA
3854	CCTAGTGCACAGGCAAATCGGGCT
3855	GGCGTTCTCCAAGATAAGGCCAAA
3856	ACTTCGATACCGTGGACCTCGCCA
3857	CTGAGCGCGCTAAACGTCCCTAGC
3858	ATCAGATAAACGATCCGACGCGTC
3859	CATGGCTGAATTTGTGACCCCTCT
3860	CGAAAGCGAGCAAATAGAATCCCC
3861	AGATTGCCCTGCGGCAGGTTGAAT
3862	AAGAGCGGCGCGATCAGTTAGAAA
3863	CTGATGCCTGTAAGGAGGCGCTCG
3864	AATCGCGAGGTTCCGGCAGACAAAAG
3865	CGTTGGGACACGGACCGTTCACTC
3866	AGATGTGTGCACTCGCGGTCATTT
3867	CAACTCGAGTGGCGGTAACATCTG
3868	ACCAAGGTTGCGATTACGGGAAGC
3869	CGAAGCGGTAGACGGCTCGCGTTA
3870	TCTCGCGAACAGGAGGGAAGGCGT
3871	GTCCCGATTTGCGCTGTGAGGAAA
3872	TACCACGCGTCGGCACGGAAATGG
3873	AAATGCTACCCGATTGCGCGGGAT
3874	TCGATTCAAGTTTGTGCTGCGGAG
3875	CCATCTCATCCCCTATGGCATGC
3876	CTGGCCCGTGTTTGTTGAGTCGA

5

0

5

10

25

30

35

40

3877	GACACACACGTTGCAGGGCTTCCC
3878	TCGAATCGAGTCGATCGTGAAGGT
3879	GAAAGCACTCGATCGCGTTGGATT
3880	AATTACGCGAACATGGGGCGTCAA
3881	GTGCTAACACTGTGGTCGTTCCCA
3882	GGTAAGCGCCAGCCAGGAGTTGTC
3883	GGCGATCGTTCAGGAATCGCGTCA
3884	CTGGCTAGACCTCCGACACAGGCT
3885	CGGGTTAAACGCCAACTGGCCTAG
3886	ATCGCAGCCTGGCCGCCTAGTTTT
3887	GGCGTAGCCTAGCAAATTATGCCA
3888	ATGACGCGACGGAGACAATACGGC
3889	GTTGCATCACGAAAATGCCGTCTT
3890	GAGTCATGCGTTCCTCGCTTACC
3891	TCTGAACCGGTTATCCCAACCTC
3892	TGCCTCTGGTAGGCGCCCAGTTAC
3893	CTGACGGTTTTTCATTGCGCGTGCC
3894	TGAACACGAGCAAACTCCAACGC
3895	CGGCGCGCGAAAGACTTGAAGTTG
3896	GCTACGAGTACCCGTCCGAAACGC
3897	ATACCCAACAGCATGGAGCGACCA
3898	ATCGCATCGCATCGTATTACGGG
3899	CGGCCTAGAGGTGCGAAAGCTATC
3900	TAACGCTTTTCCGAGGCCGATTCT
3901	TCTGTCTAGCACGCCGACCTGCT
3902	CTCATCGTTCAGTCGGTCGTCGTA
3903	TCGTCGAGCAGATAGCGGGGTAGG
3904	TCGACCACAGTCAGGACACTACCG
3905	TGCGATTCTATGATGTCCGAACGC
3906	CAAATGCAATGGCAAGCACTCACC
3907	TCTAATCCATCGTTTTTTGGGCGA
3908	TCTCAACTCCGGTACGACGAAACA
3909	CTGAAGAGGGTAGCCTGGGAGCGG
3910	GGCACAATTAACGCGCCGCGTT
3911	CAAAGGAGGGTCAAAGGCCAGAAA
3912	TTTGCGGCCGTGACGAGCAAAAAT
3913	AGGAATGTGCGTGGCACCTGTGGA
3914	TCGTGATGACTGCCTTCCGAATCA
3915	CACGTCGACATGTTTGTTACCTCG
3916	TTGCGGTAGTTTGTTACCACCGT
3917	GCAGTGCGGACAAATACAGCTGAG
3918	ACGGCATGATGGAGGGATAAACGT

3919	TGGGATAATCCGCAAGCGCATAGC
3920	CCTAGCTCTGCTGCGTCTTTGCGC
3921	TCCTGGAAGTCTGAAGGCGACTT
3922	CGAAGGCGGCATGGTGTAGTCTCC
3923	AACATTGTTCCCATCCCAGAGCAC
3924	CCAGGCAAGAAACAACCACGCGCT
3925	AAATCCACAGGCGCGCCAAAGCTG
3926	GCTCACCAGACTCCGCGCGATA
3927	TAGGTGGCGAGAGAGCGCCACAA
3928	GGCGTTGGTGTGTCGGGACCATGA
3929	TCTGAATGCTTCCGTGCTTTCGTG
3930	ACGCTCTGGACCTCGCTCATTGA
3931	TCCTTTATGCGCAGCGCTCGTGTT
3932	TTGCCGTCCTGCAGCAGGTAGCTC
3933	GGTCTAGTGGCAGCAAGGAGCGAT
3934	GGTAACGCGACCAGCTTAGACACC
3935	GTGGCGATTGGCTTCCTATGCATA
3936	TCAAAATACGCCAGGAAGGGCAA
3937	TGCCATGCAGTCAGGTACGATGGT
3938	ACAGGTTACGTGCTGTGTTCCCGT
3939	CTCATGACGAACGAGCGGTCTGCA
3940	GTCGTGCGAGAGGCCAAGACCTTA
3941	GCTGGCTGACGCTGTTGTCAGAGG
3942	GCTACAGTGCTGCGTCCCGTGCT
3943	TTTACGAGCACCAAGCTGGCGTAG
3944	ACGAGTTGACGGTCGTAGGGACCG
3945	TCGGATGGTAGGAGGCGAGATCGG
3946	ATTATGCAGATCCTGTGCATCCGC
3947	AGGGATGGAGACGAAGGAAGCATT
3948	ACCCCAGGACCCGTATTCCCTAGC
3949	GCACCATCCTGGGGCTTCTCAATG
3950	TACAATCCGTGGACGTTTGCTCAG
3951	GGTAGGCGAATCCGACTGGCATAG
3952	AGGACCGAACCCATGTGCAGCATC
3953	ATACACCGCACAGAAGCACAGCTG
3954	TCCTTGGCGGCCGTGTGTTTATTG
3955	CTCCACGCGAAGGGCGCTTGTAAC
3956	TGGCCCTGCCATCCTCGGATTGAG
3957	TGTCTATTCGCCAGCGTGAGCATC
3958	TGTTGTTGGCACGCCTCTACGGCA
3959	GTGCCTCAACCGTATCGTGGCGGT
3960	TCCTCGAAGTAGCGTGACCGAACC

5

0

5

10

15

30

35

40

3961	AAACAATTTCTGCACTCTCGGCC
3962	CACAACTCGTCGAGGCACACAGT
3963	GACGAAACGCTCGGCAGAAAGCCT
3964	TCAACTCACACGGGACAGCAGTTC
3965	TCACGTGGATGGGCTTAGCTGGGC
3966	AGGTGTTTGTTCGACTGGCCACA
3967	TCAACCCTCTATTCCCGAGCATTG
3968	ACCTCACACAAGCGTTCTCGTCGA
3969	AACAGCATGCGGTCGCTGGCTTTC
3970	CACGGACACGTGTTACATCCGATG
3971	CTGGGAGCCTGCTGATACATGGTG
3972	CGTCCTATGGGCCATGGCCAGGAT
3973	GTCCCCAAATCTCGCTTTACAGGC
3974	TCACAAACCTGTGCGTGCAATTGTC
3975	CACACTCGTGGCCTGCGTTGGGAA
3976	GCCTGCACTTACGGCTATCTCGCC
3977	TTGGCGTGGCGATTACCTGTTATT
3978	TTTGCGGCTGAAGTTTACAGGGTG
3979	CACTTAAGGGGCTGACCGAGCAAC
3980	AGAAAACGTCAATCCGCCACCTTT
3981	AACAAAACGGCGCTCCAACAAACG
3982	GCCTCAATATCTGGTTGCCGCTG
3983	TTCCACAGTCAATGATGGGCGTGC
3984	GATTCCCAGTCTACCCGCGAGCAT
3985	AGGCCAATTACGACCCTGTACGG
3986	CATGCGAACGTTCCGAGGAGACGG
3987	CACACGCGATGGGTTGTGTGACGC
3988	TCCGGTATTGCGCAGGAACCATAG
3989	AAGATTAGGTGTGCCCGCCTCAGG
3990	TCGTTACGCCCCGACTCGACGATG
3991	ACTAAAATCGCCAGGTTGCTCCCT
3992	AGGATGGCCACGCCGAATCAAAGT
3993	TGATGAAGCAGCTCATCGCTGGCG
3994	CCCCGATGGGTCTTTGTTGGA CT
3995	ACACGAGGGCTGCTGGTGAGGGCT
3996	TGGTCACCAATTTGATGATCCGAG
3997	AAGGCCGCTTG CATGCGACAAATT
3998	CCAGTGTTGTT CATCGGTGGCGT
3999	CCGACCGCTACATAGGTGTGCGAA
4000	TGTTGAAGCCGTTCCAGATGACA

TABLE 2

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1	TTCGCCGTCGTGTAGGCTTTTCAA	TTGAAAAGCCTACACGACGGCGAA
2	TTCGAAGCGCACGTCCCTTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
3	AACGCGTGGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCGTTGCAA
7	CGCATAGGTTGCCGATTTTCGTCAA	TTGACGAAATCGGCAACCTATGCG
8	CCGTTTGCGGTCGTCTTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
9	TTGCTTTTCGTGGCTGCACTTCAA	TTGAAGTGCAGCCACGAAAGCGAA
10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
11	TTGCCGCACCGTCCGTCATCTCAA	TTGAGATGACGACGGTGCGGCAA
12	CATCGTCCCTTTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
13	GCACGGGAGCTGACGACGTGTCAA	TTGACACGTCGTACGCTCCCGTGC
14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
16	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCGGTACTTGCAGCGATG
17	GGCTGGTTCGGCCCCGAAAGCTTAG	CTAAGCTTTCGGGCCGAACCAGCC
18	GTTCCCAAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTTAGGGCACCGGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGGTTCATTGACCGTTC
22	GCGGCCCTTGGTTCAATATGAATCG	CGATTTCATATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTCTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TTGCTCACTGCCGGACTAGGTCCA
25	ATAAACTACCCAGGACGGGCGGAA	TTCCGCCCCGTCCTGGGTAGTTTAT
26	CATCGGTTTCGCGCCAATCCAGATA	TATCTGGATTGGCGCGAACCAGTG
27	GTCGGGCATAGAGCCGACCACCT	AGGGTGGTCGGCTCTATGCCCGAC
28	CTTGGGTCATGATTCACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTTGAGGCGTCCCACACT	AGTGTGGGACGCCTCAAAACAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTCTTGGTCTGA
34	GACATCGCTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTTTC
36	TGTCATGAATGATTGATCGCGCGA	TCGCGCGATCAATCATTATGACA
37	ATATCGGGATTTCGTTCCCGGTGAA	TTACCGGGGAACGAATCCCGATAT



5

10

15

20

25

30

35

40

38	GCGAGCGTACCGAAGGGCCTAGAA	TTCTAGGCCCTTCGGTACGCTCGC
39	TTACCGGCAGCGGACTTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAAGTCATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGCGCGTAGTGCATGTACC
44	AATTCATCTCGGACTCCCGCGGTA	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCTGCCAATCCAGATTTGGC
46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
51	CCAACAACCTGGAACGGGAACCGGC	GCGGGTCCCGTTCCAGTTGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC
54	TCACATCCAAATATGGTCCGCGAA	TTGCGGACCATATTTGGATGTGA
55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTCACACCGGCAGAC
56	CATCGCAGAGCATAAACACCTCA	TGAGGGTGTTTATGCTCTGCGATG
57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
59	GGAATGAGTGAGCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
62	CACCGCGGTGTTCCCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
64	TTAACCTGCGTCTGCCCTTTCTCT	AGGAAAGGGGCAGACGCAGGTAA
65	AGGCGCGTTCCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
67	TGCATAGAGCCAAAGTCGGCGATG	CATCGCCGACTTTGGCTCTATGCA
68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCTCTCAA
69	TCCGCATTGTGAGAAAAACGAGC	GCTCGTTTTTCTCACAATGCGGA
70	GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAACCGCC
71	GGTGAAAATTTTCGTAGCCACGGGC	GCCCCGTGGCTACGAAATTTTCACC
72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCCTCCGTCGG
73	CCAGTTTGGCCCAATTCGCCAAAA	TTTTGGCGAATTGGGCCAAACTGG
74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCCTAATAGATCC
75	CGGATGTCACCGTTTGGACTTTCA	TGAAAGTCCAAACGGTGACATCCG
76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTTGCGAT
77	CAGGGCATGCAATAATCGAGGTTT	GAACCTCGATTATTGCATGCCCTG
78	CATGCGTTGATATATGGGCCCAAG	CTTGGGCCCATATATCAACGCATG

	79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
	80	TTGTATGTCTGCCGACCGGCGACC	GGTCGCCGGTCGGCAGACATACAA
	81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
	82	ATGAGAATCGCCGGCAATCTGCTA	TAGCAGATTGCCGGCGATTCTCAT
5	83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTCAAGTCAAAT
	84	CAGGGAGAACGGTTAAGTTCCCGT	ACGGGAACCTAACCCTTCTCCCTG
	85	AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACCTCCTCGATCGCCGGCCT
	86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
	87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCTCGGCGTTGCAC
10	88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
	89	TGAAATACCACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTTC
	90	GCATCGTGTACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
	91	CAGTGTCTAACGGCGCGCGTGAA	TTCACGCGCGCCGTTAGAACTG
	92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
15	93	CGAAAACTAGTGGGCTCGCCGCG	CGCGGCGAGCCCACTAGTTTTTCG
	94	CTTTCAGGGGAAGTCCCGAGTCG	CGACTCCGGCAGTTCCCCTGAAAG
	95	TTGTGGCCTTCTTGTAAGGCACG	CGTGCCCTTACAAGAAGGCCACAA
	96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTCCGCGTTTCGTGGA
	97	CGACCTTGACAGAAACCTAACGAG	CTCGTTAGGTTTCGTGCAAGGTCG
20	98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
	99	CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTCGCACGAAAGCG
	100	TGCGCTTACAGGCTCCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
	101	CACGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAAGCGCGTG
	102	CGGAGGGAGGGAGCTAGCCTTCGA	TGGAAGGCTAGCTCCCTCCCTCCG
25	103	GCATCCGGCCTGTTGATGACGCCT	AGGCGTCATCAACAGGCCGGATGC
	104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
	105	CCTTCCAATGATTGCATACGCCCA	TGGGCGTATGCAATCATTGGAAGG
	106	AACACTTGATCAGGCGGGTCGTCT	AGACGACCCGCCTGATCAAGTGTT
	107	TGGAATCAAGGCCGTAAAGGACAG	CTGTCTTTACGGCCTTGATTCCA
30	108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
	109	AGTGGTGAATGGCCGCTACCCTGA	TCAGGGTAGCGGCCATTCACTACT
	110	TGTTGAAGCGAGCTAAAACGGCCA	TGGCCGTTTTAGCTCGCTTCAACA
	111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
	112	AAGGTGGTGCCATTCAATTTGGCTA	TAGCCAAATGAATGGCACCACCTT
35	113	CGTTAAACCGCAATCCGTTCCGGCT	AGCCGAACGGATTGCGGTTTAACG
	114	CACGAGATACGGGCGTAAGGGTGG	CCACCCTTACGCCGGTATCTCGTG
	115	CTACGGCAAACGTGTGGAATGGGT	ACCCATTCCACACGTTTGCCGTAG
	116	GTAGGGCGATGACGGGCGAAGTAC	GTAGTTCGCCCGTCATCGCCCTAC
	117	AATCGACCTCCGCACACATTTCGCA	TGCGAATGTGTGCGGAGGTCGATT
40	118	GAGTCAGCATGGCGGCGGAGATTG	GAATCTCCGCCGCCATGCTGACTC
	119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTTGCCAGCGTCTTTATCT

5	120	GGTACCTCAACGCGAACCACTTGT	ACAAGTGGTTCGCGTTGAGGTACC
	121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
	122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
	123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCTGCGTGAGACCGAT
	124	TAGGTTGCCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
	125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
	126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGAAACTTTCATCA
	127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
10	128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
	129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC
	130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTACGGGGACAGCTCGA
	131	GTCTTGGGGGCCGCTTAGTGAAAA	TTTTCACTAAGCGGCCCCCAAGAC
	132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
	133	AGGACCATTTCGGAAGGCGAAGATA	TATCTTCGCCCTTCCGAATGGTCTT
15	134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
	135	AATAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCGGTTTATT
	136	TTGTACGTGCGGTCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
	137	CGCACCAAACAGATTTCCAGAC	GTCTGGGAAACTCAGTTTGGTGCG
	138	ACCTGATCGTTCCTTATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
20	139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCCTCGCTCTGTTCC
	140	CCCTGCCTTGGCGTGTGCGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGGAGTTGGCGTGTGAGAGT
	142	CTGACGGTTTTTCATTTCGGCGTGCC	GGCACGCCGAATGAAAACCGTCAG
	143	TGCGGTGGTTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
25	144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
	145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTCGCTTTACGGCCT
	146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTCTG
	147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
	148	GGACGGTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
30	149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
	150	GATGGCCTATTTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
	151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
	152	AATAACTCGCGCGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
	153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
35	154	CTTTGGTATGGCACATGCTGCCCCG	CGGGCAGCATGTGCCATACCAAAG
	155	AGAAAGGCTCGAGCAACGGGAAC	AGTTCCCGTTGCTCGAGCCTTTCT
	156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAAGTGCGGTAGATT
	157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAACTGTGGCCGCCACG
	158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
40	159	GGCCCAAAGCCCCAGACCATTTTA	TAAAATGGTCTGGGGCTTTGGGCC
	160	CGCCTGTCTTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG

5	161	TGAGGCAACAGGGGCCAAAACTA	TAGTTTTTGGCCCCTGTTGCCTCA
	162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
	163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
	164	GCACGTGAAGTTTAACCGCGATTG	GAATCGCGGTTAAACTTCACGTGC
	165	AGCGGCAGAAACGTTCCCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
	166	TCGTGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
	167	TCTTTGCCGCGTAACTGACTGCTT	AAGCAGTCAGTTACGCGGCAAAGA
	168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
10	169	TGTTACTGTGGTTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
	170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
	171	ACAAATGCGTGAGAGCTCCCACT	AGTTGGGAGCTCTCACGCATTTGT
	172	CGCGCAGATTATAGACCCGAATGT	ACATTCGGGTCTATAATCTGCGCG
	173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTCAGCGGCGTTATTTG
	174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
15	175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTTGCTCGTGTTCA
	176	CAGCAGATCCTTCGTAGCGGTGCT	ACGACCGCTACGAAGGATCTGCTG
	177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACCTACCAGGTTCC
	178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTGCTTATGA
	179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
20	180	TGTCAGAGCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182	CTCAGAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
	183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCGCGGAGTAGATAAAAGGAT
	184	AGGCGTGACGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
25	185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
	186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTGTCGATGGACCTGGCAA
	187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCGAGTTATAGTGGA
	188	GCCCAGTCGGCTCTAACAAAGTTCG	CGAACTTGTTAGAGCCGACTGGGC
	189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
30	190	TAAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
	191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
	192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAACCT
	193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
	194	TTCGCAGCACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTGCTGCGAA
35	195	TAACCCGATTTTTCGACTCTGCC	GGCAGAGTCGCAAAAATCGGGTTA
	196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
	197	GAGCTGACGTCACCATCAGAGGAA	TTCTCTGATGGTGACGTCAGCTC
	198	GGAGGCTGGGGGTGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
	199	TTGTGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCACAA
40	200	CCCTCGCACTGTGTTACCCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
	201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA

202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTGCTTTCATGTCCGCGC
206	CTTATTGGGTGCCGGTGTCTGGATT	AATCCGACACCGGCACCCAATAAG
207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTTGGTAACCGCCCC
208	GCTAAAGCGTGCTCCGTAAGTACC	GGCAGTTACGGAGCACGCTTTAGC
209	ATCTCATGCATCTCGGTTCTGCTGT	ACGACGAACCGAGATGCATGAGAT
210	ACGAAAAAAGTGTGCGGATCCCCCT	AGGGGATCCGCACACTTTTTTCGT
211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTACTTGG
212	ATCGTGCGTGGAGTGTGCGATCTA	TAGATGCGACACTCCACGCACGAT
213	TCCAGATACCGCCCCGAAGTTTGA	TCAAAGTTCGGGGCGGTATCTGGA
214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
215	TTGAAATTGCTCTGCCGTCAGTCA	TGACTGACGGCAGAGCAATTTCAA
216	AGTCAGGCGAGATGTTTCAGGCAGC	GCTGCCTGAACATCTCGCCTGACT
217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGGCTTAACGTCGGCTTGT
218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
219	GTGAGACACACATCCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
220	CGACGGATGCAGAGTTTCAAGTGGC	GACCACTGAACTCTGCATCCGTCG
221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
222	TTAGCAAAGCGGCGCCGTTAGCAA	TTGCTAACGGCGCCGCTTTGCTAA
223	CCCGACACGGGTCAGCGTAATAAT	ATTATTACGCTGACCCGTGTCTGGG
224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
226	TCTCGAAGCACAGCCCGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
227	ATGCTAACCGTTGGCCATGGAAC	AGTTCCATGGCCAACGGTTAGCAT
228	CTTGCGGAGTGTTAGCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
230	CCAATGCCTTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
231	AGCAGATAACGTCCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGCAACACGTAATGGTCAA
233	TCGCGTATTTGCGGAATTCGTCTG	CAGACGAATTCGCAATACGCGA
234	CTGCGTGTCAACAATGTCCCGCAG	CTGCGGGACATTGTTGACACGCAG
235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCGTGGCACCAGA
236	CTCCGGGAGGTCACTTAATTGCGG	CCGCAATTAAGTGACCTCCCGGAG
237	TTTTCGTGATTGCCCGGAGGAGGC	GCCTCCTCCGGGCAATCACGAAAA
238	TCGGGATGTAGCTGGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
239	CGAGCCAACGCAAACAGTCTCTTG	CAAGGACGTGTTTGCGTTGGCTCG
240	GCAAAGCCTTTGTGGGGCGGTAGT	ACTACCGCCCCACAAAGGCTTTGC
241	ATTCGACCGGAAATGAGGTCTTCG	CGAAGACCTCATTTCCGGTCAAT
242	TTGCTTGTGCTGAGTTGCTCTGTT	GAACAGAGCAACTCAGCAAGCGAA

	243	CGCGTGAAGACCCCATTCCCGAGT	ACTCGGGAATGGGGTCTTCACGCG
	244	AACCGTATTCGCGGTCACTTGTGG	CCACAAGTGACCGCGAATACGGTT
	245	GGGGCCAACCGTTTCGAGGCGTAT	ATACGCCTCGAAACGGTTGGCCCC
	246	TTCGGCTGGCAGTCCAAACGGCTT	AAGCCGTTTGGACTGCCAGCCGAA
5	247	GGGTGTGGTTAGAATGCACGGTTC	GAACCGTGCATTCTAACCACACCC
	248	GCGAGGACCGAACTAGACAAACGG	CCGTTTGTCTAGTTCGGTCCTCGC
	249	ACGCACGCGTGACCGAAGTTGCTG	CAGCAACTTCGGTCACGCGTGCCT
	250	TAAAGGTCGCTTTGAAAGGGGGA	TCCCCCTTCAAAGCGACCTTTTA
	251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTTAGCGATCGCA
10	252	GGAGGTATAAGCGGAGCGGCCTCA	TGAGGCCGCTCCGCTTATACCTCC
	253	ATGCTGACATGTCGTGCACCTCGT	ACGAGGTGCACGACATGTCAGCAT
	254	TGTGGTTAAAGCGTCCGTTCAACG	CGTTGAACGGACGCTTTAACACA
	255	CGTTCACACCGGCGTAAGCTGCGT	ACGCAGCTTACGCCGGTGTGAACG
	256	CCTATCCCGGCGGAGAACTTCTGTG	CACAGAAGTTCTCGCCGGGATAGG
15	257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTGCAGAC
	258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC
	259	AACGTGCGACGACACAGTTTCGTC	GACGAACGTGTGTCGTGCGACGTT
	260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
	261	TCACGTTTTCGTCTCGACATGAGG	CCTCATGTCGAGACGAAAACGTGA
20	262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCCTAAGGATGAGGCACA
	263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCACCT
	264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGCAGTCCCTTCGATCCAG
	265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
	266	GATCCTGCGGAGAAGAGAGTGCAAG	CTGCACTCTCTTCTCCGCAGGATC
25	267	TACGTGTGGAGATGCCCCGAACCG	CGGTTGCGGGCATCTCCACACGTA
	268	GCGCTATGTCAATCGTGGGCGTAG	CTACGCCGACGATTGACATAGCGC
	269	AGCGAGGTTTCTAGCGTCGACACC	GGTGTGCGAGCTAGAAACCTCGCT
	270	ACCCAGGTTTTGCCGTTGTGGAAT	ATTCCACAACGGCAAAACCTGGGT
	271	CCCTGTTAACGGCTGCGTAGTCTC	GAGACTACGCAGCCGTTAACAGGG
30	272	AGGCCGATTTACCCGCCAATTGC	GCAATTGGCGGGTGAAATCGGCCT
	273	GAGCCCTCACTCCTTGCCCTTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
	274	GGGTGGACATCCGCCTCGCAGTCA	TGACTGCGAGGCGGATGTCCACCC
	275	GATGGCTGAGAACCGTGCTACGAT	ATCGTAGCACGGTTCTCAGCCATC
	276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTCGA
35	277	CGAATGGGTCTGGACCTTGATAG	CTATGCAAGGTCCAGACCCATTG
	278	GTGCACCAGACATTCGAACTCGGA	TCCGAGTTGCAATGTCTGGTGCAC
	279	AGAGGCCCGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
	280	AACGCCTGTTGAGAGCATCAGCGG	CCGCTGATGCTCTGAACAGGCGTT
	281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTGAGCCTT
40	282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
	283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTTACATGGGACAT

284	ATGGAGTCTGCTCACGCCCAAAGG	CCTTTGGGCGTGAGCAGACTCCAT
285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTTGTGGAGGCCG
286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
287	TCATTTGAATGAGGTGCGCACCGG	CCGGTGCGCACCTCATTCAAATGA
288	GACGTACCGGAAGCGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
289	ATGCGAGCAATGGGATCCGGATTC	GAATCCGGATCCCATTGCTCGCAT
290	AGAGTGAGGCCTCCCTGACCAGTG	CACTGGTCAGGGAGGCCCTCACTCT
291	CGCACCGTAAGTAGATTTGCCCGC	GCGGGCAAATCTACTTACGGTGCG
292	TGAACCTTTGAGCACGTCTGCGC	GCGCACGACGTGCTCAAAGGTTCA
293	TCCGCCTTTTTGGTTACCTCGAAG	CTTCGAGGTAACCAAAAAGGCGGA
294	GAACGCCAACGGCACTAACACATC	GATGTGTTAGTGCCGTTGGCGTTC
295	CCGACAGCAGCCAAGACGTCCCAG	CTGGGACGTCTTGGCTGCTGTCCG
296	CATAAAAAACCTGGGGCTCTGCG	CGCAGAGCCCCAGGTTTTTTTATG
297	TGCCAACTGTGCAGACCGGACTTA	TAAGTCCGGTCTGCACAGTTGGCA
298	GGCGAAAGAGCGAAACCGGCTCGT	ACGAGCCGGTTTCGCTCTTTCGCC
299	GGGATGCGTATTTTAGCGAACACG	CGTGTTGCTAAAATACGCATCCC
300	TGGGATTCAGCGACCAGTACGCGA	TCGCGTACTGGTCGCTGAATCCCA
301	CCCGATATTCGCCCCGGCCTATTCTG	CGAATAGGCCGGGCGAATATCGGG
302	CGAGAAGATGCCTCACGCAACCAA	TTGGTTGCGTGAGGCATCTTCTCG
303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
304	GGCTAGACGATGGATAACCGTGCC	GGCACGGGTATCCATCGTCTAGCC
305	GCCTCTTCTCGACGATGCGATTTT	AAAATCGCATCGTCGAGAAGAGGC
306	GCTTCCGGATGAACGGGATGGTTG	CAACCATCCCGTTCATCCGGAAGC
307	CCCTCCATGTTCTTCGAACGGTTT	AAACCGTTCGAAGAACATGGAGGG
308	TTGATGGGCGGCAATGCTCTTGCT	AGCAAGAGCATTGCCGCCCATCAA
309	ATTGTGAGATGCGCCAAATTCCCC	GGGGAATTGGCGCATCTCACAAT
310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
311	ACTCCACTCCTCGGTGGCAAATA	TAGTTTGCCACCGAGGAGTGGAGT
312	TCTGGGCATGCCTGGACGGAGACG	CGTCTCCGTCCAGGCATGCCCAGA
313	TCTCAACTCCGGTACGACGAAACA	TGTTTCGTCGTACCGGAGTTGAGA
314	TTGCGTGGTCAAAGGCGCAACGTG	CACGTTGCGCCTTTGACCACGCAA
315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGCGGATCGCTGTCT
316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACGCG
317	AGGCGCACATGTACGGACATTCAG	CTGAATGTCCGTACATGTGCGCCT
318	GATGAGTGGCACGTGGTGTGTAA	TTACACACCGACGTGCCACTCATC
319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAAACGCCAATGCT
322	GGTAATATTCAGCGCAGCCGCTCA	TGAGCGGTGCGCTGAATATTACC
323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA

	325	ACTGCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGGCAGT
	326	CCTTTGGCCTGAAGTTGTCGTAGC	GCTACGACAACTTCAGGCCAAAGG
	327	GTGCCCCACGAGCGTATCGTTGTA	TACAACGATACGCTCGTGGGGCAC
	328	AGGCGCTACGTGGGCCTGGAGCAA	TTGCTCCAGGCCACGTAGCGCCT
5	329	GGGTGCTACCATTGCATTAGTCCG	CGGACTAATGCAATGGTAGCACCC
	330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGGT
	331	CCATGATGCATTGGGTGCATTTAG	CTAAATGCACCCAATGCATCATGG
	332	GGTCCGGCCCTACGAAACGTTCTGA	TCGAACGTTTTCTGAGGGCCGGACC
	333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGCCACACGG
10	334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
	335	GGGTCAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
	336	GCCGTGAAGTCGAATGCAGATCGA	TCGATCTGCATTCTGACTTCACGGC
	337	GCCACCACCCAGTGCATTCAGGTA	TACCTGAATGCACTGGGTGGTGGC
	338	GAGCTTAGTTTGCGGTCATCGGGC	GCCCGATGACCGCAAACCTAAGCTC
15	339	TGTTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCCAAACA
	340	GCTCCGCTGGATGTGCCGTTTAG	CTAAACCGGCACATCCAGCGGAGC
	341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTCGCATGCTACCG
	342	CTACGCTCTACCAGTTGCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
	343	GTGCCTCCTGCTGTATTTGCCAAG	CTTGGCAAATACAGCAGGAGGCAC
20	344	TTGCGACTCGACTTGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
	345	TCTGGGAGCTGTTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
	346	TGCACGCGGAACTCCCTTTACCAT	ATGGTAAAGGGAGTTCCGCGTGCA
	347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTTCGATTCATTTGCTGCCA
	348	AACTGGTGACGCGGTACAGCGAAG	CTTCGCTGTACCGCGTCACCAGTT
25	349	AGACGATTACGCTGGACGCCGTCG	CGACGGCGTCCAGCGTAATCGTCT
	350	ATGCCCTCCTTCATGGAAAGGGTT	AACCCTTTCCATGAAGGAGGGCAT
	351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATACGCTCCGAGAAT
	352	ATAGCGGAGTTTGGGTACGCGAAC	GTTTCGCTACCCAACTCCGCTAT
	353	ACCTACGCATACCGCTTGCGGAGG	CCTCGCCAAGCGGTATGCGTAGGT
30	354	GATTACCTGAATGGCCAAGCGAGC	GCTCGCTTGCCATTGAGGTAATC
	355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
	356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATCATCCG
	357	TGAGAGAGGCGTTGGTTAAGGCAA	TTGCCTTAACCAACGCCTCTCTCA
	358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
35	359	TCACGACAGACGGGCGAGATTAC	GTAATCTCGGCCCGTCTGTCTGTA
	360	AAGCAATTTGGCCTCGTTTGTGA	TCACAAAACGAGGCCAAATTGCTT
	361	GCTGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
	362	TTGTGAATCCGTTCTGTCCCCGAC	GTCGGGGACAGAACGGATTACAAA
	363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTCGCCTCAGAGGAGCCCA
40	364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTCGATTCACCTCTATCC
	365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGACGTTCCGGTGCA



	366	GCCAGTATTCTCGGGTGTGGACG	CGTCCAACACCCGAGAATACTGGC
	367	TCGCTACCTAAGACCGGGCCATAC	GTATGGCCCGGTCTTAGGTAGCGA
	368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
	369	CGCGTCCCAGCGCCCTTGGAGTAT	ATACTCCAAGGGCGCTGGGACGCG
5	370	ATGAAGCCTACCGGGCGACTTCGT	ACGAAGTCGCCCCGGTAGGCTTCAT
	371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCCAGGCCATCTGTCTGG
	372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTTGAGATGGTCCCACGCCA
	373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
	374	GCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGGC
10	375	ATTACGGTCGTGATCCAGAAAGCG	CGCTTTCTGGATCACGACCGTAAT
	376	TGCGAGGTGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
	377	GGGCCGCATTCTTGATGTCCATTC	GAATGGACATCAAGAATGCGGCC
	378	CCTCGGATGTGGGCTCTCGCCTAG	CTAGGCGAGAGCCCACATCCGAGG
	379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCTA
15	380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTCGTATCG
	381	TACGCCGGTTAGCACGGTGCCTA	TAGCGCACCGTGCTAACCGGCGTA
	382	CATACGATGTCCGGGCGGTGTGCG	GCGACACGGCCCGACATCGTATG
	383	ATCCGCAGTTGTATGGCGCGTTAT	ATAACGCGCCATACAACTGCGGAT
	384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATCTTTGTCCCTTACCC
20	385	ATTGGAGTGTTTTGGTGAATCCGC	GCGGATTCACCAAAACACTCCAAT
	386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTTT
	387	GCCGTCAAGCTTAAGTTTTGGGC	GCCCCAAACCTTAAGCTTGACGGC
	388	ACCTGCTTTTGGGTGGGTGATATG	CATATCACCCACCCAAAAGCAGGT
	389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTTGCTGCGCCACGATT
25	390	GTCGCCGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
	391	ACCCGTCGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGGT
	392	ATCCGGGTGGGCGATACAAGAGAT	ATCTCTTGATCGCCCACCCGGAT
	393	TTCCGCATGAGTCAGCTTTGAAAA	TTTTCAAAGCTGACTCATGCGGAA
	394	GCAAAGTCCCACTGGCAAGCCGAT	ATCGGCTTGCCAGTGGGACTTTGC
30	395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTG
	396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAACTGCGCTCATGAG
	397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
	398	TCAAAGGCTCTTGGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTTGA
	399	TCCGCTAATTTCCAATCAGGGCTC	GAGCCCTGATTGGAAATTAGCGGA
35	400	ACGCACGGCGCTTTTGCCTTAATG	CATTAAGGCAAAAGCGCCGTGCGT
	401	TGACAACGTCACAAGGAGCAGGAC	GTCCTGCTCCTTGTGACGTTGTCA
	402	CTTAGTTGGGGCGCGGTATCCAGA	TCTGGATACCGCGCCCCAACTAAG
	403	GCTCTAATGCCGTGGAGTCGGAAC	GTTCCGACTCCACGGCATTAGAGC
	404	CCGATTACAAATTGACTGACCGCA	TGCGGTCAGTCAATTTGTAATCGG
40	405	AGACGTACGTGAGCCTCCCGTGTC	GACACGGGAGGCTCACGTACGTCT
	406	AATGGAGCGATACGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT

	407	GGAGGCGCTGTACTGATAGGCGTA	TACGCCTATCAGTACAGCGCCTCC
	408	TGTTTTGAATTGACCACACGGGA	TCCCGTGTGGTCAATTCAAAAACA
	409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
	410	GCCCGCTAATCCGACACCCAGTTT	AAACTGGGTGTCGGATTAGCGGGC
5	411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
	412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTCCGGTGATTC
	413	AACCAGCCGCAGTAGCTTACGTCTG	CGACGTAAGCTACTGCGGCTGGTT
	414	TTTTCTGAGGGACACGCGGGCGTT	AACGCCCGCGTGTCCCTCAGAAAA
	415	GGTGCTCCGTTTGATCGATCCTCC	GGAGGATCGATCAAACGGAGCACC
10	416	CCGCTTAGGCCATACTCTGAGCCA	TGGCTCAGAGTATGGCCTAAGCGG
	417	TAAGACATACCGACGCCCTTGCT	AGGCAAGGGCGTCGGTATGTCTTA
	418	GTTCCCGACGCCAGTCATTGAGAC	GTCTCAATGACTGGCGTCGGGAAC
	419	TAAAAGTTTCGCGGAGGTCGGGCT	AGCCCGACCTCCGCGAAACTTTTA
	420	CGGTCCAGACGAGCTGAGTTCGGC	GCCGAACTCAGCTCGTCTGGACCG
15	421	CGGCGTAGCGGCTACGGACTTAAA	TTTAAGTCCGTAGCCGCTACGCCG
	422	GCTTGATGCCCATGCGGCAAGGT	ACCTTGCCGCATGGGCATCCAAGC
	423	AGCGGGATCCCAGAGTTTCGAAAA	TTTTCGAAACTCTGGGATCCCGCT
	424	GAGCTTGAGAGCGAGGTCATCCTC	GAGGATGACCTCGCTCTCAAGCTC
	425	GCATCGGCCGTTTTGACCATATTC	GAATATGGTCAAAACGGCCGATGC
20	426	CATAGCGCTGCACGTTTCGACCGC	GCGGTCGAAACGTGCAGCGCTATG
	427	ACCCGACAACCACCAATTCAAAAA	TTTTTGAATTGGTGGTTGTCGGGT
	428	GCGAACACTCATAAGAGCGCCCTG	CAGGGCGCTCTTATGAGTGTTCCG
	429	CCGCCGAGTGTAGAGAGACTCCGA	TCGGAGTCTCTTACACTCGGCGG
	430	GACATCGGGAGCCGGAACATGAG	CTCATGTTTCCGGCTCCCGATGTC
25	431	TCGTGTAGACTCGGCGACAGGCGT	ACGCCTGTCGCCGAGTCTACACGA
	432	ATGCGCATATACTGACTGCGCAGG	CCTGCGCAGTCAGTATATGCGCAT
	433	ACAAGCGAACCCGAGTTTTGATGA	TCATCAAACTCGGGTTCGCTTGT
	434	GCATGAGACTCCGCGAAGACATGT	ACATGTCTTCGCGGAGTCTCATGC
	435	TCCTACATGTCGCGTCACGATCAC	GTGATCGTGACGCGACATGTAGGA
30	436	GACCGATCGCGAAGTCGTACACAT	ATGTGTACGACTTCGCGATCGGTC
	437	GTCGCCAGGACTGGGCCGATGTGA	TCACATCGGCCCAGTCCTGGCGAC
	438	ACCGATAAGACTTGCATCCGAACG	CGTTCGGATGCAAGTCTTATCGGT
	439	TCCATAACCAGTCCGAAGTGCCGG	CCGGCACTTCGGACTGGTTATGGA
	440	ACGCGCCCTGCATCTCGTATTTAA	TTAAATACGAGATGCAGGGCGCGT
35	441	AGACCGCATCAATTGGCGCGTACC	GGTACGCGCCAATTGATGCGGTCT
	442	AGAGGCTTGGAAGTAGGGACCCT	AGGGTCCCTACTTGCCAAGCCTCT
	443	GCAATGGACGCCAGACGATACCGG	CCGGTATCGTCTGGCGTCCATTGC
	444	GCTGGACTTAGTCGTGTTGCGCGG	CCGCCGAACACGACTAAGTCCAGC
	445	AGGCATCGTGCCGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCCT
40	446	TGCGCATGTGACGTTGAACAAAG	CTTTGTTCAACGTCGACATGCGCA
	447	TTCGGGTCACATCCGATGCCATAC	GTATGGCATCGGATGTGACCCGAA

5	448	ACCCATCGCCGAAAGCGATGTTG	CAACATCGCTTTCCGGCGATGGGT
	449	AAGCGCTGACTCGGCTAAGAATCA	TGATTCTTAGCCGAGTCAGCGCTT
	450	ACTTCCAAGTCCTTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAAGT
	451	TCTCAATATTCCCGTAGTCGCCCA	TGGGCGACTACGGGAATATTGAGA
	452	AACAGTTCCTCTTTTCTGGCGC	GCGCCAGGAAAAAGAGGAACTGTT
	453	CGTCCTCCATGTTGTACGAACAG	CTGTTCTGTACAACATGGAGGACG
	454	TGCGCAGACCTACCTGTCTTTGCT	AGCAAAGACAGGTAGGTCTGCGCA
	455	ATGGACGGCTTCGCAGTCCTCCTT	AAGGAGGACTGCGAAGCCGTCCAT
10	456	TGAACGCTTTCTATGGGCCACGTA	TACGTGGCCCATAGAAAGCGTTCA
	457	TGAACCCTGCCGCGAGCGATAACC	GGTTATCGCTCGCGGCAGGGTTCA
	458	GTTCTTGCGCGATGAATCAGGACC	GGTCCTGATTCATCGCGCAAGAAC
	459	AGGGTACGTGTCGCAGCTTCGCGT	ACGCGAAGCTGCGACACGTACCCT
	460	ACCCTTGCTCCGCCATGTCTCTCA	TGAGAGACATGGCGGAGCAAGGGT
15	461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTTCAATCCTTGTCCC
	462	TGTCGTTGCTCCCGAGTACCATTG	CAATGGTACTCGGGAGCAACGACA
	463	GTTGTCCGAGACGTTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC
	464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCTGTAGTGTTACCAGC
	465	GCAGACAGGGCAAATCGGTGCAAA	TTTGACCGATTTGCCCTGTCTGC
20	466	CCCATCACAAAGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
	467	GCTTCTACAGCTGGCGTGCTAGCG	CGCTAGCACGCCAGCTGTAGAAGC
	468	GAATGTGTGCCGACCATTCTAGCC	GGCTAGAATGGTCGGCACACATTC
	469	CCAGCGGAAGTTAGAGCTCTGTGG	CCACAGAGCTCTAACTCCGCTGG
	470	TTTTTACCGACCACTCCATGTCCG	CCGACATGGAGTGGTCGGTAAAAA
25	471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTCATCATAGCCGC
	472	AGTACACGGGCGTGTTAGCGCTCC	GGAGCGCTAACACGCCCGTGTACT
	473	TCCTGTGTGGTGGCGCACTCCAC	GTGGGAGTGCGCCACCACACAGGA
	474	CCAACTAACCAATCGCGCGGATGA	TCATCCGCGCGATTGGTTAGTTGG
	475	AGTGAGTGACCAAGGCAGGAGCAA	TTGCTCCTGCCTTGGTCACTCACT
30	476	CATCTTTCGCGGAGTTTATTGCGG	CCGCAATAAACTCCGCGAAAGATG
	477	CTTCGTCCGGTTAGTGCGACAGCA	TGCTGTGCGACTAACCAGGACGAAG
	478	CTCACGAAAACGTGGGCCCGAAAT	ATTCGGGCCCACGTTTTCTGTGAG
	479	CGCAGCAGCTGAACTCTAGCATTG	CAATGCTAGAGTTCAGCTGCTGCG
	480	AGGAGACATACGCCCAAATGGTGC	GCACCATTGTTGGCGTATGTCTCCT
35	481	ATTGAGAACTCGTGCGGGAGTTTG	CAAACCTCCGCACGAGTTCTCAAT
	482	CTCTTTGTAGGCCCAGGAGGAGCA	TGCTCCTCCTGGGCCTACAAAGAG
	483	GCCGCAGGGTCGATAATTGGTCTA	TAGACCAATTATCGAACCCTGCGGC
	484	AAACGCCGCCCTGAGACTATTGGG	CCCAATAGTCTCAGGGCGGCGTTT
	485	CTGAGTTGCCTGGAACGTTGGACT	AGTCCAACGTTCCAGGCAACTCAG
40	486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
	487	CTGACCTTTGGGGGTTAGTGCGGT	ACCGCACTAACCCCCAAAGGTCAG
	488	GGAAATGAGAACCTTACCCAGCG	CGCTGGGGTAAGGTTCTCATTTCC

5	489	AACGCATCGTCCGTCAACTCATCA	TGATGAGTTGACGGACGATGCGTT
	490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCTCCA
	491	TTGCGCTCATTGGATCTTGTCAGG	CCTGACAAGATCCAATGAGCGCAA
	492	AGCGCGTTAAAGCACGGCAACATT	AATGTTGCCGTGCTTTAACGCGCT
	493	AGCCAGTAACTGTGGGCGGCTGT	ACAGCCGCCACAGTTTACTGGCT
	494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
	495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
	496	GCGCAAATCCACGGAACCCGTACC	GGTACGGGTTCCGTGGATTTGCGC
10	497	ACGCAGTTTATTCCCCTGGCTTCT	AGAAGCCAGGGGAATAAACTGCGT
	498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCGCGGAGGTTCT
	499	AAAGGAGCTTTCGCCAACGTACC	GGTACGTTGGGCGAAAGCTCCTTT
	500	AGTGATTGTGCCACTCCACAGCTC	GAGCTGTGGAGTGGCACAATCACT
	501	GCGATCGTCGAGGGTTGAGCTGAA	TTCAGCTCAACCCTCGACGATCGC
	502	GGGAGACAGCCATTATGGTCCTCG	CGAGGACCATAATGGCTGTCTCCC
15	503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTGCCGGAGTGACAGCGTCTC
	504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG
	505	CGGCATAACGTCCAGTCCTGGGAC	GTCCCAGGACTGGACGTTATGCCG
	506	AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
20	507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
	508	AGGGAACCGCGTTCAAACCTCAGTT	AACTGAGTTTGAACGCGGTTCCCT
	509	GAATTACAACCACCCGCTCGTGTT	AACACGAGCGGGTGTTGTAATTC
	510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
	511	TTAGTTTGGCGTTGGGACTTCACC	GGTGAAGTCCCAACGCCAAACTAA
25	512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
	513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCCACGTTAACGTTTCGG
	514	TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTCGCCTTGTTACTTTA
	515	TAATGATTTAGTCGCGGGGTGGG	CCCACCCCGCGACTAAAATCATT
	516	GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
30	517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCGCCA
	518	GGGCGTTAGGCGTAATAGACCGTC	GACGGTCTATTACGCCTAACGCC
	519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCCGTCTAAAGGTGGC
	520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTTACACATCTC
	521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGAGGGCCACGAGCTA
35	522	GTGTCGGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
	523	CCAGGGAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTTCCCTGG
	524	TTCCGAAACTAAGCCAGAACCGCT	AGCGGTTCTGGCTTAGTTTCGGAA
	525	GCAAACCCGGTAACCCGAGAGTTC	GAAGTCTCGGGTTACCGGGTTTGC
	526	GCAAATGGCGTCATGCACGAACGT	ACGTTTCGTGCATGACGCCATTTGC
40	527	AGTACTTTCGCGCCAGTTTAGGG	CCCTAAACTGGGCGCGAAAGTACT
	528	AAGATCTGCGAGGCATCCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
	529	GCAAGTGTATCGCACAGTGCGATT	AATCGCACTGTGCGATACACTTGC

530	CCGACAAGGCCTCAATTCATTCTG	CAGAATGAATTGAGGCCTTGTCGG
531	GTCTCGTCTCAACTTTAAGGCGCG	CGCGCCTTAAAGTTGAGACGAGAC
532	ATCCAGAGATCCGTTTTGCAGCGT	ACGCTGCAAAACGGATCTCTGGAT
533	GTCACCAGGAGGGAAGTTTCACCC	GGGTGAAACTTCCCTCCTGGTGAC
534	TTCCGTCAGGCGGATCAACGGAAT	ATTCCGTTGATCCGCTGACGGAA
535	ATGCCGGACACGCATTACACAGGC	GCCTGTGTAATGCGTGTCCGGCAT
536	TGGGCCGCTTGGCGCTTTCATAGA	TCTATGAAAGCGCCAAGCGGCCCA
537	CCTAGCGCGAGCTTTACTGACCAG	CTGGTCAGTAAAGCTCGCGCTAGG
538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATATTCCTGGCCAA
539	GTCTGCGGCCGACTTGCTATGCAT	ATGCATAGCAAGTCGGCCGAGAC
540	AAC TTGCTCATTCTCAAGCCGACG	CGTCGGCTTGAGAATGAGCAAGTT
541	ACGTCAGCGATTGTGGCGAAATAT	ATATTTGCCACAATCGCTGACGT
542	ACGGCCTGCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
543	ATACCTCCGCAGAACCATTCGGTT	AACGGAATGGTTCTGCGGAGGTAT
544	AGTTCGCGGTCCCACGATTCACCT	AAGTGAATCGTGGGACCGCGAACT
545	TGCTCAATTTGTGCAGAAAACGCC	GGCGTTTTCTGCACAAATTGAGCA
546	TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
547	GACGCGACGTGAGTAGTGGAAGCG	CGCTTCCACTACTCACGTGCGGTC
548	ATGGTAGGGGCATTGGGCTTTCCT	AGGAAAGCCCAATGCCCTACCAT
549	CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGCTATATTTGG
550	GCAAACCGTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
551	TAGCGTCTTGCGTGAAACCATGGG	CCCATGGTTTCACGCAAGACGCTA
552	CCACCCGACAGCGCTGGACTCTT	AAGAGTCCAGCGCTGTGCGGGTGG
553	ACGAGCACTGAAGGCTGCTTTACG	CGTAAAGCAGCCTTCAGTGCTCGT
554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTGCGGGCC
557	GGCTCCAGGGCGAGATTATGAATG	CATTCATAATCTCGCCCTGGAGCC
558	CAAAATCCGATGGGCGGAAATTA	TAATTTTCCGCCCATCGGATTTTG
559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
560	TAGCTATTGCCCCGATGGGCTACT	AGTAGCCCATCGGGGCAATAGCTA
561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
562	GACGCTGTGGCTCGGAACTGTTC	GAACAGTTTCCGAGCCACAGCGTC
563	CCTGGGTTGCGCGCGTGGTAACTG	CAGTTACCACGCGGCGAACCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
565	TTCCGCGGATTGCTGCCGCATAACA	TGTTATGCGGCAGCAATCCGCGAA
566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTTCGGTGCCATTTTT
567	CATTCCGCGCGAGTTGAAATCCAG	CTGGATTTCAACTCGCGCGGAATG
568	ACGCACGTTTTTTGGCACGGTTAA	TTAACCGTGCCAAAAACGTGCGT
569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
570	TCTCAGTCGGA CTGATGCCAGA	TCTGGCATACGAGTCCGACTGAGA

571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGTGCGTTTGGAG
572	TTCAACCAAGCGGGGTGTTCTGTGA	TCACGAACACCCCGTTGGTTGAA
573	GGTGTGCGAGGGTGGTGACCTCGA	TCGAGGTCAACACCCTCCGACACC
574	AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAGCGCT
575	CCGAGGACTTACGTCTGCCCAGGA	TCCTGGGCAGACGTAAGTCCTCGG
576	GCCCAATCCAGTTCTTATGCGCCC	GGGCGCATAAGAACTGGATTGGGC
577	CGGGTTAACCACGCAAGTTATGA	TCATAACTTGCGTGGGTTAACCCG
578	TGATTAGCGCTCAATACACGCGTG	CACGCGTGTATTGAGCGCTAATCA
579	AAGGGCAGACCTTTGGTTCGACTG	CAGTCGAACCAAAGGTCTGCCCTT
580	GCGCCACAAGATTCACATGTCATT	AATGACATGTGAATCTTGTGGCGC
581	GCCATGTTCAAGGGCCTTTTGAAG	CTTCGAAAGGCCCTTGAACATGGC
582	CGCGGTGTTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
584	CGATACGCGCCGGTTTGTTAAATC	GATTTAACAAACCGGCGCGTATCG
585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTTATAGCC
586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTACCCA
587	GTCTTCATCGCCCCGCGCAAGCTA	TAGCTTGCGCGGGCCGATGAAGAC
588	GCGACACACCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCCG
589	GTAGCAGGGTCCGCAAGACCAAGC	GCTTGGTCTTGCGGACCCCTGCTAC
590	TCGCCAACGCAGGGTAACTGCCAT	ATGGCAGTTACCCTGCGTTGGCGA
591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGAGT
592	TCCCGCCCACTAGACTGACTCGTA	TACGAGTCAGTCTAGTGGGCGGGA
593	ACCTTCTGGGGTTCGCTCACCAATA	TATTGGTGAGCGACCCCAAGGT
594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
595	CGCTGGACTGGCCTATCCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
596	CGGTCTCAGCAAACTGTGCGAAA	TTTGCAGAGTGTTGCTGAGACCG
597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTCCG
598	ATACCGTGCAGACAAGCCCTCTGA	TCAGAGGGGCTTGTCGCACGGTAT
599	AGCTCATTCCCGAGACGGAACACC	GGTGTTCCGTCTCGGGAATGAGCT
600	TTTCATGCGGCCGTTGCAAATCAT	ATGATTTGCAACGGCCGCATGAAA
601	ACTCGAACGGACGTTCAATTCCCA	TGGGAATTGAACGTCCGTTCCGAGT
602	CTGCATGGTGTGGGTGAGACTCCC	GGGAGTCTCACCCACACCATGCAG
603	CCGCGAGTGTGGATGGCGTGTGA	TCAACACGCCATCCACACTCGCGG
604	AATGTGTGCGTCTTAAGCCGGGTG	CACCCGGCTTAGGACCGACACATT
605	TAAGACGAGCCTGCACAGCTTGCG	CGCAAGCTGTGCAGGCTCGTCTTA
606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCACGCC
607	TGCTCCATGTTAGGAACGCACCAC	GTGGTGCGTTCCTAACATGGAGCA
608	CGGTGTTGGTCGGACTGACGACTG	CAGTCGTCACTCCGACCAACACCG
609	CCGCGCGTATCTATCAGATCTGGG	CCCAGATCTGATAGATACGCGCGG
610	AAAGCATGCTCCACCTGGAGCGAG	CTCGCTCCAGGTGGAGCATGCTTT
611	ACTTGCATCGCTGGGTAGATCCGG	CCGGATCTACCCAGCGATGCAAGT

	612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
	613	ATGCAGATGAACAAATCGCCGAAT	ATTCGGCGATTGTTCATCTGCAT
	614	GCAATTCTGGGCCATGTATTCGTC	GACGAATACATGGCCCAGAATTGC
	615	AGGGTTCCTTACGCGTCGACATGG	CCATGTCGACGCGTAAGGAACCCT
5	616	GTGGAGCTAATCGCGAGCCTCAGA	TCTGAGGCTCGCGATTAGCTCCAC
	617	TCGTAGTCTCACC GGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
	618	TTATAGCAGTGCGCCAATGCTTCG	CGAAGCATTGGCGCACTGCTATAA
	619	CGAACAGTGCTGTCCGTCGCTCAA	TTGAGCGACGGACAGCACTGTTTCG
	620	TCCGCGTGGACTGTTAGACGCTAT	ATAGCGTCTAACAGTCCACGCGGA
10	621	CATTAGCCCGCTGTCCGTAACGTG	ACAGTTACCGACAGCGGGCTAATG
	622	GGAAAGAACTCAGACGCGCAATG	CATTGCGCGTCTGAGTTTCTTTCC
	623	CGACTCGCTGGACAGGAGAATCGT	ACGATTCTCCTGTCCAGCGAGTCG
	624	CATGATCCTCTGTTTCACCCGCGG	CCGCGGGTGAAACAGAGGATCATG
	625	GGCGTAGCGCTCTAAAGCTTCGG	CCGAAGCTTTTAGAGCGCTACGCC
15	626	AGTGATGCCATCAGGCCCGTATAC	GTATACGGGCCTGATGGCATCACT
	627	TATGGAAAGGGCAACAGCGCTATC	GATAGCGCTGTTGCCCTTTCCATA
	628	CTGTGGTTGATGGAGGATCCACAC	GTGTGGATCCTCCATCAACCACAG
	629	ACTCGCTGGAATTTGCGCTGACAC	GTGTCAGCGCAAATTCAGCGAGT
	630	CAGGCCCGAACCACGCGGTTACAG	CTGTAACCGCGTGTTTCGGGCCTG
20	631	GGCGCAATGGGCGCATAAACTACTA	TAGTATTTATGCGCCCATTGCGCC
	632	GGTCAATTCGCGCTACATGCCCTA	TAGGGCATGTAGCGCGAATTGACC
	633	GATGGTGGACTGGAGCCCTTCCGC	GCGGAAGGGCTCCAGTCCACCATC
	634	CCGCGCATAGCGCAATAGGGGAGA	TCTCCCTATTGCGCTATGCGCGG
	635	TCTTCTGGCTGTCCGGCACCCGAA	TTCGGGTGCCGGACAGCCAGAAGA
25	636	GCGTTCGCAATTCACGGGCCCTTA	TAAGGGCCCGTGAATTGCGAACGC
	637	TCGTTTCGGCCTTGAGAGTATCG	CGATACTGTTCCAAGGCCGAAACGA
	638	AGGTGCAAGTGCAAGGCGAGAGGC	GCCTCTCGCCTTGCACTTGACCT
	639	CGCCAGTTTCGATGGCTGACGTTT	AAACGTCAGCCATCGAACTGGCG
	640	GCTTTACCGCCGATCCCAGATATC	GATATCTGGGATCGGCGGTAAAGC
30	641	GTGCTTGACGAAGAGGCGAAATGT	ACATTTGCGCTCTTCGTCAAGCAC
	642	CAGTCCGTGCGCTTCATGTCTCA	TGAGGACATGAAGCGCACGACTG
	643	TACGCGTAAGAGCCTACCCTCGCG	CGCGAGGGTAGGCTCTTACGCGTA
	644	GGCGAGTCTTGTTGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
	645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTTCGCTTTGG
35	646	GCCGTAGGTTGCTCTTCACCGAAC	GTTCCGTGAAGAGCAACCTACGGC
	647	AAATCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGCGGATTT
	648	GGCTTCGCACCCGTACCAATTTAG	CTAAATTGGTACGGGTGCGAAGCC
	649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGGACTCTACA
	650	CACTAGTCTGGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
40	651	TGTACTCGGCAGGCGCAATAGATT	AATCTATTGCGCCTGCCGAGTACA
	652	AACGGGTATCGGAAGCGTAAAGC	GCTTTTACGCTTCCGATACCCGTT

	653	CGGACTGCCCGTTTGCAAGTTGAG	CTCAACTTGCAAACGGGCAGTCCG
	654	ATCGTTCAGCACTGGAGCCCGTAA	TTACGGGCTCCAGTGCTGAACGAT
	655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
	656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
5	657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGCAC
	658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTTAGGACGATGAG
	659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACCGCCGAAGTGCCATT
	660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCACGG
	661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTCACCAACGAGAATTT
10	662	TTGCTCTTATCCTTGCTCGGGCG	CGCCCAGGACAAGGATAAGAGCAA
	663	TTAAGGATCAGGCGGAGCTTGCA	CTGCAAGCTCCGCCTGATCCTTAA
	664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGCAGCACCTTAGTCGCG
	665	GCTCGATTTACGGCCCGTTGTTC	GAACAACGGGCCGTGAAATCGAGC
	666	AGCAGAGTGCGTTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
15	667	TGGAGGTGAGGACGACGTGCACTA	TAGTGCACGTGTCCTCACCTCCA
	668	AACCGTTTAGGGTACATTCGCGGT	ACCGCGAATGTACCCTAAACGGTT
	669	TATGATCGCTCGGCTCACAGTTTG	CAAAGTGTGAGCCGAGCGATCATA
	670	GACTTTTTGCGGAAACGTCATGGT	ACCATGACGTTTCCGCAAAAAGTC
	671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAAGTGGAATAACCGACA
20	672	CTATGGTTTGCACTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
	673	AGCAGGGAAATTCAATCGTTTCGA	TGCGAACGATTGAATTTCCCTGCT
	674	CCTAACCGAGCGCTTAGCATTTCC	GGAAATGCTAAGCGCTCGGTTAGG
	675	CCCGACCCTAACTCGCATTGAATA	TATTCAATGCGAGTTAGGGTCGGG
	676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAAGCAA
25	677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAAGTAAACACGGCGAGCATC
	678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAACTCGTCATCCGA
	679	ATGCGGTCTACTTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
	680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
	681	AACCTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAATTAAGTT
30	682	GTGACCGCGAACTTGTTCCGACAG	CTGTGCGAACAAGTTCGCGGTCAC
	683	TGCGGATTACCGATTGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
	684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
	685	TCGCTCCGTAGCGATTATCGTAG	CTACGATGAATCGCTACGGAGCGA
	686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
35	687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
	688	TCACTCAGCGCTGTGACTGCCTGA	TCAGGCAGTCACAGCGCTGAGTGA
	689	GTTTGCGCTATAGTGGGGGACCGT	ACGGTCCCCCACTATAGCGCAAAC
	690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGAGAATGCGAC
	691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
40	692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTCACCCAAGGTCCCTT
	693	TCAAATGGCCACCGCGTGTCAATC	GAATGACACGCGGTGGCCATTTGA



5	694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
	695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGGAATAGCC
	696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
	697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
	698	GCCACAGAGTTTTAGCAGGGACCC	GGGTCCCTGCTAAACTCTGTGGC
	699	CCCACGCTTTCCGACCACTGACCT	AGGTCAGTGGTCGGAAAGCGTG
	700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCAATG
	701	AGCCACTCGACAGGGTTCCAAAGC	GCTTTGGAACCCTGTCGAGTGGCT
10	702	CAGGATGAGCAAAGCGACTCTCCA	TGGAGAGTCGCTTTGCTCATCCTG
	703	CAAGGTATGGTCTGGGGCCTAAGC	GCTTAGGCCCCAGACCATACCTTG
	704	GGTGTTGCGCCTAAACTCTTCGG	CCGAAAGAGTTTAGGCCGAACACC
	705	TTTAGTCGACCCCTGTGGCAATTC	GAATTGCCACAGGGTCCGACTAAA
	706	CACACGTTTCCGACCAGCCTGAAC	G TTCAGGCTGGTCGGAAACGTGTG
	707	CTGGACGAACTGGCTTCCTCGTAC	GTACGAGGAAGCCAGTTCGTCCAG
15	708	TTCACAATCCGCCGAAAACCTGACC	GGTCAGTTTTCGGCGGATTGTGAA
	709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATATCCTGTT
	710	TACGTCGGATCCATTGCGCCGAGT	ACTCGGCGCAATGGATCCGACGTA
	711	CATGGATCTCTCGGTTTGATCGCC	GGCGATCAAACCGAGAGATCCATG
	712	AGCCAGGCGCGTATATACGCTCGG	CCGAGCGTATATACGCGCCTGGCT
20	713	ATTTGGCACGTGTCGTGCCATGTT	AACATGGCACGACACGTGCCAAAT
	714	CCGCGTTGCACCACTTTGAGGTGC	GCACCTCAAAGTGGTGCAACGCGG
	715	TTGGACGTGACAAGCATGGCGCTC	GAGCGCCATGCTTGTCACGTCCAA
	716	CTGAATCGCGCAAGTAAATGGGGG	CCCCATTTACTTGCGCGATTACAG
	717	GATAAGGTCCACCAGATTGCGCGC	GCGCGCAATCTGGTGGACCTTATC
25	718	CTAACAATTGCCAACCGGGACGGC	GCCGTCCCGTTGGCAATTGTTAG
	719	GGTAACCTGGGTGCTTGCAAGTTA	TAACCTGCAAGCACCCAGGTTACC
	720	ATCGGAGCCACCATTGCGATTGGG	CCCAATGCGAATGGTGGCTCCGAT
	721	GTGAACTGGCTTGCCCCAGGATTA	TAATCCTGGGGCAAGCCAGTTCAC
	722	AGGCGATAGCATGGTCCCATATGA	TCATATGGGACCATGCTATCGCCT
30	723	AACGGTATCGTGGCTAATGCACGA	TCGTGCATTAGCCACGATACCGTT
	724	AGTAGTGGTCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCACTACT
	725	CCGTTGAATTGGACGGGAGGTTAG	CTAACCTCCCGTCCAATTCAACGG
	726	GCATAAGTGCGGCATCGGAAGGG	CCCTTCGCGATGCCGCACTTATGC
	727	CGACAAGATGCAGCTGCTACATGC	GCATGTAGCAGCTGCATCTGTGCG
35	728	TCGCAGTGATTCCCGACCGATAAG	CTTATCGGTGCGGAATCACTGCCA
	729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCTCGAGTGGACTCGCCTTG
	730	GCAACTTGACGGCATAAGTGGCC	GGCCACTTATGCCGTGCAAGTTGC
	731	TCCGAGCTTGACGTTGCGGACGTC	GACGTGCGGAACGTCAAGCTCGGA
	732	AGCGCTGGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
40	733	TTCATGTCGCTGAGTAACCTCGC	GCGAGGGTTACTCAGCGACATGAA
	734	CGAACCGCTAATGCCCATTTGTCAG	CTGACAATGGGCATTAGCGGTTGCG

	735	CACGGAAGGTGGGACAAATCGCCG	CGGCGATTTGTCCCACCTTCCGTG
	736	CACAGATGGAGACAAACGCGCCTT	AAGGCGCGTTTGTCTCCATCTGTG
	737	TTTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAAA
	738	ACGTTACGTTTCCGGCGCCTCTAA	TTAGAGGCGCCGGAACGTAACGT
5	739	TATCGGATTGCGTGGGTTTCAATC	GATTGAAACCCACGCAATCCGATA
	740	CTTCCACAATTGTCTGCGACGCAC	GTGCGTCGCAGACAATTGTGGAAG
	741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACCTTTGTGCA
	742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
	743	CTGAAACCGTGCGAATCGAGGTGA	TCACCTCGATTGCGACGGTTTCAG
10	744	CGGTGTTCCGCGTGTGAAAAAAT	ATTTTTTCGACACGCGGAACACCG
	745	TCTAGCAGGCCTTTTGAATCGCCA	TGGCGATTCAAAGGCCTGCTAGA
	746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
	747	TCTTCTGTCATCCTGCAGCAGCAT	ATGCTGCTGCAGGATGACAGAAGA
	748	GCGGATGAAACCTGAAAGGGGCCCT	AGGCCCTTTTCAGGTTTCATCCGC
15	749	GGGGCCCCAACTGGTATCAAGCC	GGCTTGATAACCAGTTTGGGGCCCC
	750	GCATTGGCTTCGGATTCTCCTACA	TGTAGGAGAATCCGAAGCCAATGC
	751	AGGCGGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGGCCGCCT
	752	ACACCATGTGCTCCGCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
	753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCGATTTCATGTTTCATCGT
20	754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
	755	GTGCCGTATTTGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
	756	GCAGTGCGCACTTCAGTTCAAAG	CTTTTGAAGTGAAGTGCGCACTGC
	757	GCGATTTTAAGCGATGCCTTGACG	CGTCAAGGCATCGCTTAAATCGC
	758	TAGGTGACCTAGGCTTGCTTGCGG	CCGCAAGCAAGCCTAGGTCACCTA
25	759	CTGGATACCTTGCTGTGCGGCGC	GCGCCGCACAGGCAAGGTATCCAG
	760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
	761	GCGCTTGCCCGATGCGATGCATTA	TAATGCATCGCATCGGGCAAGCGC
	762	TTTCTGTAAGCGGCCTGGGGTTCA	TGAACCCAGGCCGCTTACAGAAA
	763	GGCTGAGGTGAGCGGTAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
30	764	TCTTGGCCTCCCCGATCTAATTTG	CAAATTAGATCGGGGAGGCCAAGA
	765	GGAGGTAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
	766	GTAATCCATTTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
	767	CAAACCCATTCCAGCAGACGCCTG	CAGGCGTCTGCTGGAATGGGTTTG
	768	TAGGAGGAATTTGGCATGCGGGCG	CGCCCGCATGCCAAATTCCTCCTA
35	769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGGCACATCCTACCTAT
	770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
	771	CTGGCTGTGTCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
	772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
	773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
40	774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTCTGCTCCTGCT
	775	TTCAAGCACCATCGTGCAATCCAA	TTGGATTGCACGATGGTGCTTGAA

5	776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
	777	TACATTCCCTGCCTCCGTGGGCTT	AAGCCCACGGAGGCAGGGAATGTA
	778	CGCTTCGCGTATTCAGTAGCGGTT	AACCGCTACTGAATACGCGAAGCG
	779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTCGACGCGTCCGA
	780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGCTCAGA
	781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGAATTCAA
	782	AGTTTTCGCCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAACT
	783	GTTTCATAGGCCACGCGTGCTAAA	TTAGCACGCGTGCCCTATGAAAC
10	784	GGAGCGAAGACTTCGTCTGCCCAA	TTGGGCAGACGAAGTCTTCGCTCC
	785	ATTGGCCGAGGGTGAATGCAGCCT	AGGCTGCATTACCCCTCGGCCAAT
	786	TGATCCATCCGAATGCTTTTCCAT	ATGGAAAAGCATTGGGATGGATCA
	787	GCACACAGTTGTCTTGGCCCATGA	TCATGGGCCAAGACAACTGTGTGC
	788	CTGGCGGGCAGTGGAACAAAC	GTTGTTTTTCCACTGCCC GCCAG
15	789	ATCTCCATGCGTAAGACTGCTCCG	CGGAGCAGTCTTACGCATGGAGAT
	790	TCTCCTCTCGTCGCAGTTCGTGGA	TCCACGAACTGCGACGAGAGGAGA
	791	TAGCGTATTCACTCTTGCCGAGCA	TGCTCGGCAAGAGTGAATACGCTA
	792	CAATCAAAAGCCACGGCGCGATGG	CCATCGCGCCGTGGCTTTTGATTG
	793	AGCGTCACGGAATTCAGCAGATCT	AGATCTGCTGAATTCGGTGACGCT
	794	GACTCCCTGTTAATGCGCCCAAGG	CCTTGGGCGCATTAAACAGGGAGTC
20	795	TAGGCACTGCCGGTTCAGATTCAA	TTGAATCTGAACCGGCAGTGCCTA
	796	AACAGGGTGATAACGGTGGCCAAT	ATTGGCCACCGTTATCACCCGTGT
	797	CGTGCGTACCATGTGTAAGTGCGT	ACGCACTTACACATGGTACGCACG
	798	GACCAATTCTACTTCGGCAGCCCA	TGGGCTGCCGAAGTAGAATTGGTC
	799	ATCGGACCGATTGCTTTTGGCTG	CAGCCAAAAGCAAATCGGTCCGAT
25	800	TCCGCCGAAGCACACGCTTATTCG	CGAATAAGCGTGTGCTTCGGCGGA
	801	AACGGTACGCATTGTGAGCAGTGT	ACACTGCTCACAATGCGTACCGTT
	802	TGGCGACTACTGTTCCCTGAATC	GATTCAGGGGAACAGTAGTCGCCA
	803	CAGAGGGGACAGCCGTATGCCTTA	TAAGGCATACGGCTGTCCCCTCTG
	804	CGGTGGTTTTATCGGAATCTGCGA	TCGCAGATTCCGATAAAACCACCG
30	805	TTGGCCTCCGACCTCACGACATAT	ATATGTCGTGAGGTGCGAGGCCAA
	806	CGTTTCGCTAGCATCTGGCGCCGA	TCGGCGCCAGATGCTAGCGAAACG
	807	ACTAAGCGGTGGAGCCGGTGGATG	CATCCACCGGCTCCACCGCTTAGT
	808	ATATTGGCTGCGTTTACGGGCCGC	GCGGCCCGTAAACGCAGCCAATAT
	809	CCGCTATGGTGGCAATCCCGATAC	GTATCGGGATTGCCACCATAGCGG
35	810	GTTGCATGTGGCTCAGGCGGCATA	TATGCCGCCTGAGCCACATGCAAC
	811	ATTCTGGGGAGTGACCCAGGGCTT	AAGCCCTGGGTCACTCCCCAGAAT
	812	CTCTCCAAGGAGACGAGCCAATGT	ACATTGGCTCGTCTCCTTGAGAG
	813	GAAAGGACGGGATTTGGGGGCTAA	TTAGCCCCCAAATCCCGTCTTTTC
	814	TATGTAGTACCTTGGCTCGCGCCA	TGGCGCGAGCCAAGGTACTACATA
40	815	TCCCTTTCGATGAGCGGCTGTACT	AGTACAGCCGCTCATCGAAAGGGA
	816	TAGATCGGGCAGAGCCCGTATCTT	AAGATACGGGCTCTGCCCGATCTA

	817	GGAATGCTTTAGGCTGCCGAGCTG	CAGCTCGGCAGCCTAAAGCATTCC
	818	ATGGTAGCAACATTCAACGCCAGG	CCTGGCGTTGAATGTTGCTACCAT
	819	CTATGAAACGTGTGGCCAGCAAC	GTTGCTGGGCCACACGTTTCATAG
5	820	ATGTTGCTAGTGCCTTTCGGGCCT	AGGCCCCGAAAGGCACTAGCAACAT
	821	CCAATGTGCGCAGACTCAGTCATT	AATGACTGAGTCTGCGCACATTGG
	822	GATAGTGCTCGCAAACGGGCCTTC	GAAGGCCCCGTTTGCGAGCACTATC
	823	GCACCCTGTTGCCTCATTGAGCGT	ACGCTCAATGAGGCAACAGGGTGC
	824	GGCGTGAATAGAGTGACCAGGCGG	CCGCCTGGTCACTCTATTACGCCC
10	825	ACGTGCCAGCTGCGGGCACTTTAT	ATAAAGTGCCCGCAGCTGGCACGT
	826	AGTGGAATAGTCGCGTCGTGCCGC	GCGGCACGACGCGACTATTCCACT
	827	ACTCGCCTATTACCGCTGGATTGG	CCAATCCAGCGGTAATAGGCGAGT
	828	GAGACCGGATTGAGATGATCCCGT	ACGGGATCATCTCAATCCGGTCTC
	829	CTGGCAGTTTACCACCGAACCACT	ACTGGTTCGGTGGTAAACTGCCAG
	830	TTACATTGCCGATTTTCGCATGTGA	TCACATGCGAAATCGGCAATGTAA
15	831	TAAAACTGAAGGGTCGCCTCAGCA	TGCTGAGGCGACCCTTCAGTTTTA
	832	GGCTTCGCATGCCTTTGCAACATT	AATGTTGCAAAGGCATGCGAAGCC
	833	AAGACCGAAGGTCTCTCTGAGGGC	GCCCTCAGAGAGACCTTCGGTCTT
	834	GCCTATGGCTCCAGCTCAGCAGTA	TACTGCTGAGCTGGAGCCATAGGC
	835	CGTATCATAGCGTTTCGGTGGACAA	TTGTCCACCGAACGCTATGATACG
20	836	CATGCGCTCGCACTCTGCCTGTCT	AGACAGGCAGAGTGCGAGCGCATG
	837	TGGGCAATTTCGAAACGTCGGTCT	AGACCGACGTTTCCGAATTGCCCA
	838	TTGCGGAGATGCGACGGTACATTG	CAATGTACCGTCGCATCTCCGCAA
	839	ACTTTCGCACGTCGATCTGGACTG	CAGTCCAGATCGACGTGCGAAAGT
	840	CTAACTGCCGCGGCAAACTGATTA	TAATCAGTTTGCCGCGGCAGTTAG
25	841	GGCCGCGGATTTTATTCTTGGAT	ATCCAAGGAATAAAATCCGCGGCC
	842	GAATTTGGAACGGTGTTCCGATGA	TCATCGGAACACCGTTCCAAATTC
	843	GTCCATCCATCTACGGCATCAGGA	TCCTGATGCCGTAGATGGATGGAC
	844	TAAACGACCTGGCACATGTGCGTA	TACGCACATGTGCCAGGTGCTTTA
	845	CACCATCCAAGAGCCAATCCTAGG	CCTAGGATTGGCTCTTGGATGGTG
30	846	ACTCATATACGATCAGTCCGCCGC	GCGGCGGACTGATCGTATATGAGT
	847	GTGCCAACCGACGATCAACCGAAC	GTTCCGTTGATCGTCGGTTGGCAC
	848	TGGGGTTTCGTACAGGTCCGTTTCAT	ATGAACCGACCTGTACGAACCCCA
	849	AACAGTAGAGGCGAGGCCTGCGGG	CCCGCAGGCCTCGCCTCTACTGTT
	850	TGCATCGAATCCGAGATGGATCTT	AAGATCCATCTCGGATTCGATGCA
35	851	GCGTCACGTTATGTCCGCTCTGTC	GACAGAGCGGACATAACGTGACGC
	852	GGGACATGCGTAGCGCAATATCAC	GTGATATTGCGCTACGCATGTCCC
	853	CACACGTCACACCATCCAAAGTGG	CCACTTTGGATGGTGTGACGTGTG
	854	ATGCTCAGGTGCTAAATACGGCCA	TGGCCGTATTTAGCACCTGAGCAT
	855	AAAAATGTTTAGCGCGCTGACTGG	CCAGTCAGCGCGCTAAACATTTTT
40	856	ATAGTCCGTTTCCGTTCCCAACGA	TCGTTGGGAACGGAACGGACTAT
	857	TCGATCTTCTGGGTTGCAGACCAG	CTGGTCTGCAACCCAGAAGATCGA

5	858	GTCGGCGCAGCCGATCCTCATGTC	GACATGAGGATCGGCTGCGCCGAC
	859	GTTGCGGGGTGTGCGAAAAGGATCT	AGATCCTTTTCGACACCCCGCAAC
	860	ATCTCTTCCTCGGGTGGATGCCAG	CTGGCATCCACCCGAGGAAGAGAT
	861	TGATGTGCGTTTCAGCTTTTCGCG	CGCGAAAAGCTGAAACGCACATCA
	862	GTTAAGGGGTGAGAACATCCGGCC	GGCCGGATGTTCTCACCCCTTAAC
	863	AAGTCGTCTCCCTGCGTCTCGTCC	GGACGAGACGCAGGGAGACGACTT
	864	CCGACCTAATAAGGCGCAACAATG	CATTGTTGCGCCTTATTAGGTCGG
	865	CATCATTGGCACCGTACCAATGCC	GGCATTGGTACGGTGCCAATGATG
10	866	TGGAGAAAGGGAAGTGCAGCAACG	CGTTGCTGCACTTCCCTTTCTCCA
	867	TGGTACTCCTTGTCATGCCTGCCA	TGGCAGGCATGACAAGGAGTACCA
	868	GGCACAGGTTCTCTTGACGCGCGG	CCGCGCTGCAAGAGAACCTGTGCC
	869	GAATCTGGGCATTGCTACGAGACC	GGTCTCGTAGCAATGCCAGATTTC
	870	CGAAATGGGAGCGTCCACTACCAC	GTGGTAGTGGACGCTCCCATTTTCG
15	871	ACATATGAGCTCGCGTGCTTGCAT	ATGCAAGCACGCGAGCTCATATGT
	872	TCGAGCACGGTCACTGATAAAGCC	GGCTTTATCAGTGACCGTGCTCGA
	873	GAGGGTCCCTGCTCAGAGTTGGTT	AACCAACTCTGAGCAGGGACCCTC
	874	AAATGCGATCGCCCCCTTATGGAAT	ATTCCATAAGGGGCGATCGCATTT
	875	CTACCCGAATGGATTGCGGATGGC	GCCATCCGCAATCCATTCGGGTAG
20	876	AGGGACTGGCAGGTCTCTGCGCGT	ACGCGCAGAGACCTGCCAGTCCCT
	877	TAACGATCCATTCCACGAATGCAG	CTGCATTCTGGAATGGATCGTTA
	878	GGCCGCACGTACGATTACGCCTTG	CAAGGCGTAATCGTACGTGCGGCC
	879	TGGGGAATGCATCAGTTGTTGGCT	AGCCAACAACCTGATGCATTCCTCA
	880	TATCTGGGAGTAGCAGGCAGGGCC	GGCCCTGCCTGCTACTCCCAGATA
25	881	CCGAAGGTTTCACGCTCAGGTGCG	GCGACCTGAGCGTGAAACCTTCGG
	882	GAACCCAGCTGGGACATCCTTCAG	CTGAAGGATGTCCCAGCTGGGTTTC
	883	TGCATGCGAGCAAATAACCCGGAC	GTCCGGGTATTGCTCGCATGCA
	884	AATTGTCCGCCAAACGCTTTTCAG	CTGAAAAGCGTTTGCCGGACAATT
	885	GTCGGCTTCGAGCGATCGAGTGTG	CACACTCGATCGCTCGAAGCCGAC
	886	TCGCGTGCTCTACGTAGCCCATGA	TCATGGGCTACGTAGAGCACGCGA
30	887	GGCTTCCGCGATAACGTAATTCGC	GCGAATTACGTTATCGCGGAAGCC
	888	TGTAGCCGACTAGGGCCGAAGCCC	GGGCTTCGGCCCTAGTCGGCTACA
	889	AAGCGAACGCCCTGGCTGAATATT	AATATTCAGCCAGGGCGTTTCGCTT
	890	TGTCACGCGACGTGCTGCAGATTT	AAATCTGCAGCACGTGCGTGACA
35	891	CCGTGTCCGTGTTGTGACAGGCG	CGCCTGTGACAACACGGACACGG
	892	CCCCACACGTTGCGCCTATATGTG	CACATATAGGCGCAACGTGTGGGG
	893	GGCGGGCACAACCTCAACACAGATG	CATCTGTGTTGAGTTGTGCCCGCC
	894	CGACTGCGGGATACCGGTGATTA	TAATCACCGGTGATCCCGCAGTCG
	895	TCGGGACATGACCGGTACGGAGTC	GACTCCGTACCGGTATGTCCCGA
	896	TACCTCGAGTGGCCGTTGATCGGG	CCCGATCAACGGCCACTCGAGGTA
40	897	TAATTCATGGGGCTAGCCGAACCA	TGGTTCCGGCTAGCCCCATGAATTA
	898	ACACTCTAAGCCGATTCCGTTCTGA	TCGAACGGAATCGGCTTAGAGTGT

5	899	GTGGGCGTGAGTGACACGCACAAA	TTTGTGCGTGCTCACTCACGCCCAC
	900	ACGACTCCTCGGGCAAAGTACGTA	TACGTACTTTGCCCCGAGGAGTCGT
	901	TGTGGTCATGGCGCTACTGTTTTTC	GAAAACAGTAGCGCCATGACCACA
	902	CTTTCGCTAGCCAGAGCGGGTTCC	GGAACCCGCTCTGGCTAGCGAAAG
	903	ACAGGGCGTGTTAGCGTGTGACAA	TTGTCACACGCTAACACGCCCTGT
	904	GGTACTTCCGGCGTATCGGGCCAC	GTGGCCCCGATACGCCGGAAGTACC
	905	GTGGGTTTTGTTACCCCTTCTGGG	CCCAGAAGGGTGAACAAAACCCAC
	906	ACGCAATTCCGCATTACTTACCCG	CGGGTAAGTAATGCGGAATTGCGT
10	907	CGCCTCGACTGCGGTCAAGCACAA	TTGTGCTTGACCGCAGTCGAGGCG
	908	GTGAAATGGATCCAGAGAGGGCCA	TGGCCCTCTCTGGATCCATTTTAC
	909	TATAAACGCTGCAGGGCTCCGTTA	TAACGGAGCCCTGCAGCGTTTATA
	910	GTTATTCAGGCGGCTTGTAACGGG	CCCGTTACAAGCCGCCTGAATAAC
	911	GGGTTCTAGCGTGCGGTTTCACTT	AACTGAACGCGCACGCTAGAACCC
	912	TTGGGCTCGAGCGGTACACCACTA	TAGTGGTGTACCGCTCGAGCCCAA
15	913	CCGTCTTCAGGACAACGGTATGCG	CGCATACCGTTGTCCTGAAGACGG
	914	GGACCCCTTGACAGATTGCGGCAC	GTGCCGCAATCTGTCAAAGGGTCC
	915	TAAATTTTATCGCCAGGCGGCGCT	AGCGCCGCTGGCGATAAAATTTA
	916	GCCGAACGCAAGATCGCTTGAAC	AGTTCAAGCGATCTTGCGTTCCGGC
	917	TAGGCCATTGGTGCCCTAAGACGG	CCGTCTTAGGGCACCAATGGCCTA
20	918	CAAACACAGCTTACAGGCTGCGT	ACGCAGCCTGTAAGCTGTGGTTTG
	919	TAAACGGAGACTGGCACGGTAGCA	TGCTACCGTGCCAGTCTCCGTTTA
	920	TAGCGCGCATCACACTTGGAATCG	CGATTCCAAGTGTGATGCGCGCTA
	921	TGCTGACACAAACGAGCCGTTTCG	CGAAACGGCTCGTTTTGTGTCAGCA
	922	CGCTTAACGGCATTGACTGTCCAC	GTGGACAGTCAATGCCGTTAAGCG
25	923	TTCCACGGCCGTGTATTACGGATA	TATCCGTAATACACGGCCGTGGAA
	924	TTTATGCCGTTGCCGAGGAAGACT	AGTCTTCGTCGGCAACGGCATAAA
	925	AGTGCCGAGATAGGGGACTGGGCG	CGCCCAGTCCCCTATCTCGGCACT
	926	CTAGTCTCCACGCCCTCGGGACGA	TCGTCCCAGGGCGTGAGACTAG
	927	CCGCCATTCCGAAGATGGATGATG	CATCATCCATCTTCCGAATGGCGG
30	928	TGACGGTGAAAGTCGATTGCGAAG	CTTCGCAATCGACTTTCACCGTCA
	929	ATATGCGTCACCACCCGGTTCCGA	TCGGAACCGGGTGGTGACGCATAT
	930	CCATCAGTGAAGGGGTGCTGCCA	TGGCAGCAACCCCTTCACTGATGG
	931	CATATGTGCTTGGCTTGCGATGAC	GTCATCGCAAGCCAAGCACATATG
	932	TCTGCTTTGGAAGCCTGAACTGCT	AGCAGTTCAGGCTTCCAAAGCAGA
35	933	CGATTTGGTCAAGAAGGCGGAAAT	ATTTCCGCCTTCTTGACCAAATCG
	934	ATCAGAGGCCCTCCCGCCTCGTTA	TAACGAGGCGGGGAAGGCCTCTGAT
	935	ATTGTTGTCGTTGCCACATCGCAG	CTGCGATGTGGCAACGACAACAAT
	936	TGAAATGTGTCTGGACGCGAGTCT	AGACTCGCGTCCAGACACATTTCA
	937	GCGGGCGATGCTCCTTAAAGGGTA	TACCCTTTAAGGAGCATCGCCCGC
40	938	CCGCAATCTCCATGCGTCGACCGT	ACGGTCGACGCATGGAGATTGCGG
	939	TGCCGCGTAATCACCTGGAACCTG	CAAGTTCAGGTGATTACGCGGCA

5	940	TTCCAGTAGCCAGCGGTAGTGTGA	TCACACTACCGCTGGCTACTGGAA
	941	CTGAATTCGCCTATTGTTCGGCA	TGCCGAACAATAGGCGGAATTCAG
	942	GCTTGAACCTCGAGGCGATGTTCT	AGAACATCGCCTCGAGGTTCAAGC
	943	CAAGCGTGGAAGTACGACCCGCCA	TGGCGGGTCGTACTTCCACGCTTG
	944	GTGTGCACTGGATCCGAGCCCTAG	CTAGGGCTCGGATCCAGTGACACAC
	945	TCCCTGGGCTAGCATTGCGAGGTT	AACCTCGCAATGCTAGCCCAGGGA
	946	AGAACCAAAGACGCTTGTTCGCG	CGGCAAACAAGCGTCTTTGGTTCT
	947	CGTCACATGCAAACGTTCCCTCCC	GGGAGGGAACGTTTGCATGTGACG
	948	TGACCGCATGTGTATTGAGTCGCT	AGCGACTCAATACACATGCGGTCA
10	949	GCGGGCCCAATGAGTATCCGTCAT	ATGACGGATACTCATTGGGCCCCGC
	950	TAGTGACTGTGAACGCCCTGGTT	AACCAGGGGCGTTACAGTCACTA
	951	GGCACCGTCTGCCGCGCGTATATC	GATATACGCGCGGCAGACGGTGCC
	952	TCGATGCAGTCTTTTCCCGTCAA	TTGACGGGAAAAAGACTGCATCGA
	953	ACCCCGTGGGGTTTCGCCATTTT	AAAAATGGCGAAACCCACGGGGT
15	954	CTACACGCGCAGTTGTGACTTGTG	CACAAGTCACAACTGCGCGTGTAG
	955	CGCAGCGACCTCATCTCTGGAGCC	GGCTCCAGAGATGAGGTCGCTGCG
	956	CGACCCAGCACTCCTAAAATCGGT	ACCGATTTTAGGAGTGCTGGGTCTG
	957	ACGCGCCGCTCATCACTACAATCT	AGATTGTAGTGATGAGCGGCGCGT
	958	CGCAACTTCCTGTGGCAAAGCCAG	CTGGCTTTGCCACAGGAAGTTGCG
20	959	TCGTTGGGCACATAAGGCAACTGA	TCAGTTGCCTTATGTGCCAACGA
	960	CCGCTTGTAATTGCCATTCTCCGT	ACGGAGAATGGCAATTACAAGCGG
	961	GTAACCAGGGAGTCCTGGGCTGTG	CACAGCCCAGGACTCCCTGGTTAC
	962	AGCGCAAGATCTGGGGGCAAGTAC	GTGACTGCCCCCAGATCTTGCGCT
	963	GCGTACATCTGCTCATCAGCATGG	CCATGCTGATGAGCAGATGTACGC
25	964	CCTCTGTGGCAGGAAAGAAACCGT	ACGGTTTCTTTCTGCCACAGAGG
	965	CCTATGCAATGGACCTGCATCGGA	TCCGATGGAGGTCCATTGCATAGG
	966	CTCGGTGGATGGCGAATAAGGATA	TATCCTTATTCGCCATCCACCGAG
	967	CCTCACTCGTGATGGCGTGACGCA	TGCGTCACGCCATCACGAGTGAGG
	968	TACGCTCACAGAACGCCATACGCC	GGCGTATGGCGTTCTGTGAGCGTA
30	969	CCGGAGAAGTTACGCGGATCGGAC	GTCCGATCCGCGTAACCTCTCCGG
	970	GCGCCCTCACTGCATTTTGGTAT	ATACCAAAAATGCAGTGAGGGCGC
	971	ACTTTCAGCACGCGAACAGCGCAA	TTGCGCTGTTGCGGTGCTGAAAGT
	972	CTAAACGCCCTTGATGCATGAGCA	TGCTCATGCATCAAGGGCGTTTAG
	973	GCTTGCCCTTTTACGATCGTCGCTA	TAGCGACGATCGTAAAAGGCAAGC
35	974	CAGACATCGTACGCACTCGGCATC	GATGCCGAGTGCGTACGATGTCTG
	975	TAGCCGCGCGGCTCCTATGCTCTT	AAGAGCATAGGAGCCGCGCGGCTA
	976	GATGCCCTTTTGGTCCCCATGCCA	TGGCATGGGGACCAAAAGGGCATC
	977	TGAGCTGCCTTGCCACGATGCCTC	GAGGCATCGTGGCAAGGCAGCTCA
	978	CCGCCGTATACGTGCCATAGTTTG	CAAACATGGCACGTATACGGCGG
40	979	TAGTGCTCTCCGCGCTCATCCAAC	GTTGGATGAGCGCGGAGAGCACTA
	980	CCCTAGATAAGTTGGGGTGGGACG	CGTCCCACCCCAACTTATCTAGGG

5	981	TGAAGGGCCACCTGATATGGTTTC	GAAACCATATCAGGTGGCCCTTCA
	982	GCCGCCTCCGACTGGTTAACCCGA	TCGGGTTAACCAGTCGGAGGCGGC
	983	CGCACGGCTACTAACAGCGGATCA	TGATCCGCTGTTAGTAGCCGTGCG
	984	CCGGACCAATTCCAACGAGCATCG	CGATGCTCGTTGGAATTGGTCCGG
	985	CATTGAGGTCCACCGTTCACATCC	GGATGTGAACGGTGGACCTCAATG
	986	AGGACGCAGCATGTCCCAGCCGAG	CTCGGCTGGGACATGCTGCGTCCT
	987	TAATCGCGGGCCATACTACCAACG	CGTTGGTAGTATGGCCCCGCGATTA
	988	CGCAAATTTCTCCGGTCGGCAAGC	GCTTGCCGACCGGAGAAATTTGCG
	989	GTGGCTCGACTAATGCCTTGCGTG	CACGCAAGGCATTAGTCGAGCCAC
10	990	TGTGGGCGTGTTCCGGCTCACTGT	ACAGTGAGCCGGAACACGCCACACA
	991	GTTCTTCCTTTTCTGCGGTGGGAA	TTCCACCCGAGAAAAGGAAGAAC
	992	ACCTCGAGTCAGATTGTGCGCCTT	AAGGCGCACAATCTGACTCGAGGT
	993	CAAGTGGACAGACGGTTTGTTCCG	CGGAACAAACCGTCTGTCCACTTG
	994	TCCAGTTGAGTCGCGCCGACGAGG	CCTCGTCGGCGCGACTCAACTGGA
15	995	CGCAACAGGTCAGCCCTTATTTGC	GCAAATAAGGGCTGACCTGTTGCG
	996	GCCGTGACTCCTGCAATGTCGGTA	TACCGACATTGCAGGAGTCACGGC
	997	ATCAGCGCAAGCTGGTCTGAAACA	TGTTTCAGACCAGCTTGCGCTGAT
	998	CCCTGGCCAGAACGAGAGGCCATG	CATGGCCTCTCGTTCTGGCCAGGG
	999	ACGATCAAGGACTCGTCAGGGTTG	CAACCCTGACGAGTCCTTGATCGT
20	1000	TTCATGGCACCAAGACCACCGTTA	TAACGGTGGTCTTGGTGCCATGAA
	1001	ACAGCAAGGAGATGGATTGCGACG	CGTCGCAATCCATCTCCTTGCTGT
	1002	CGTAAATATCTGCGGCGGTGTGAA	TTCACACCGCCGAGATATTTACG
	1003	GGAAACACGTGTTCTGTCTGTTGGC	GCCAACAGACGAACACGTGTTTCC
	1004	CGATGTTAGGATTTCGGATAGGCCA	TGGCCTATCCGAATCCTAACATCG
25	1005	ATCGGACAAGGACAAGTGGATGGT	ACCATCCAATTGTCCTTGTCGGAT
	1006	GCCCGGAGGACAAAGTTCGAGTTA	TAACTCGAACTTTGTCTCCGGGC
	1007	AAATCCGACAAATGGGCACATGGA	TCCATGTGCCCATTTGTGCGATTT
	1008	CAGTTAGGGGATGCGGATGAGTGA	TCACTCATCCGCATCCCTAACTG
	1009	CGGCAGGTGGAGATTCCGACATTG	CAATGTCGGAATCTCCACCTGCCG
30	1010	TAGGGCAGCCAGGTTCACTCATCT	AGATGAGTGAACCTGGCTGCCCTA
	1011	GCACCGTATTAGCAGTAGGCACGC	GCGTGCCTACTGCTAATACGGTGC
	1012	ACGCATTACAGGTGTGCGAAGGGA	TCCCTTCGCACACCTGTAATGCGT
	1013	CGTGA CTGCACGTGTTCCACAGGG	CCCTGTGGAACACGTGCAGTCACG
	1014	GCTGAACTACCGCCTAAAATCGCG	CGCGATTTTAGGCGGTAGTTCAGC
35	1015	AGCACGCCAGGGAGGATCGAGTTA	TAACTCGATCCTCCCTGGCGTGCT
	1016	ATGAGGGCAAGGAATGGGTCATGC	GCATGACCCATTCTTGCCCTCAT
	1017	GGGTCTCTCGTAATCAAAGGCCGA	TCGGCCTTTGATTACGAGAGACCC
	1018	TATCTTGCGCAACGCCTCCATTTA	TAAATGGAGGCGTTGCGCAAGATA
	1019	GGTTACACCTACGGAATCCAGCGG	CCGCTGGATTCCGTAGGTGTAACC
40	1020	ACACCGAGTTGGTCCGGTCAATAG	CTATTGACCGGACCAACTCGGTGT
	1021	TCCCAGATTAAACGCTAGCCACCG	CGGTGGCTAGCGTTTAATCTGGGA



5	1022	TTGGTGAAACTGGCCCGTCGGAAG	CTTCCGACGGGCCAGTTTCACCAA
	1023	CCAGGGGAGTTGACAATGAGGCTG	CAGCCTCATTGTCAACTCCCCTGG
	1024	TCTGCGTTATTGGACCGTTTGTCTG	CGACAAACGGTCCAATAACGCAGA
	1025	TATGGGATGCTAAACCGGCGTACA	TGTACGCCGGTTTAGCATCCCATA
	1026	CACAGACGTCTGTCTGGGCTTGTGT	ACACAAGCCCCGACAGACGTCTGTG
	1027	AGAATGCCGTTCTGCCTACTCCCGT	ACGGGAGTAGGCGAACGGCATTCT
	1028	CGACGGATAATGCAGGCCTCATGA	TCATGAGGCCTGCATTATCCGTCTG
	1029	ACCCTCTAAAGCAATAGGTCGGCG	CGCCGACCTATTGCTTTAGAGGGT
10	1030	CACTCACGGCAGAAGCCTGCTTGT	ACAAGCAGGCTTCTGCCGTGAGTG
	1031	ATCAGCCCACATATTCTCGGCCGT	ACGGCCGAGAATATGTGGGCTGAT
	1032	CAAATCTGGGGTCGTCTAAACGC	GCGTTTAGGACGACCCCAGATTTG
	1033	TGTCGCCCCATGGCAGGTTAAATAC	GTATTTAACCTGCCATGGGCGACA
	1034	GGGGGCCCCATCAATTCATTATCGA	TCGATAATGAATTGATGGGCCCCC
	1035	GTCGAGCAGCTTTAGTATCGCGGG	CCCGCGATACTAAAGCTGCTCGAC
15	1036	CCGCTAAGCACC GAAGGCTCACAA	TTGTGAGCCTTCGGTGCTTAGCGG
	1037	TAGAATTAGCGAACGGTGATCCCG	CGGGATCACCGTTCGCTAATTCTA
	1038	CACATGACATTTGGCAAAGGTCCA	TGGACCTTTGCCAAATGTCATGTG
	1039	TCAACGCACTGGCGATGACTAGAT	ATCTAGTCATCGCCAGTGCGTTGA
	1040	CGGGAAATGTCTTTAGCCGTCGAA	TTCGACGGCTAAAGACATTTCCCG
20	1041	ATCAGAGCAAATCTGCAGCGGGGA	TCCCCGCTGCAGATTTGCTCTGAT
	1042	GGCCTGTTTCTGTCCAAGTGGGCT	AGCCCAGTTGGACAGAAACAGGCC
	1043	ATTTACCTCGCTGATCGCTTCCG	CGGAAGCGATCAGCGAGGTGAAAT
	1044	AGTGACGCCGAGTCGCGAGGGTTA	TAACCTCGCGACTCGGCGTCACT
	1045	AGTTGTCTCATCCTGTCCGGGACC	GGTCCCGGACAGGATGAGACAAGT
25	1046	CTTCTTTGTGCACACTTGCCAGGG	CCCTGGCAAGTGTGCACAAAGAAG
	1047	CACCTCATCGGAGCATAGCAACCC	GGGTGCTATGCTCCGATGAGGTG
	1048	ATGCGATCCATGACAAGGGTTGCT	AGCAACCCTTGTCATGGATCGCAT
	1049	CCCGTGGAGATGATGTGCGGCTTA	TAAGCCGCACATCATCTCCACGGG
	1050	CCCAATAGACGCCACAGCCAGTGA	TCACTGGCTGTGGCGTCTATTGGG
30	1051	AACGACCACGACCCTCGCCGAGTA	TACTCGGCGAGGGTCGTGGTCGTT
	1052	GGTGCTTTGTCTGAGGCGAGTGAA	TTCACTCGCCTCAGACAAAGCACC
	1053	CTGTGCGCGCTGCTCTCCGAATTT	AAATTTCGGAGAGCAGCGCCGACAG
	1054	CTCGCCGGAGTGTTGTAAGCATTG	CAATGCTTACAACACTCCGGCGAG
	1055	AGCAATCATGAGAGGTGGCCGGTG	CACCGGCCACCTCTCATGATTGCT
35	1056	ATTTGCCACCGGCGACAAAAAGAT	ATCTTTTGTGCGCCGGTGGCAAAT
	1057	CCGCCCCTGTTGGCATGTCTTTTG	CAAAAGACATGCCAACACGGGCGG
	1058	ATCGGAAGTGCTGACTGACACACG	CGTGTGTCAGTCAGCACTTCCGAT
	1059	CCTCAGACCCTATCTGGGTTGACG	CGTCAACCCAGATAGGGTCTGAGG
	1060	CTGTGTGGTCTGGTCCGGCTGTTT	GAACAGCCGGACCAGACCACACAG
40	1061	GTCCCCATTATCGGTGAGTGCAAC	GTTGCACTCACCAGATAATGGGGAC
	1062	ACAGGCACGTAAGTGCTCAATCGG	CCGATTGAGCACTTACGTGCCTGT

	1063	AGCAAGATAGCGGGAGTGCCCTA	TAGGGGCACTCCCGCTATCTTGCT
	1064	GGTTTACGCCATGACATCCCGTCA	TGACGGGATGTCATGGCGTAAACC
	1065	GTGCAGGCCTTTGTGTGTGAATCG	CGATTACACACAAAGGCCTGCAC
	1066	CTTCGAGGGTAGGGCTTCGAAACG	CGTTTCGAAGCCCTACCCTCGAAG
5	1067	AGTCGACACTTGGGTTTACCACGG	CCGTGGTAAACCCAAGTGTCGACT
	1068	ACATAAATCTCGCCCGCTGCACTC	GAGTGCAGCGGGCGAGATTTATGT
	1069	GTTTGGTTTTCCACGGAGGTTTGA	TCAAACCTCCGTGGAAAACCAAAC
	1070	GCAGGAACCAGATTAGTGTCCCGG	CCGGGACACTAATCTGGTTCCTGC
10	1071	TTTGCTAGAGCGCGGAGCTAAAGC	GCTTTAGCTCCGCGCTCTAGCAA
	1072	CTATGTGGCATCGCTGACATGCTC	GAGCATGTCAGCGATGCCACATAG
	1073	CCTAAGTCGGTTTGCAGCTGCTCT	AGAGCAGCTGCAAACCGACTTAGG
	1074	GCGTTCGTCCACAGGAACGGAAGG	CCTTCCGTTCTGTGGACGAACGC
	1075	TAACCCGCGCCCGAGAAATTGTCT	AGACAATTTCTCGGGCGCGGGTTA
	1076	TATGGTGCTCAGAGCTGTTGCCAA	TTGGCAACAGCTCTGAGCACCATA
15	1077	TCATCGACCCACTAACGTCAGGGC	GCCCTGACGTTAGTGGGTCGATGA
	1078	TGCTCAAGCTACGCGTCACTTCCC	GGGAAGTGACGCGTAGCTTGAGCA
	1079	AGCGGGAAGGTCTGAGGAGGGAAA	TTTCCCTCCTCAGACCTTCCCGCT
	1080	CCGATGTAGCACCACCGCAGTGGC	GCCACTGCGGTGGTGCTACATCGG
20	1081	AAGTTCTGGGAATCACACGGCGCG	CGCGCCGTGTGATTCCCAGAACTT
	1082	CACCAGCCTTACGTGCGGCGTTAA	TTAACGCCGCACGTAAGGCTGGTG
	1083	CGTTTCGCCTCCTCTTCCGAATGC	GCATTGGAAGAGGAGGCGAAACG
	1084	GAGGAGGCCAATAGAGCAGCGCGC	GCGCGCTGCTCTATTGGCCTCCTC
	1085	AGTAATCTTGCGGCACACAAGCGG	CCGCTTGTGTGCCGAAGATTACT
	1086	TGAGGACAAACCGCGCGTAGGATA	TATCTACGCGCGGTTTGTCTCA
25	1087	TCGTAGAGACGCAGTGCCCATCTC	GAGATGGGCACTGCGTCTCTACGA
	1088	CGAAGCTACACCCCGAGTGCGGTG	CACCGCACTCGGGGTGTAGCTTCG
	1089	ATGATGTGATCTTCCCATGGCTGG	CCAGCCATGGGAAGATCACATCAT
	1090	TGTACACGTATCGCGTTCGCCTAG	CTAGGCGAACGCGATACGTGTACA
	1091	GGTGTGCTTTTACGCATGTACGCA	TGCGTACATGCGTAAAGCACACC
30	1092	AGGCGGGATACGTGGATGCTAGCC	GGCTAGCATCCACGTATCCCGCCT
	1093	AAATTAGGCACAGCCCTCCACAG	CTGTGGGAGGGCTGTGCCTAATTT
	1094	ATAAGTTTGGTGAGCCATTGCGCA	TCGCGAATGGCTCACCAAACCTTAT
	1095	CCTATTTGCGCGGACCTCGATGCC	GGCATCGAGGTCCGCCGAATAGG
	1096	TTACCGGAATATGCACTTGCCGCG	GCGGCCAAGTGCAATTCCGGTAA
35	1097	CCTCTCGGACGGTCCCTTTGATCG	CGATCAAAGGGACCGTCCGAGAGG
	1098	CAAGCGAATGCTGTATTACGGCCT	AGGCCGTAATACAGCATTGCTTG
	1099	GCATTTCCCATGCCAGAACGTTGA	TCAACGTTCTGGCATGGGAAATGC
	1100	GTTTTGGCTAACCGTCCTGCCTTG	CAAGGCAGGACGGTTAGCCAAAAC
	1101	AGGTTTTGTCCGGGCGAATGATGT	ACATCATTCGCCCGGACAAAACCT
40	1102	ATGTCCACGAGTGCGTCCGATATC	GATATCGGACGCACTCGTGGACAT
	1103	AGACGCGTACGAGGGTTCTGCGCC	GGCGCAGAACCCTCGTACGCGTCT

	1104	AATACCGTTCCCATCTGTGCGAGG	CCTCGCACAGATGGGAACGGTATT
	1105	ACACAAGGTGCCTCATCGAATGGT	ACCATTGATGAGGCACCTTGTGT
	1106	GCCGGCAAATCCTACAAAATCCA	TGGATTTTGTAGGATTTTGCCGGC
	1107	CTTATCCCATGTGCCGGTCTGACT	AGTCAGACCGGCACATGGGATAAG
5	1108	GCGGCCATAATGCATAGCACGGAA	TTCCGTGCTATGCATTATGGCCGC
	1109	TACGGTGCATCGCAGTATGGGTAA	TTACCCATACTGCGATGCACCGTA
	1110	CACCAGATGTCGAGGATCATCGCC	GGCGATGATCCTCGACATCTGGTG
	1111	GCTCCTACGCCCAAAGAGGTATGG	CCATACCTCTTTGGCGTAGGAGC
	1112	AGAATATGGGCAGCAGCAGCACTC	GAGTGCTGCTGCTGCCCATATTCT
10	1113	CTGCAGTCGCACGCAGTAGACCCG	CGGGTCTACTGCGTGCGACTGCAG
	1114	ATGTCCCTGACCGGAATCTTTCCA	TGGAAAGATTCCGGTCAGGGACAT
	1115	TTCGCCACGAGGCATTAGTCCGAC	GTCGGACTAATGCCTCGTGCGGAA
	1116	ACGTCGTTCCCGAGAATACGGTCT	AGACCGTATTCTCGGGAACGACGT
	1117	ATCCGCTGGCGCTTTGACGAAGAA	TTCTTCGTCAAAGCGCCAGCGGAT
15	1118	TGAACCAAATTCTTACCGCGTGGA	TCCACGCGGTAAGAATTTGGTTCA
	1119	CACGCGTAGGCTGGTGTGTCTTTC	GAATGACACACCAGCCTACGCGTG
	1120	TCGATCCCGCGATCTGGCCTATTG	CAATAGGCCAGATCGCGGGATCGA
	1121	GGAACACTCAACCACCGTGGATCT	AGATCCACGGTGGTTGAGTGTTC
	1122	TCACACACCAACTGGCCACAGATG	CATCTGTGGCCAGTTGGTGTGTGA
20	1123	TGTGCTTAGGACACCAGGCAACCC	GGGTTGCCTGGTGTCTTAAGCACA
	1124	GACATTTAACCCGACCGATTGTGC	GCACAATCGGTCGGGTAAATGTC
	1125	GGCACCGAGCCAGTAGGCCTCTGA	TCAGAGGCCTACTGGCTCGGTGCC
	1126	CTCAAGCGTGCATGTTGGTAACCA	TGGTTACCAACATGCACGCTTGAG
	1127	AGGAAGGCCACCATCCAATATTCTG	CGAATATTGGATGGTGGCCTTCCT
25	1128	TACGAACGCCAAGGTTATGCCAAT	ATTGGCATAACCTTGCGCTTCGTA
	1129	CGCACCAGAGTTATGCAGGCTCAA	TTGAGCCTGCATAACTCTGGTGCG
	1130	CCAGCTTGGACGAGGAAGGATGTG	CACATCCTTCCTCGTCCAAGCTGG
	1131	GTCACGCCTTTCAAATGACCCACA	TGTGGGTCATTTGAAAGGCGTGAC
	1132	TGCTAGACCCAGCCCGAGTCTCGG	CCGAGACTCGGGCTGGGTCTAGCA
30	1133	TATTGTGGCACTTGGGTCCAGTGC	GCACTGGACCCAAGTGCCACAATA
	1134	CACGTGTGAGACCGGAAGTGCATC	GATGCACTTCCGGTCTCACACGTG
	1135	GGCAGCCTGATGCTACAGCACCGT	ACGGTGCTGTAGCATCAGGCTGCC
	1136	CGGTCCGTCCATCCTTCAGAGTTA	TAACTCTGAAGGATGGACGGACCG
	1137	CTATTGCGCGACCCCTACGCAGTTT	AAACTGCGTAGGGTCCGCGAATAG
35	1138	ACCTGTGCAGTCAGCACGAGTGCG	CGCACTCGTGCTGACTGCACAGGT
	1139	GAGAACCACAGGTGGTCCACCCTA	TAGGGTGGACCACCTGTGGTTCTC
	1140	CCTCGCTAGAGAAATCCACGGGAT	ATCCCGTGGATTTCTCTAGCGAGG
	1141	TAACATCGGTGCAAACCGTGCGC	GCGCCACGGTTTGACCCGATGTTA
	1142	ACCCAGAAGACATGGCATTGCGCT	AGGCGAATGCCATGTCTTCTGGGT
40	1143	AAAAGCGCTGCTCTAACACCGCCG	CGGCGGTGTTAGAGCAGCGCTTTT
	1144	CAAGTCTGTCCATTTCCTAACGGT	ACCGTTGGGAAATGGACAGACTTG

	1145	CCGACACATGGTGGGCTTTTTAAG	CTTAAAAAGCCCACCATGTGTCGG
	1146	ACAGACCAGCTTTTGCAGATT	AATCTGCGCAAAAAGCTGGTCTGT
	1147	CGGCGATCCATTTCACTCAAAGT	ACTTTGAAGTGAAATGGATCGCCG
	1148	GACGTTATCATGACACAGGTCGCG	CGCGACCTGTGTCATGATAACGTC
5	1149	GGCAGAGTTGGATCGGATCCTCAA	TTGAGGATCCGATCCAACCTCTGCC
	1150	CCTCAATGCCACCGAATTCGGTAT	ATACCGAATTCGGTGGCATTGAGG
	1151	GGAGTTAGCGTGATTAGTCGCCCCA	TGGGCGACTAATCACGCTAACTCC
	1152	GAAGTCGACGTGTCACGGAAGGGT	ACCCTTCCGTGACACGTCGAGTTC
	1153	CACAAGCGACATTTCTGGTGCACG	CGTGACCCAGAAATGTGCGTTGTG
10	1154	CCAGAATGCGTGAATTCGCGTCCT	AGGACGCGAATTCACGCATTCTGG
	1155	CAAGGGAGCCCTGCGAATTAGAGT	ACTCTAATTCGCAGGGCTCCCTTG
	1156	ATTCTTGCTTCGGACGACTAGCCG	CGGCTAGTCGTCCGAAGCAAGAAT
	1157	TGCCACTTTGATTTCCAGATTGCC	GGCAATCTGGAAATCAAAGTGCCA
	1158	GATGGTCGGCAGATAAGTGGTGGG	CCCACCACTTATCTGCCGACCATC
15	1159	GTTACACGGGTTGACCAACATGT	ACATGTTGGTCAACCCGTGTGAAC
	1160	GATTCAATTGCCCCATTCCTGCAT	ATGCAGGAATGGGGCAATTGAATC
	1161	TACCGGAACTGAGCCTCGTGCTA	TAGCACGAGGCTCAGTTCCGGTA
	1162	GGATCTTTACTCAGGGGCAGAGCC	GGCTCTGCCCTGAGTAAAGATCC
	1163	CGCGAGTGCTTTGTTCTGTGTGGA	TCCACACAGAACAAAGCACTCGCG
20	1164	GTCGTCGCGATGGCGTACATCCTT	AAGGATGTACGCCATCGCGACGAC
	1165	ACGGGAATCTCCCGAAGTGCAGC	GCTCGCACTTCGGGAGATTCCCGT
	1166	GGTCGAAATGAGCCAGCAGCAGAT	ATCTGCTGCTGGCTCATTTGACCC
	1167	CCATTGGAATACTGCGTGCGGCTT	AAGCCGCACGCAGTATTCCAATGG
	1168	GGAAGACTTCGCGAGGGCACAATG	CATTGTGCCCTCGCGAAGTCTTCC
25	1169	AGGGTGACTTCGAAGGTCCGAAC	AGTTCGGACCTTCGAAGTCACCTT
	1170	TCGTCCCTCTGGTGGTGAATCAC	GTGATTCGACCACCAGAGGGACGA
	1171	TGTGCAAATTATGCTGGGCGTGAG	CTCACGCCAGCATAATTTGCACA
	1172	GTCGCCAACTGTCATGTGTGCCCA	TGGGCACACATGACAGTTGGCGAC
	1173	CCTCGAACCTCAAGACGAAACGA	TCGTTTCGTCTTGAGGGTTCGAGG
30	1174	CTTCATCACGTGACCTTTGTTGCC	GGCAACAAAGGTCACGTGATGAAG
	1175	CCTTCATTCCAGCAGGATGGCTT	AAGCCATCCTGCTGGGAATGAAGG
	1176	CGGGGACCTCAATGGAGCGTCTTA	TAAGACGCTCCATTGAGGTCCCCG
	1177	CGCCTCTAGCGCTTGTTACGTCGA	TCGACGTAACAAGCGCTAGAGGCG
	1178	CTGCCAGACTCAAAACAGGGACGG	CCGTCCCTGTTTTGAGTCTGGCAG
35	1179	CTCCTTACACCGTGTGAGGGAACC	GGTTCCTCACACGGTGTAAAGGAG
	1180	TTTCATGCCATATCGCCTCGCGCA	TGCGCGAGGCGATATGGCATGAAA
	1181	GTCTGACTGTCTGCCCTGTATGCG	CGCATACAGGGCAGACAGTCAGAC
	1182	GGTTAATGGAACGGCGTTAACGCG	CGCGTTAACGCCGTTCCATTAACC
	1183	CTTCGCACTGCGGAATCTCAAGCT	AGCTTGAGATTCCGCAGTGCGAAG
40	1184	TGCCAGAGGCGTAGGAGTCCTGGA	TCCAGGACTCCTACGCCTCTGGCA
	1185	GACGGGCGAGCCAGTATTAACCTCA	TGAGTTAATACTGGCTCGCCCGTC

	1186	GACCTCCAAAGTCAGTCTTGGCGG	CCGCCAAGACTGACTTTGGAGGTC
	1187	CGTTAGAGCATGACCGAACACGTC	GACGTGTTCCGGTCATGCTCTAACG
	1188	GTGGGCTCAAAAATTGGGTACGCC	GGCGTACCCAATTTTTGAGCCAC
5	1189	GGGGCAGAGATCACGCGTTCCTCT	AGAGGAACGCGTGATCTCTGCCCC
	1190	TTTCGCCCTACGAAGCGAAGTTTC	GAAACTTCGCTTCGTAGGGCGAAA
	1191	TACGGGGTGATGTTAAGCTACGCG	CGCGTAGCTTAACATCACCCCGTA
	1192	CCTGTGAGTCTGAGATCGCCGTGT	ACACGGCGATCTCAGACTCACAGG
	1193	ACTGAAGCTGGAACAGGCCATTCTG	CGAATGGCCTGTTCCAGCTTCAGT
10	1194	AGCACTGGTTCACATGGGAGTCCA	TGGACTCCCATGTGAACCAGTGCT
	1195	TAAGGAAGATCACACTCCCTGCGC	GCGCAGGGAGTGTGATCTTCCTTA
	1196	CACCACACGCTAAAATTGAAGCCG	CGGCTTCAATTTTAGCGTGTGGTG
	1197	GCTGTCGCCAGGATCATGTATCGT	ACGATACATGATCCTGGCGACAGC
	1198	TTCGTTCTGTCACCTGGATTCTTGA	TCAAGAATCCAGTGCACGAACGAA
15	1199	TCAGCTCTCCTTGTGCTTGCACTG	CACTGCAAGCACAAAGGAGAGCTGA
	1200	ACGACGAGGTGAACTTCGTGGGAA	TTCCACGAAGTTCACCTCGTCGT
	1201	AGCATTGCCGCGGGCCTTGTTTAA	TAAACCAAGGCCCGCGGCAATGCT
	1202	CAGAGGGCAGATGTGACTCCTCAA	TTGAGGAGTCACATCTGCCCTCTG
	1203	CGATATTTAGCCTCTCAAACGCG	CGCGTTTGAGAGGCTGAAATATCG
20	1204	TGCCAGAAATGTTGCCGATTGCAA	TTCGAATCGGCAACATTTCTGGCA
	1205	TAGGCCACCCGGTGTTACAAATTC	GAATTGTGAACACCGGGTGGCCTA
	1206	GAGAGTCAGACCGAGGGACACGAG	CTCGTGCCCTCGGTCTGACTCTC
	1207	GAGGCGATCCTGGAACACGCAAC	GTTGCGTGGTTCAGGATCGCCTC
	1208	CCAGAGAGGCGGGCTACTGACTCA	TGAGTCAGTAGCCCGCCTCTCTGG
	1209	CACACAGTCCCATCGTACGGCAGT	ACTGCCGTACGATGGGACTGTGTG
25	1210	TTACGTTGCGGAAGCGTGCCTCTA	TAGAGGCACGCTTCCGCAACGTAA
	1211	ATGTACACGCTGCAATCGTGTCCC	GGGACACGATTGCAGCGGTACAT
	1212	ACTCGTCGTCGGAAGCGCCAGGT	ACCTGGGCGCTTCCGACGACGAGT
	1213	ATGCGAGAGCAGAATTGAGCCGGT	ACCGGCTCAATTCTGCTCTCGCAT
	1214	AAGTTGGTTCGTATTACGCGTGC	GCACGCGTGAATACGAACCAACTT
30	1215	TGGGCTTATCGCCGAAGATTGCTA	TAGCAATCTTCGGCGATAAGCCCA
	1216	CAACGGCGAAGACCCAGAATTTTA	TAAAATTCTGGGTCTTCGCCGTTG
	1217	AGCGTACGGCGAAAGTCTAGGGAC	GTCCCTAGACTTTCGCCGTACGCT
	1218	ATGCATCCAGCGTCCCCTTGATTA	TAATCAAGGGGACGCTGGATGCAT
	1219	ACCGTCATCAGTCGCAGGCTTCTG	CAGAAGCCTGCGACTGATGACGGT
35	1220	TCTTGACGGCTGGGCATGATTGGA	TCCAATCATGCCAGCCGTCAAGA
	1221	TTAACATTGCGACCCAGGACCTGG	CCAGGTCCTGGGTCCGAATGTAA
	1222	TGGTGTCGAACTCCCTTGCGTGTT	AACACGCAAGGGAGTTCGACACCA
	1223	TACTCCAGTCGCCTGCGCGCAAAC	GTTTGCGCGCAGGCGACTGGAGTA
	1224	CGCAATGCCGTAAGCATGCCAAGC	GCTTGGCATGCTTACGGCATTGCG
40	1225	AGTCCGCGCGAAATACGAACAGTA	TACTGTTCTGATTTTCGCGCGGACT
	1226	ATGTTGCACGCGCACTGTATCACA	TGTGATACAGTGCGCGTGCAACAT

5	1227	ATCGCCTAACTACCCGCGGCGTGC	GCACGCCGCGGGTAGTTAGGCGAT
	1228	TGGCCAGGGAACACAAGCTCGGTA	TACCGAGCTTGTGTTCCCTGGCCA
	1229	AAACATGGGTGCGCTCTGAGATCA	TGATCTCAGACGCGACCCATGTTT
	1230	GCGAGAGCTGCGATTCCCTTTTAG	CTAAAAGGGAATCGCAGCTCTCGC
	1231	CCGGCCAAACAAGAGACGAGCGGA	TCCGCTCGTCTCTTGTGTTGGCCGG
	1232	AATGGGGCACAGTCTCGCTTGACA	TGTCAAGCGAGACTGTGCCCCATT
	1233	TGTCTCGGGCCTTCAGGACACACT	AGTGTGTCCTGAAGGCCCGAGACA
	1234	TCCACCTTCATTAAGTGGTTCGGC	GCCGAACCACTTAATGAAGGTGGA
10	1235	GCTTCGGAATCATCCACCTGTCAT	ATGACAGGTGGATGATTCCGAAGC
	1236	GAGCCGATGGGCTATCGTCGTCGG	CCGACGACGATAGCCCATCGGCTC
	1237	CACGAATTACGCACGCACAGAGGA	TCCTCTGTGCGTGCGTAATTCGTG
	1238	GCTGTGACGCTCCCCTCACTAGG	CCTAGTTGAGGGGAGCGTCACAGC
	1239	CGCTCTGAAAACGCGGGCTACGTT	AACGTAGCCCGCGTTTTTCAGAGCG
15	1240	GAGTGCTGGACACCGTAGCCAGGA	TCCTGGCTACGGTGTCCAGCACTC
	1241	CCAACCCCAAGTGTAGGCGCAAATG	CATTTGCGCCTACACTGGGGTTGG
	1242	GAAGTAGGGGATGTTGGCCGGCGG	CCGCCGGCCAACATCCCCTACTTC
	1243	CAACGTGGGCACCTGTTTTAGCAG	CTGCTAAACAGGTGCCACGTTG
	1244	CTAGCTGCGATCCGAACCTCTACG	CGTAGAGGTTCCGATCGCAGCTAG
	1245	CATTGAACCATCAGCCAAGCTGCG	CGCAGCTTGGCTGATGGTTCAATG
20	1246	AGACTGGCAATTTTTTCGAGGCCAA	TTGGCCTCGAAAAATTGCCAGTCT
	1247	CTGGCCGTCCATGAGTTGGTCCAG	CTGGACCAACTCATGGACGGCCAG
	1248	CATGCTGAAACACGGGATTGCCAT	ATGGCAATCCCGTGTTTCAGCATG
	1249	CGATATGTAAGACAGCCGTCGCAA	TTGCGACGGCTGTCTTACATATCG
	1250	AGCGTAACCTACTGGGAAGGCACC	GGTGCCTTCCCAGTAGGTTACGCT
25	1251	GTTCTGAACCCCGCGATGTTAAATG	CATTTAACATCGCGGGGTTCGAAC
	1252	GTTGTTAGGAGGCTCGAGGCTGCT	AGCAGCCTCGAGCCTCCTAACAAC
	1253	ACTGGTGCTACGCGGGATATTTGA	TCAAATATCCCGCGTAGCACCAGT
	1254	CTGGGAGCTATCCTCAGCCGAATC	GATTCGGCTGAGGATAGCTCCAG
	1255	GAACCTGCGCGCTGCCGAAGGGTAG	CTACCCTTCGGCAGCGGCGAGTTC
30	1256	TTCGATCGAGGAGCAAGGAGAGTC	GACTCTCCTTGCTCCTCGATCGAA
	1257	GGGGAAAATTGAGGCCTTAGCCAT	ATGGCTAAGGCCTCAATTTCCCC
	1258	CTAAGGTCAAAGCGCTGTGCCAG	CTGGCGACAGCGCTTTGACCTTAG
	1259	CCGTAGCGGTGCTCGACCAGTTTC	GAACCTGGTCGAGCACCGCTACGG
	1260	TGGGGACGAATCCGAATGTAGTGA	TCACTACATTTCGGATTCGTCCCCA
35	1261	GTCATGTAATTGCATCCCACGGGT	ACCCGTGGGATGCAATTACATGAC
	1262	CTTTGCGCGGTGGTCAATAAAAAG	CTTTTTATTGACCACCGCGCAAAG
	1263	CTCGGGGATGCCCTCTTGGCATTA	TAATGCCAAGAGGGCATCCCCGAG
	1264	CGAAACGTGGTGCAGAAACCTGAA	TTCAGGTTTCTGCACCACGTTTCG
	1265	GGAGTTCACGAGTCGAGCAGTCGC	GCGACTGCTCGACTCGTGAACCTCC
40	1266	AGCCGTTTTCAAAGATCTCGACGA	TCGTCGAGATCTTTGAAAACGGCT
	1267	TGGCTGGACATTGTCTGCAATGCA	TGCATTGCAGACAATGTCCAGCCA

1268	ATCGGCTGCCTCAGTCCCTAATTT	AAATTAGGGACTGAGGCAGCCGAT
1269	CCAGCATGGAGTTAAGTGAGCGCG	CGCGCTCACTTAACTCCATGCTGG
1270	TTCATATTTACGAATGCCGGGTGC	GCACCCGGCATTTCGTAAATATGAA
1271	CGAAATCGCACAGGAATTCGCGTC	GACGCGAATTCCTGTGCGATTTCCG
1272	GGCAATTTCTGGGACACTCGTTTCA	TGAAACGAGTGTCCCCGAAATTGCC
1273	TTTGTGATTGGGGGTATAACCCGA	TCGGGTATACCCCCAATCACAAA
1274	CCCAGCTAATCCAGCTTGGGCTGT	ACAGCCCAAGCTGGATTAGCTGGG
1275	AAAATCGTTTGGCTGTAACGTCGC	GCGACGTTACAGCCAAACGATTTT
1276	AGGAGATTCATCGACTTCCGGGAA	TTCCCGGAAGTCGATGAATCTCCT
1277	GCACGGGGTCTCAATGCTTAGGGT	ACCCTAAGCATTGAGACCCCGTGC
1278	GCGCAACAAGTAGCCTACCGAGGC	GCCTCGGTAGGCTACTTGTTGCGC
1279	TAGCAGGCTGATGCCGTCTACACA	TGTGTAGACGGCATCAGCCTGCTA
1280	GCAAGCGGCGATCGTACAACCTGT	ACAAGTTGTACGATCGCCGCTTGC
1281	GCACCTCTGGTAAGCCTGAAAGGG	CCCTTTCAGGCTTACCAGAGGTGC
1282	CGAGGGCGGTGAGTGCATACCGTG	CACGGTATGCACTCACCGCCCTCG
1283	GGATTAACCGGAACTGCCCTTCTG	CAGAAGGGCAGTTCGGTTAATCC
1284	GATATTGGGTCCGGCGCGCATTAC	GTAATGCGCGCCGGACCCAATATC
1285	GGCCTTTAATCTCCGGTCGCAATG	CATTGCGACCGGAGATTAAAGGCC
1286	AACCTTAGTGCGGCTAGGTGGGGT	ACCCACCTAGCCGCACTAAGGTT
1287	CACGCTGACGCCAGTGTGGTGAGG	CCTCACCACACTGGCGTCAGCGTG
1288	GGTTCCTTGACCCACCGAATTGA	TCAATTCGGTGGGTCAAGGGAACC
1289	TTCTGACAACATCGACCCTGGCTC	GAGCCAGGGTCGATGTTGTAGAA
1290	GCGAGCGAAGATAATCCCCAACT	AGTTTGGGGATTATCTTCGCTCGC
1291	GTAATCTGTGCAACGGTCCCGAGT	ACTCGGGACCGTTGCACAGAGTAC
1292	ACACGCCAGGAACAGTGTCTGTGA	TCACAGACACTGTTCTCGCGTGT
1293	AAGGGAATTTAGCGCGCGTGA	AAGTCACGCGCGCTAAATCCCTT
1294	TGACGTACGCGTTTAAAGTGGGGA	TCCCCACTTAAACGCGTACGTCA
1295	CTTAGAGGGACGAGGCCATGAATG	CATTCATGGCCTCGTCCCTCTAAG
1296	GGACGACTCCGCAAAAAGGTCGT	ACGACCTTTTTTGCGGAGTCGTCC
1297	TCAATCCCAACATCCAAAGCCTCA	TGAGGCTTTGGATGTTGGGATTGA
1298	GCACTGGTCTACCAAGCTTGTCCC	GGGACAAGCTTGGTAGACCAGTGC
1299	ACTTGTCGGAACGAGACCGAGCA	TGCTCGGTCTCGTTCCGACAAGT
1300	TCAGGAAAGGCCTAAAGGCGAAAG	CTTTCGCCTTTAGGCCTTTCCTGA
1301	GGAATGTAGTCAAGGAGGACGGGG	CCCCGTCCTCCTTGACTACATTCC
1302	GCACGTGGTAAATGAATTGGCGAG	CTCGCCAATTCATTTACCACGTGC
1303	GATCATCAGGGGTATGCGTCCGG	CGCGACGCATAACCCCTGATGATC
1304	CTCACTATTCTGATTGCCGCGG	CCGCGGGCAATCAGAATGAGTGAG
1305	GGGGTGATCTCTCGAACGTCACCC	GGGTGACGTTGAGAGATCACCCC
1306	AAGGTTGCTGCTAGCGTACCTCGA	TCGAGGTACGCTAGCAGCAACCTT
1307	TATAGATCGCCCAACAGGCAGGAG	CTCCTGCCTGTTGGGCGATCTATA
1308	GTTTGGACCTGTTGGGAGTGGGCA	TGCCCCACTCCCAACAGGTCCAAAC

5	1309	ATTGGGGAAAACCCGGTCTCAAGG	CCTTGAGACCGGGTTTTCCCAAT
	1310	TCGACGATAAAGTGCTCACGGGAC	GTCCCGTGAGCACTTTATCGTCGA
	1311	CGATAGAATTCAATGCAGGGCGGA	TCCGCCCTGCATTGAATTCTATCG
	1312	CGGTTTCGCTACGGCGGCTGGTTTC	GAAACCAGCCGCCGTAGCGAACCG
	1313	CCAGGTTTCGGTTAGTCGCGCTAG	CTAGCGCGACTAACCGAAACCTGG
	1314	ACGACCTTACACTCGGATCCGACG	CGTCGGATCCGAGTGTAAGGTCGT
	1315	TCGCGTTAAATGGACCAAGGGGCC	GGCCCCCTGGTCCATTTAACGCGA
	1316	CCAGAAAGAAAATGGCGCCCGGAT	ATCCGGGCGCCATTTCTTTCTGG
10	1317	GATACATCGCCGCCTGCTAGGCAC	GTGCCTAGCAGGCGGCGATGTATC
	1318	GAGATCACACTCGGAAACCGGATG	CATCCGGTTTCCGAGTGTGATCTC
	1319	ACTTCGCGGAAAAAGGCTGGCATT	AATGCCAGCCTTTTTCCGCGAAGT
	1320	CCGAGCTGCACGAGCACACAAAGT	ACTTTGTGTGCTCGTGCAGCTCGG
	1321	TTCCACAAGGCGGCATAGTGAGGC	GCCTCACTATGCCGCCTTGTGGAA
	1322	AGCAAACCTGGAATCCGGA AAAACC	GGTTTTTCCGGATTCCAGTTTGCT
15	1323	CGCTATGTCGCGAGCATGCATTTAC	GTAAATGCATGCTGCGACATAGCG
	1324	AGTCACGCCCAACGTCGGTTCTTT	AAAGAACCGACGTTGGGCGTGACT
	1325	AGTGGGCGCACTTGGCCTTAAATA	TATTTAAGGCCAAGTGCGCCCACT
	1326	ACTTGCAACTTCGGCCGTTTGACT	AGTCAAACGGCCGAAGTTGCAAGT
	1327	CAAACATCAGGTTTCATGCCGTACG	CGTACGGCATGAACCTGATGTTTG
20	1328	AGCGTGACCACCCTACAATGGCAA	TTGCCATTGTAGGGTGGTCACGCT
	1329	GCAGGCATCCGGCAGAGATGTCTC	GAGACATCTCTGCCGGATGCCTGC
	1330	GAGCGGCTAAGAGGCCAGACCAAA	TTTGGTCTGGCCTCTTAGCCGCTC
	1331	CACAGAACAGGGTGTTTCCCGCTA	TAGCGGGAAACACCCTGTTCTGTG
	1332	ACTTTGCAGAAGGCCCAACACAAG	CTTGTGTTGGGCCTTCTGCAAAGT
25	1333	CCTTCCTGGTACTTTGTGGGCGAC	GTCGCCACAAAGTACCAGGAAGG
	1334	CTACATGCTACCCCCACCAGAGTG	CACTCTGGTGGGGTGAGCATGTAG
	1335	ATTTTCAGAATAGCCCCGCTCGA	TCGAGGCGGGGCTATTCTGAAAT
	1336	CAATTGCTACGTTGACGCCCTCTG	CAGAGGGCGTCAACGTAGCAATTG
	1337	CTGTGCGCTAATCCTCGGTGGCCG	CGGCCACCGAGGATTAGGCGACAG
30	1338	TTTGTGTTGGCTCCGTACATTGGA	TCCAATGTACGGAGCCAACACAAA
	1339	ACGTGACGGGAAGGTGGTTGAATC	GATTCAACCACCTTCCCGTCACGT
	1340	AGTTCCTGCGTTGCACGAAACAGA	TCTGTTTCGTGCAACGCAAGAACT
	1341	GCTCGCCGCGCGTCTTTATGTCTG	CAGACATAAAGACGCGCGGCGAGC
	1342	ATGAACATCGCGAGGCAAGCCTTT	AAAGGCTTGCCTCGCGATGTTTAT
35	1343	CAACCGCGCCCAACCAATTAAGG	CCTTAATGTTGGTGGGCGCGGTTG
	1344	TGATCGAGGACGGCTTGGTAGCCT	AGGCTACCAAGCCGTCTCGATCA
	1345	GGAGGCATGCCTTCCGAGAGCAAC	GTTGCTCTCGGAAGGCATGCCTCC
	1346	CACCGATCCTCAACGCAATTGCTA	TAGCAATTGCGTTGAGGATCGGTG
	1347	GGCCATGAATTGGGAAATCCATGT	ACATGGATTTCCCAATTCATGGCC
40	1348	CTGTTCCAGGCGTAACCAGCGGGC	GCCCGCTGGTTACGCCTGGAACAG
	1349	TATGTCTGGCTCGCCATCAGAAGA	TCTTCTGATGGCGAGCCAGACATA



5	1350	GGAGTGACCAGCACAAAGCATCGAG	CTCGATGCTTGTGCTGGTCACTCC
	1351	TCGGACTGGAAGTAACTCGCATGA	TCATGCGAGTTACTTCCAGTCCGA
	1352	GTAGGGTCAAGCACGATTGAAGCC	GGCTTCAATCGTGCTTGACCTAC
	1353	CACCGGCGGTTCTGACTAACGTGAC	GTCACGTTAGTCGAACCGCCGGTG
	1354	GAATGACGCGCAGTGCATTTGAAC	GTTCAAATGCACTGCGCGTCAATC
	1355	GTGCTCGTCTAACC GCGGATAGAG	CTCTATCCGCGGTTAGACGAGCAC
	1356	GCGGACCTGGGTTAATTGACGCGC	GCGCGTCAATTAACCCAGGTCCGC
	1357	TTTTTGATGTTGCGCACCGGGCTA	TAGCCCGGTGCGCAACATCAAAAA
10	1358	TTGCGTCAGCGCATCTGCTCGATT	AATCGAGCAGATGCGCTGACGCAA
	1359	ATGAGCACGCCAGTTCGTTCTTT	AAAGGAACGAACTGGCGTGCTCAT
	1360	TCAACGGTAAAGAATCGCCCCGA	TGCGGGGCGATTCTTTACCGTTGA
	1361	CGCGATTGACTGAACCACACCTCT	AGAGGTGTGGTTCAGTCAATCGCG
	1362	GCGTGAAAGATGACGGCCGGTATA	TATACCGGCCGTCATCTTTCACGC
15	1363	CATGATTCCACCTCGATCGGCTAG	CTAGCCGATCGAGGTGGAATCATG
	1364	CTACGACAAAGCAACCGTGCAAAA	TTTTGCACGGTTGCTTTGTCGTAG
	1365	ATGCCGTGTTTCATCTTGATGGTCC	GGACCATCAAGATGAACACGGCAT
	1366	TTCGTGGAGGGACTTTGGAGATCC	GGATCTCCAAAGTCCCTCCACGAA
	1367	GAAGCGCCGTAACGTACACCGTCG	CGACGGTGTACGTTACGGCGCTTC
20	1368	AGCGTGCGCTTGGCTATAAGGCTA	TAGCCTTATAGCCAAGCGCACGCT
	1369	ACAGTCAGGAGTAACGCCGCTCAA	TTGAGCGGCGTTACTCCTGACTGT
	1370	TTTAGCCGCTGCGACTGTAGGAAA	TTTCCTACAGTCGCAGCGGCTAAA
	1371	ACTGTGTGCGCAATCAACCCGCAAA	TTTGCGGGTTGATTGCGACACAGT
	1372	TGCAGCCAATGCGGAACCTAGAGG	CCTCTAAGTTCGCGATTGGCTGCA
25	1373	CCCGCTATCCCGGTCTTGACGTTT	GAACTGCAAGACCGGGATAGCGGG
	1374	GAGGGCGCAACATATGCAGTGCTG	CAGCACTGCATATGTTGCGCCCTC
	1375	CGTACGGACATCGATGACGCAACG	CGTTGCGTCATCGATGTCCGTACG
	1376	AGTCTCCCGAGAAACGCATAAGGC	GCCTTATGCGTTTCTCGGGAGACT
	1377	AGGAAGTGGATGAACGCGGCTGCA	TGCAGCCGCGTTTCATCCACTTCCT
30	1378	GGGTTGCTCACCTCTGTCATCAGG	CCTGATGACGAGGGTGAGCAACCC
	1379	TAGGAATGCGAGTTCCGGCGGTAA	TTACCGCCGGAACTCGCATTCTTA
	1380	CTCCTCACTTCCAAGCTGCGGATA	TATCCGCAGCTTGGAAGTGAGGAG
	1381	TCAATAGCACCTAGCATGCTCCCG	CGGGAGCATGCTAGGTGCTATTGA
	1382	TGATTCCTGCGCTTTTACAGGTCG	CGACCTGTGAAAGCGCAGGAATCA
35	1383	GTATGTGCGGGATGGAAATCACGC	GCGTGATTTCCATCCCGCACATAC
	1384	TACGGCAACTGTCGATACGAGGGC	GCCCTCGTATCGACAGTTGCCGTA
	1385	GGTTCCTATCCAGCACTCCTCGC	GCGAGGAGTGCTGGATAGGGAACC
	1386	ATAAGCGCGCCACAGGTATGTACC	GGTACATACCTGTGGCGCGCTTAT
	1387	GAAAGTCGCCAACAGACTCGAGCA	TGCTCGAGTCTGTTGGCGACTTTC
40	1388	CGCTAATGCCTCATAGGCGTGTGC	GCACACGCCTATGAGGCATTAGCG
	1389	ATCCCCGCCGCACGAAGTACCAAG	CTTGGTACTTCGTGCGGCGGGGAT
	1390	GACGCTGCTGATGGCTTTATCGAT	ATCGATAAAGCCATCAGCAGCGTC

	1391	CTCTCCCCGTCGCTTCAGAGATTA	TAATCTCTGAAGCGACGGGGAGAG
	1392	TCATGTGGGCCGTCGTATCAGTTT	AAACTGATACGACGGCCACATGA
	1393	GGCCTGAAGGTGAATGGTTACGTG	CACGTAACCATTACCTTCAGGCC
5	1394	AGCCTCCAAAGCCGGTAGAGTTCC	GGAAGTCTACCGGCTTTGGAGGCT
	1395	TTGTCGTAGGCGCTCACCTTAGGA	TCCTAAGGTGAGCGCCTACGACAA
	1396	GCCTGAGTCCGGGTCGGGAAAGAA	TTCTTTCCCGACCCGGACTCAGGC
	1397	GGCACTATACCGGTTCTGGACGCG	CGCGTCCAGAACCGGTATAGTGCC
	1398	CCGTGTATACGAAAGGTACGCCA	TGGCGTACCTTTCCGTATACACGG
10	1399	CCCAAGGCAAGTGTGCATCAGTCC	GGAAGTATGCACACTTGCCTTGGG
	1400	GGAGTGCATCATGGCCAAATCTGG	CCAGATTTGGCCATGATGCACTCC
	1401	CCATGTTACGTCTGCGCACCACAG	CTGTGGTGCGCAGACGTAACATGG
	1402	GGCGTTGAGCTTAAAAGCAGCGAC	GTCGCTGCTTTTAAGCTCAACGCC
	1403	TTGGCACTCTGCAAGATACGTGGG	CCCACGTATCTTGACAGAGTGCCAA
	1404	GATCTGCACTGCAAGGTCTTGGGG	CCCCAAGACCTTGCAAGTGCAGATC
15	1405	CGATCAACTTGCGGCCATTCTGCG	GCAGGAATGGCCGCAAGTTGATCG
	1406	CGGCTGGGGTCACAGAAACGAGTA	TACTCGTTTCTGTGACCCAGCCG
	1407	GCGGCTAGTTGTACCTAGCGGCTG	CAGCCGCTAGGTACAAGTAGCCGC
	1408	TCGTCACTGTTAGAGAGGCCTCCG	CGGAGGCCTCTCTAACAGTGACGA
	1409	AGTGTGCTGAGCCCTAGCGGCGCT	AGCGCCGCTAGGGCTCAGGACACT
20	1410	AGGACGCAAGGATTCAAGTGCAAC	GTTGCACTTGAATCCCTGCGTCTT
	1411	ACCGATGCGCGGTCTGCTCATAC	GTATGAGACCGACCGCGCATCGGT
	1412	GGCAGAGGGTTAGGGGGTTTTTTT	AAAAAAACCCCTAACCCTCTGCC
	1413	GGCAAAGGGTGTATATGGGAGACC	GGTCTCCATAAACACCCCTTTGCC
	1414	ACAAGGCTTCGGCTGGCAGAATAC	GTATTCTGCCAGCCGAAGCCTTGT
25	1415	CATATCCGTTCTATCGCCAGACG	CGTCTGGCGATAGGAACGATATG
	1416	AAGCCTTTGTGGCCAAGGCCGCGT	ACGCGGCCTTGCCACAAAGGCTT
	1417	CCGAACCATGGCTTTATCCAGTGT	ACACTGGATAAAGCCATGGTTCCG
	1418	GTTTACGAGTAGCTCCCTCCTCGA	TCGAGGAGGGAGCTACTGCTGAAC
	1419	GCGCAGTGACACCATGATGCTTTC	GAAAGCATCATGGTGTCACTGCGC
30	1420	ACGATCCATTTTGCCAGCATGCAA	TTGCATGCTGGCAAAATGGATCGT
	1421	TCCCTTCATTTCCGGGTTTTTAGCC	GGCTAAAAACCCGAAATGAAGGGA
	1422	TCTTCTTGCCACATTCCCTTTTG	CAAAAGGGAATGTGGGCAAGAAGA
	1423	TGCCCTTTGATTGGTGGTCACGGT	ACCGTGACCACCAATCAAAAGGCA
	1424	GACCCTCACGGTCATCAGAGGGAG	CTCCCTCTGATGACCGTGAGGGTC
35	1425	CCGTTCAACACAGTGATACACGCG	CGCGTGTATCACTGTGTTGAACGG
	1426	CACCAGGGGATAGGTGCGGTACGC	GCGTACCGCACCTATCCCTGGTG
	1427	GGTCGGAAGTATCTGTGCGATCC	GGATCGCACAGATCAGTTCCGACC
	1428	TGCTCCTTCCTAGGGTCATCCGTG	CACGGATGACCCTAGGAAGGAGCA
	1429	GTGGACTTTGACGCCGGCTACCGC	GCGGTAGCCGGCGTCAAAGTCCAC
40	1430	CTGATCTGTGCGCGGTTACTTGCC	GGCAAGTAACCGCCGACAGATCAG
	1431	AGAGGAGCGGAAAAAACCGGACGA	TCGTCCGGTTTTTCCGCTCCTCT

5	1432	GCGACGAAGAGATCCAGCAAGCTC	GAGCTTGCTGGATCTCTTCGTCGC
	1433	GGGACTTCCAGCTGAGGGACGAAA	TTTCGTCCCTCAGCTGGAAGTCCC
	1434	GGCGCACTCCAATACCCACTGTTT	AAACAGTGGGTATTGGAGTGCGCC
	1435	GCGCTTGAGACTGTCAGGACGTG	CACGTCCTGACAGTCTCCAAGCGC
	1436	CAAACCGCTGGTTTCTCCACCTGT	ACAGGTGGAGAAACCAGCGGTTTG
	1437	GCGATTGCTTGGGATCGGTGACTA	TAGTCACCGATCCCAAGCAATCGC
	1438	CTCAGCGACATTTTTCTGGTGGCG	CGCCACCAGAAAAATGTCGCTGAG
	1439	CAGCGGCGTCGTTTACTCAGGACT	AGTCCTGAGTAAACGACGCCGCTG
10	1440	GACAGCCGTGAACGCTCAGCCGTT	AACGGCTGAGCGTTCACGGCTGTC
	1441	GGGCCGTAGAGGCATCGGGTAAAG	CTTTACCCGATGCCTCTACGGCCC
	1442	CGCCGCTCACCTGCTTAAAGCATT	AATGCTTTAAGCAGGTGAGCGGCG
	1443	TGCCAAATCGCAACTCTTGAGACA	TGTCTCAAGAGTTGCGATTTGGCA
	1444	CCCCGATCGGGTGTAAATTCTCCCT	AGGGAGAATTACACCCGATCGGGG
	1445	CAAGGTCCAGGTGACGCAACCACT	AGTGTTTGCCTCACCTGGACCTTG
15	1446	CGAGCCTTCAGTGGTATGCATGCG	CGCATGCATACCACTGAAGGCTCG
	1447	CAGCAGCGTGCCCATCTCGACTTA	TAAGTCGAGATGGGCACGCTGCTG
	1448	CGGACCAAGATGGCAGTAATCCAG	CTGGATTACTGCCATCTTGGTCCG
	1449	CTACCACGCTCTGCGCGGGCTGTA	TACAGCCCCGCGCAGAGCGTGGTAG
20	1450	ACGTGGTTAGGCATGAGCTGCCTC	GACGCAGCTCATGCCTAACCACGT
	1451	CGACATATCCGACATGACCGGATG	CATCCGGTCATGTCGGATATGTCG
	1452	GCGCCCAGGCTGTGTTAGAAAATA	TATTTTCTAACACAGCCTGGGCGC
	1453	AGCTGGGACTCCGGACCTTGAGTG	CACTCAAGGTCCGGAGTCCAGCT
	1454	CGGTGTAACCGCTGCTACAACCTT	AAGTTGTAGCAGCGGTTACGACCG
	1455	TCGTTCTCTGGAACAATTCAGCA	TGCTGAATTGTTCCAGAGGAACGA
25	1456	CGGCATCTCCGGACAAAGGTTAAC	GTTAACCTTTGTCCGGAGATGCCG
	1457	TATCTTGTCGAGCGCCACTCGGAG	CTCCGAGTGGCGCTCGACAAGATA
	1458	TGCAAGGGAGAAAGCCCCATGAGC	GCTCATGGGGCTTTCTCCCTTGCA
	1459	ACTGCATAGCCCAGATCCGCTTGC	GCAAGCGGATCTGGGCTATGCAGT
	1460	TGTGATTCAAGTGAAGCAAGGCCG	CGGCCTTGCTTCGACTGAATCACA
30	1461	CATCCATCTACAATTCGGGCCAGT	ACTGGCCCGAATTGTAGATGGATG
	1462	ATGAGCCGTTTCAGAAAGCCAAAGA	TCTTTGGCTTTCTGAACGGCTCAT
	1463	ACACTGGAATTGCTAGACCCCGCG	CGCGGGGTCTAGCAATTCCAGTGT
	1464	CTGAGCTGCGTGGGACAACTCCGC	GCGGAGTTGTCCACGCAGCTCAG
	1465	CAGCTACTAGGGCGCGATGTACCC	GGGTACATCGCGCCCTAGTAGCTG
35	1466	ATAATGATGGGACGAGAAGGCCCC	GGGGCCTTCTCGTCCCATCATTAT
	1467	CGACCGAGTGTTACGACATGGTGC	GCACCATGTCGTAACACTCGGTGC
	1468	TGCAGTACCCGCCGCTCCACTAGT	ACTAGTGGAGCGGCGGGTACTGCA
	1469	ATGCTAGCGCGCCTGTCAACGTAC	GTACGTTGACAGGCGCGCTAGCAT
	1470	AGACTCACTGCCGGCTGATCAAAT	ATTTGATCAGCCGGCAGTGAGTCT
40	1471	GCCTGGTGCGAAGATAGGGATTCC	GGAATCCCTATCTTCGCCACCAGGC
	1472	GGAAAGTTGGCGGATCCGAGCACT	AGTGCTCGGATCCGCCAACTTTCC

5	1473	GGCAGTGAGCAATGTGTGACGAGG	CCTCGTCACACATTGCTCACTGCC
	1474	TGAGGTCCCTCCCGGCGGACTACGA	TCGTAGTCCGCCGGGAGGACCTCA
	1475	CTCGCCTTAGATCGTGGTTCCGCA	TGCGGAACCACGATCTAAGGCGAG
	1476	GTCGAGGAATATCATCGCAGCCAG	CTGGCTGCGATGATATTCTCGAC
	1477	GCGAATGCAACGAGACAAGAAGGA	TCCTTCTTGTCTCGTTGCATTGCG
	1478	TTCGCCACCAAGTCGGCATTGT	AACAAATGCCGACTTGGTGCGAA
	1479	CGGTGGCTGACACTTGCCGGATT	GAATCCGGCAAGTGTCAGCCACCG
	1480	CAAGGAGCAATCAGATGGTCGGAG	CTCCGACCATCTGATTGCTCCTTG
10	1481	GTGACCCGGTCCGTTCTAGCTGTG	CACAGCTAGAACGGACCGGGTCAC
	1482	CTCTCGCCACATAACTGCACAAA	TTTGTGCAGTTATGTGGGCGAGAG
	1483	AAACCTGCCTAAGCAAGCACTGGA	TCCAGTGCTTGCTTAGGCAGGTTT
	1484	TTCCATATTGTACCCCGCGCATGC	GCATGCGCGGGGTACAATATGGAA
	1485	TGCTTGCGATATCACGATACTGCG	CGCAGTATCGTGATATCGCAAGCA
	1486	TTAGTGTTGAGCCTTGAGCCGGC	GCCGGCTCAAGGCTCGAACACTAA
15	1487	CTTGTTGCGCAGTCCGTCTGGGA	TCCAGACGGACTCGCGCAACAAG
	1488	GTCAGCTGCCTGCTGGTGCTCTTC	GAAGAGCACCAGCAGGCAGCTGAC
	1489	CATCCCTCGAGGTGTAGGCAACAC	GTGTTGCCTACACCTCGAGGGATG
	1490	CAGATGCACTCCGACGGGATTCAG	CTGAATCCCGTCGGAGTGCATCTG
20	1491	CTGAGCCTCGCGAAGCTGTGGCAT	ATGCCACAGCTTCGCGAGGCTCAG
	1492	GCTATGCCACGCCGCAGATAGAGC	GCTCTATCTGCGGCGTGGCATAGC
	1493	AACACCAACCATAACCGTCCGTTCA	TGAACGGACGGTATGGTTGGTGTT
	1494	GCCCAGAGCTAAAGCATGTCTGGG	CCCAGACATGCTTTAGCTCTGGGC
	1495	AATGCTGCAATGCTAGCGTCGCTA	TAGCGACGCTAGCATTGCAGCATT
25	1496	TCCGGACGCAGTATCCAATCCGGA	TCCGGATTGGATACTGCGTCCGGA
	1497	TAAGACCATGTGGCACCAAGGTGC	GCACCTTGGTGCCACATGGTCTTA
	1498	ACAGCCACACACACGCGCCCACTA	TAGTGGGGCGTGTGTGTGGCTGT
	1499	TAGAACCGAGCACGGCGCCTTGTA	TACAAGGCGCCGTGCTCGGTTCTA
	1500	TTCGAGTAAGCTGGCAGGACCACT	AGTGGTCTGTCAGCTTACTCGAA
30	1501	CTTTCGCAGGTCGCAGACAATCC	GGATTGTCTGCGAACCTGCGAAAG
	1502	TACGTCCTGTGCTGTTGACACCGG	CCGGTGTCAACAGCACAGGACGTA
	1503	GTTCCGGTCAATGTTTCGGGGAGA	TCTCCCCGAAACATTGACCCGAAC
	1504	CCCTGTTGTGAAGGGGTTTTGTGA	TCACAAAACCCCTTCACAACAGGG
	1505	GGCAGATTGGTGAACCCAGATAA	TTATCTGGGGTTCACCAATCTGCC
35	1506	CCCTCGGTGTGTTCAAGCCAAATC	GATTTGGCTTGAACACACCGAGGG
	1507	CCCGCGAACATTTGAACAGCTTAA	TTAAGCTGTTCAAATGTTGCGGGG
	1508	CCGTGTCAGTTGCTCCCTGGCACG	CGTGCCAGGGAGCAACTGACACGG
	1509	TCCGTCTCAGCCGCTCCCTATCC	GGATAGGGAGGCGGCTGAGACGGA
	1510	ATAGCTGGGTACCCACAGGCGGTC	GACCGCCTGTGGTGACCCAGCTAT
40	1511	ATAGGCAAGCGGTGTAGCACAGCG	CGCTGTGCTACACCGCTTGCCAT
	1512	TTAGAAGCCGGTCTGGATTTGCGT	ACGCAAATCCAGACCGGCTTCTAA
	1513	TGCCGACCTTTACCAGGATCCTCG	CGAGGATCCTGGTAAAGGTCGGCA

	1514	GCCCACACTATAACCAAGCTGGCA	TGCCAGCTTGGTTATAGTGTGGGC
	1515	TTGCGCCACTAGTACGGATCTCAA	TTGAGATCCGTAAGTGTGGCGCAA
	1516	CTTGCAAGTTTATGCTGACCCGTCC	GGACGGGTGAGCATAACTGCAAG
5	1517	TGCCTCCAAATTACTTACCGCCGT	ACGGCGGTAAAGTAATTTGGAGGCA
	1518	CCCGTATGCGGAAGCTATGGGCTA	TAGCCCATAGCTTCCGCATACGGG
	1519	TCGTTCAACCCACACTTCAGTTG	CAACTGAAGTGTGGGGTTGAACGA
	1520	CAATGTGGGGGACATTTCAAGGTT	AACCTTGAAATGTCCCCACATTG
	1521	TAGCGTCGCACAAATGGCTGACCG	CGGTCAGCCATTTGTGCGACGCTA
10	1522	GGTGGCTTCGTGACAATATCGGCC	GGCCGATATTGTCACGAAGCCACC
	1523	CAGCGGCGTCCGAAATTGGCTCTC	GAGAGCCAATTTCCGACGCCGCTG
	1524	GGCTTGCTCTCGTTTTTGATTGCA	TGCAATCAAAACGAGAGCAAGCC
	1525	ATGCGAGGAGGACACGACCGTTCC	GGAACGGTCTGTCTCCTCGCAT
	1526	CCTGTTCACTACGACCCACGGGAA	TTCCCGTGGGTCGTAGTGAACAGG
	1527	GTGCCACGGAGTGCAGCTGTTGCT	AGCAACAGTCGCACTCCGTGGCAC
15	1528	ACACATCCAAGTCTGACGATGGCC	GGCCATCGTCAGACTTGGATGTGT
	1529	CAGCCCGAAAGGAAAGCCTCCGTG	CACGGAGGCTTTCCTTCGGGCTG
	1530	AACTGAATGTAGGTGGGCCCTGT	ACAGGGGCCACCTACATTCAGTT
	1531	ATTTTCGACGATAAGCTGGCCGGT	ACCGGCCAGCTTATCGTCGAAAAT
	1532	TGAGGGAGAACCCGAAATCTGCTT	AAGCAGATTTCGGGTTCTCCCTCA
20	1533	GGCGACTACATCCCAATTGCTTG	CAAGCAATTGGGGATGTAGTCGCC
	1534	GCAGACGCGCCTTCCATACTTTT	AAAAGTATGGAAGGCCGCTCTGC
	1535	ACAACCACATGACGTGTAGCTGCA	TGCAGCTACACGTCATGTGGTTGT
	1536	CTGCTGGGCGCGCAAAGCTTGTTG	CAACAAGCTTTGCGCGCCCAGCAG
	1537	AAGCCTTCTTTGGCTTGCTCCGCT	AGCGGAGCAAGCCAAAGAAGGCTT
25	1538	TACCTGCTGCCTGGAGCAAGGCAT	ATGCCTTGCTCCAGGCAGCAGGTA
	1539	GACGCCGCAGCCATGAGTGAGTGT	ACACTCAGTCATGGCTGCGGCGTC
	1540	AGTTGGCCGCTTATTTTGCTCACC	GGTGAGCAAAATAAGCGGCCAACT
	1541	CCAGGCGCCTTCGACAGATCCTCA	TGAGGATCTGTGCAAGGCGCCTGG
	1542	GTGTCCCCTCCAGCTAGCCAGTTT	AAACTGGCTAGCTGGAGGGGACAC
30	1543	GACAACAAGCCAAGGTGACACGTC	GACGTGTCACCTTGGCTTGTGTC
	1544	CTACACCGCTCGTGACTCGGCAAA	TTTGCCGAGTCACGAGCGGTGTAG
	1545	TGGTGCCATCAAAGCACGTTGTAC	GTACAACGTGCTTTGATGGCACCA
	1546	ACAATGCGTGTTGCGAAACGCATA	TATGCGTTTCGCAACACGCATTGT
	1547	TTGTCCAGCCATTGTATTTGCGC	GCGCAAAATACAATGGCTGGACAA
35	1548	ACGAGAGATAGCGGACTCCTCCGA	TCGGAGGAGTCCGCTATCTCTCGT
	1549	AGCTTTGTGCTCAGGCGAGCTCTT	AAGAGCTCGCCTGACGACAAAGCT
	1550	GACAGTCGGCGTGCAGTTTGTGT	ACAACAACTGCACGCCGACTGTC
	1551	AGCTAGCGACGGCCAACTCACGTA	TACGTGAGTTGGCCGTCGCTAGCT
	1552	CTCCTGTTGCGGGCCGTTACTGGT	ACCAGTAACGGCCCCGAACAGGAG
40	1553	ACTGACCGACGCAGTGCCACATAG	CTATGTGGCACTGCGTCGGTCAGT
	1554	AGGTAGGGTCTGGTTTACTCGCA	TGCGAGTCAAACCAGACCCTACCT

5	1555	CCTCCATTTTAGCGCGTTGCCAAT	ATTGGCAACGCGCTAAAATGGAGG
	1556	TTCTTAGGATCCGCGCACTCTTGG	CCAAGAGTGCGCGGATCCTAAGAA
	1557	GTCGAAGGTGTCTACCGTGCGCAG	CTGCGCACGGTAGACACCTTCGAC
	1558	GTCAC TCGGCGGCCCAATCACTCG	CGAGTGATTGGGCGCCGAGTGAC
	1559	TCTCGGTCACCCGTCTTGACCCTT	AAGGGTCAAGACGGGTGACCGAGA
	1560	GCCCTCGACGAAC TACCTGAAC	GTT CAGGATGAGTTCGTCGAGGGC
	1561	TCCGGCGTACTCTGACACGGCGAT	ATCGCCGTGTCAGAGTACGCCGGA
	1562	AGCCAAATGCTTTCGTGGTTCGGA	TCCGAACCACGAAAGCATTTGGCT
10	1563	ACTCCACGCCGCATGTTGCTGTGA	TCACAGCAACATGCGGCGTGAGT
	1564	GCTTCGAGTCGGTGGCATCTGTAT	ATACAGATGCCACCGACTCGAAGC
	1565	GGTCTTGGGCCATCGACTTGCTGC	GCAGCAAGTCGATGGCCCAAGACC
	1566	GGTATCGGACTGCACTAAGGGCAA	TTGCCCTTAGTGCAGTCCGATACC
	1567	AGCCCATGCGTTCCGGATGATTTG	CAAATCATCCGGAACGCATGGGCT
	1568	GCCAGGGTTAAAAGTGATGGGCTC	GAGCCCATCACTTTTAACCCTGGC
15	1569	GACGACGTGCTGGCTACGAAGGGG	CCCTTCGTAGCCAGCACGTCGTC
	1570	TCCTATTGACCGTGATCGTGATC	GATCACGATGCACGGTCAATAGGA
	1571	ACCCGCCTCGACTCCACAATAAA	TTTAGTTGTGGAGTCGAGGCGGGT
	1572	GATGTGGATCACGACCTGCCAGTA	TACTGGCAGGTCGTGATCCACATC
	1573	GTGCCATTGCCACCCATAATGCGT	ACGCATTATGGGTGGCAATGGCAC
20	1574	TTAGCCTGTGCACCCAGTCAGGAG	CTCCTGACTGGGTGCACAGGCTAA
	1575	TCCGATGGGAGAGGCTGATCTCAC	GTGAGATCAGCCTCTCCCATCGGA
	1576	CACTACTGAAGTGGCCTGGCGCTG	CAGCGCCAGGCCACTTCAGTAGTG
	1577	TGCGGCCATAGCGATGTGATAGAT	ATCTATCACATCGCTATGCCGCA
	1578	GATTGCGCTTAACGGAGATGCACG	CGTGCATCTCCGTTAAGCGCAATC
25	1579	TCACGTTTGACAACGCCAAGCATT	AATGCTTGGCGTTGTCAAACGTGA
	1580	GCATTGTTTGCTAAAGGCGGCATT	AATGCCGCCTTTAGCAAACAATGC
	1581	AGTCGCTCTACGCGTGCAACGCTG	CAGCGTTGCACGCGTAGAGCGACT
	1582	TAGCTCCATGGAGGTCCGAAAGGG	CCCTTTCGGACCTCCATGGAGCTA
	1583	GACCGGTTGGACCTCACTGGCTTC	GAAGCCAGTGAGGTCCAACCGGTC
30	1584	AAGCCGGACAGTCAATGTGCGTAT	ATACGCACATTGACTGTCCGGCTT
	1585	TGCCTCGCTGAGTTCTTCACCGTG	CACGGTGAAGAACTCAGCGAGGCA
	1586	TCGTAGACCTTGCTTTTGGGCTCA	TGAGCCCAAAAGCAAGGTCTACGA
	1587	ACCGCTATGCGCCCTACAAAGCAT	ATGCTTTGTAGGGCGCATAGCGGT
	1588	TAGCGTCACCGTAGCTTGGGGCAG	CTGCCCCAAGCTACGGTGACGCTA
35	1589	CTCTCAGCAACTGATGGCACCGGA	TCCGGTGCCATCAGTTGCTGAGAG
	1590	AAAGGAAATGTGGTGCTGGTCCGC	GCCGACCAGCACCACATTTCTTTT
	1591	CCGGCTTAGATGGAGAACAAGTGC	GCACTTGTTCTCCATCTAAGCCGG
	1592	AAGTAAATCGCTCGCCCAAACCG	CGGTTTGGGCGAGGCGATTACTT
	1593	TGGGCTGTT CAGCCTACCGGACGT	ACGTCCGGTAGGCTGAACAGCCCA
40	1594	GTTTCGGTTCAGCCATGGGCCTAC	GTAGGCCCATGGCTGAACCGAAAC
	1595	GGCCAACATTTCTAGGGGAGTGCC	GGCACTCCCCTAGAAATGTTGGCC

	1596	TTCTTCGTTGGGATTGTCTCACC	GGTGAGGACAATCCCAACGAAGAA
	1597	TGCACATTGGGGTACGGATCTGAC	GTCAGATCCGTACCCCAATGTGCA
	1598	GGCAGTTAGACGGCAAACCTGCAGG	CCTGCAGTTTGCCGTCTAACTGCC
5	1599	CGCGTCAGGCTATGAATGGCTCTT	AAGAGCCATTCATAGCCTGACGCG
	1600	GCTGAATGCAAACCTCGGAGCCAT	ATGGCTCCGAGGTTTGCAATTCAGC
	1601	CGCTCTGGCGGATTCAATTGTTTTT	GAAAACAATGAATCCGCCAGAGCG
	1602	TTTTCAATCAACCCTCCGGACGTA	TACGTCCGGAGGGTTGATTGAAAA
	1603	GTGGTGGAGTCTGAAGCACGACAG	CTGTCTGTGCTTCAGACTCCACCAC
10	1604	AAACAGGTCCGGATGATGTCTGGA	TCCAGACATCATCCGGACCTGTTT
	1605	GTACCGCGTGTACGCCACCGTTAG	CTAACGGTGGCGTACACGCGGTAC
	1606	TCCAACCTACATTTGCGGAAGGAA	TTCTTCCGCAAATGTAGGTTGGA
	1607	GACGTACCGTCGTCCCGTGAGTTG	CAACTCACGGGACGACGGTACGTC
	1608	GGCAATCCTACAACCGACGCTGAT	ATCAGCGTCGGTTGTAGGATTGCC
	1609	GGCGGCTGCAGGGTCTACATCGAG	CTCGATGTAGACCTGCAGCCGCC
15	1610	ATACTACGCTGCAGCTGCGCGGGC	GCCCGCGCAGCTGCAGCGTAGTAT
	1611	GGATCGCAATCCCTCCGATGACGA	TCGTCATCGGAGGGATTGCGATCC
	1612	TGGCCTTGACGCGGAGCCGAATCT	AGATTGGGCTCCCGTGCAAGGCCA
	1613	AGGTGCCGACGAAACGACGAATAT	ATATTCGTCTGTTTCTGTCGGCACCT
	1614	GCTGTTTACCGTCGTCTGTTGTTG	CAACAACGACGACGGTGAACAGC
20	1615	CGGTCCCAATGTTACAACCCAGAC	GTCTGGGTTGTAACATTGGGACCG
	1616	GCAATTCCAGCCACTTTTGACCAA	TTGGTCAAAAGTGGCTGGAATTGC
	1617	ACGGGCGAAAGCTCGGTACGGATA	TATCCGTACCGAGCTTTCGCCCGT
	1618	CGACCCGACTTTTGCTTTCGAGTG	CACTCGAAAGCAAAAGTCGGGTCCG
	1619	AATTCAGTGTGTCGTCATGGTCG	CGACCATGACGCAAACACTGAATT
25	1620	CCTGTATGAGGTTCTGGGTCGGCT	AGCCGACCCAGAACCTCATACAGG
	1621	TGGCATACTTGGTGCAAACGCCGT	ACGGCGTFTGCACCAAGTATGCCA
	1622	TCGCCAGTACAGAAACATGCGGGC	GCCCGCATGTTTCTGTACTGGCGA
	1623	CCCGCTGTTGCTCTCATCGTGAG	CTCCACGATGAGAGCAACAGCGGG
	1624	GCCACAATCTGACCCTGGGAATCA	TGATTCCCAGGGTCAGATTGTGGC
30	1625	GCTCAGTCTCGGAAGTTTCGGCTA	TAGCCGAAACTTCCGAGACTGAGC
	1626	CTTCACGGGCCAACGACGGTCGAG	CTCGACCGTCGTTGGCCCGTGAAG
	1627	CGACAGTTCCGTCCGTCTTGAGGA	TCCTCAAGACGGACGGAAGTGTCCG
	1628	ACGGAGACGCAGTCGAAACGTCCC	GGGACGTTTCGACTGCGTCTCCGT
	1629	CATGCATCCGATTAAGGGGATCAC	GTGATCCCCTTAATCGGATGCATG
35	1630	ATTGCGGGAGTCCCTAGCTTTCTG	CAGAAAGCTAGGGACTCCCGCAAT
	1631	GTGTGGAAGATGCAATTGGAACGG	CCGTTCCAATTGCATCTTCCACAC
	1632	ATACAACGGTAGGTGACAGGGGCG	CGCCCCGTGCACCTACCGTTGTAT
	1633	GCCGTGGGAGTAAGGGTACAAAGG	CCTTTGTACCCTTACTCCACGGC
	1634	GCACGTAGGTCGGCTACTACTCGG	CCGAGTAGTAGCCGACCTACGTGC
40	1635	ACTGTGATCTCTTGGGCAAAGGGC	GCCCTTTGCCCAAGAGATCACAGT
	1636	CATGCCTGAACAATCTCGCATCCC	GGGATGCGAGATTGTTACGGCATG

5	1637	GAGCCTGGCTCCACAGCTGTGCTC	GAGCACAGCTGTGGAGCCAGGCTC
	1638	CTTTCGATACCATCGTTGGCGATC	GATCGCCAACGATGGTATCGAAAG
	1639	CCCGGAGGTGAGGCATTGAATATG	CATATTCAATGCCTCACCTCCGGG
	1640	CTCATTAGCTAAAAGCGGCTGGA	TCCAGCCGCTTTTAGCTGAATGAG
	1641	GAAATGCCCTGGGGACTTTTTGCC	GGCAAAAAGTCCCCAGGGCATTTC
	1642	TTTGCTTCACAACAGACGCAGCA	TGCTGCGTCTGTTGTGAAGGCAAA
	1643	AAATCCCAAGACGTCGGGGCGTAT	ATACGCCCCGACGTCTTGGGATTT
	1644	CAACGGGGCGGTAGCTAAACCGTAA	TTACGGTTTAGCTACCGCCCGTTG
10	1645	GGCCAACGACAATGCGAAACCTTC	GAAGGTTTCGCATTGTGCTTGGCC
	1646	GACATCACGCAAAATCTCAGCGCA	TGCGCTGAGATTTTGCCTGATGTC
	1647	ACGTTCCGTCCACAACCGTATGTT	AACATACGGTTGTGGACGGAACGT
	1648	GCTCATAGGTCTTCCGTAGCCCGT	ACGGGCTACGGAAGACCTATGAGC
	1649	GAAACGAGTCTCTCGCGCCCTAGA	TCTAGGGCGCGAGAGACTCGTTTC
	1650	CGGGACAGAAGCAAGTTACATCGG	CCGATGTAACCTGCTTCTGTCCCG
15	1651	TGACCGCTCGATACCAGGAGGGTG	CACCCTCCTGGTATCGAGCGGTCA
	1652	CTGGCAATAAAGACCTTCCGACCA	TGGTCGGAAGGTCTTTATTGCCAG
	1653	TGCGCGACGTCATGTTGGTGATTA	TAATCACCAACATGACGTCGCGCA
	1654	GTTGGTTGTGGGAACACACCCGCT	AGCGGGTGTGTTCCCAACCAAC
20	1655	TGTGGGTTTCGGAACACAGGAAGT	ACTTCCTGTGTTTCCGAACCCACA
	1656	GGAAAAACGGCAATTAGCCGAGT	ACTCGGCTAATTGCCGTTTTTCC
	1657	TGGTGCGGAGTGCCCTCTATTGGG	CCCAATAGAGGGCACTCCGCACCA
	1658	AACCAACAGGCTGCAGCCCAGACT	AGTCTGGGCTGCAGCCTGTTGGTT
	1659	AAACAGATCCATCTGCACGCCAGG	CCTGGCGTGCAGATGGATCTGTTT
25	1660	GGAATACCGCGGCGATTATGGCTT	AAGCCATAATCGCCGCGGTATTCC
	1661	TACTGTTTCGCGGCAAACCGTCACT	AGTGACGGTTTGCCGCAACAGTA
	1662	GATCTCTCGTGGAGCACGTTTTCC	GGAAAACGTGCTCCACGAGAGATC
	1663	GGCATAGCAAACCTTGACCTCCAA	TTGGAGGTCAAGGTTTGCTATGCC
	1664	ATCTGGGATTCGCGAGCCAATATC	GATATTGGCTCGCGAATCCAGAT
30	1665	CGATCAGGATATCATTTACGCCCG	CGGGCGTAAATGATATCCTGATCG
	1666	ACGGTACCGAAACGGTCTCAGCGT	ACGCTGAGACCGTTTCGGTACCGT
	1667	CTCCCATACCTGCGTTCTTACCGA	TCGGTAAGAACGCAGGTATGGGAG
	1668	GCACGAGAACCTAATTGTGCACACA	TGTGCGACAATTAGGTTCTCGTGC
	1669	GCCACACGATCAAGACAGCGCATG	CATGCGCTGTCTTGATCGTGTGGC
35	1670	CCCGTTAACTCACGAGCGGTCAAT	ATTGACCGCTCGTGAGTTAACGGG
	1671	AGAGAAGGTCATTGCCTGTCGGTG	CACCGACAGGCAATGACCTTCTCT
	1672	CGGGCCCTCTTAAAGTAGAGCAGG	CCTGCTCTACTTTAAGAGGGCCCCG
	1673	ACATCGCGTCCGAGGGAGTTAGCG	CGCTAACTCCCTCGGACGCGATGT
	1674	AATGCCTAATCGAGCCAGCGGATC	GATCCGCTGGCTCGATTAGGCATT
	1675	CTCGATCTTTTTAAACCGGCGCTT	AAGCGCCGGTTTAAAAAGATCGAG
40	1676	CGTTCCTGGAAGGCAGGGTCTCAC	GTGAGACCCTGCCTTCCAGGAACG
	1677	CCTGTGCTTACTATCGGCGATCCA	TGGATCGCCGATAGTAAGCACAGG



	1678	GTTAGTCGCCCTATTGGCCTGGTT	AACCAGGCCAATAGGGCGACTAAC
	1679	CCGGTGAGATGACTGTAAATGCCA	TGGCATTACAGTCATCTCACC GG
	1680	CGTGGTTTAAACATCGCGCTTCG	CGAAGCGCGATGTTTTAAACCACG
5	1681	TAAGACGCAGAAGATGGGGTCCAC	GTGGACCCCATCTTCTGCGTCTTA
	1682	CACCACAGCTTCTTTGTTGACCC	GGGTCGAACAAAGAAGCTGTGGTG
	1683	TCGGGTCCGTACCACCACTTTTGC	GCAAAAGTGGTGGTACGGACCCGA
	1684	CCAAGCCCCGAGTACCGAAGATTT	AAATCTTCGGTACTCGGGGCTTGG
	1685	TCCGTGATATGGTCGTGGCGCGGT	ACCGCGCCACGACCATATCACGGA
10	1686	TGTCTGTGTCATGGCACCTCGCAT	ATGCGAGGTGCCATGACACAGACA
	1687	AGGACTGCACTGTGCACGTCTGAT	ATCAGACGTGCACAGTGCAGTCTT
	1688	CCATCCTCATGTACAGCGCCGCTG	CAGCGGCGCTGTACATGAGGATGG
	1689	GTACCCGCGCCTTCCTCGACACAG	CTGTGTCGAGGAAGGCGCGGGTAC
	1690	ACGGGTCTTGGTCGACTAAGGCTT	AAGCCTTAGTCGACCAGGACCCGT
15	1691	CGTATCGAAGGCGTGTACAACCGG	CCGGTTGTACACGCCTTCGATACG
	1692	TGCCCCGCCCTTTATGCAACGCTCA	TGAGCGTTGCATAAAGGGCGGGCA
	1693	AAACTTACGAGACGGCGGCTGCCA	TGGCAGCCGCCGTCTCGTAAGTTT
	1694	AAGTCTGACAAACGGAACGGGTGT	ACACCCGTTCCGTTTGTGAGACTT
	1695	TAAGCGCAGACCAAAGTATGCGGC	GCCGCATACTTTGGTCTGCGCTTA
20	1696	GCAGTTTTTCAGATCCTCCGCAA	TTTGCGGAGGATCTGAAAACTGC
	1697	TCGGAAGCATTTACGCGATCTCAG	CTGAGATCGCGTAAATGCTTCCGA
	1698	CACAGAAACGGTTGAACGAACGCC	GGCGTTCGTTCAACCGTTTCTGTG
	1699	GCATGCTCAGATGGTCGTGCTCAC	GTGAGCACGACCATCTGAGCATGC
	1700	AAGGATTCTCGCTTCCGGCATGAT	ATCATGCCGGAAGCGAGAATCCTT
25	1701	GGTGGGGTAGCGCTGGTATGAAAA	TTTTCATACCAGCGCTACCCACC
	1702	ATTATTACGGGACCGAACCAACGG	CCGTTGGTTCGGTCCCGTAATAAT
	1703	GCGCGAGTGTGTCATGATGTTACGT	ACGTGAAGATCATGACACTCGCGC
	1704	GACATTCGTGACTTGGTCGTCCGC	GCGGACGACCAAGTCACGAATGTC
	1705	TCATTAGTGCAGGCACCGATCAAG	CTTGATCGGTGCCTGCACTAATGA
	1706	GAGTTGTGCGGAGTCATCGGAGTC	GACTCCGATGACTCCGCACAACCTC
30	1707	GCCTTTACAGATTTGGCGGGCTAT	ATAGCCCGCCAAATCTGTAAAGGC
	1708	ATGGCGTTTGCGAAGTCGATACAG	CTGTATCGACTTCGCAAACGCCAT
	1709	TGCATCGGCCTCAATCAGAGAACT	AGTTCTCTGATTGAGGCCGATGCA
	1710	ACAATCATGGCAATCTGGCAAATG	CATTTGCCAGATTGCCATGATTGT
35	1711	GACGTGGAAGAGTGCAGATCAGCA	TGCTGATCTGCACTCTTCCACGTC
	1712	AGGGCAGGGGACGGACAGTAAGTC	GACTTACTGTCCGTCCCCTGCCCT
	1713	GCATAGGGCGAATCTAGTACGGGC	GCCCGTACTAGATTCCGCCCTATGC
	1714	TCCGGCGCATCCTCATTAGCAACT	AGTTGCTAATGAGGATGCGCCGGA
	1715	TGGCCGCTTCCACTAATATTGGAC	GTCCAATATTAGTGGAAGCGGCCA
40	1716	CCGGCGGACGGCTCTTGTCATGA	TCATTGACAAGAGCCGTCCGCCGG
	1717	CGAGCAACCCAAAAGGAAGCAGTA	TACTGCTTCCTTTGGGTTGCTCG
	1718	GCGTATGATTCGGCAATCCGCCAG	CTGGCGGATTGCCGAATCATACGC

	1719	AGTACCGCTACAACGCTGGTTCGC	GCGAACCAGCGTTGTAGCGGTACT
	1720	GGGCAGGCCAGGTCCACCTGAGAA	TTCTCAGGTGGACCTGGCCTGCCC
	1721	CCACTTCTGTGACCGAACCGTGCT	AGCACGGTTCGGTCACAGAAGTGG
5	1722	CCTGGTACCAGGCAGCAGTTGATT	AATCAACTGCTGCCTGGTACCAGG
	1723	TTAGGGTACCGTCGAGAGACGCCA	TGGCGTCTCTCGACGGTACCCTAA
	1724	GGTTGCTTGTGCGCGTGAGGTAGT	ACTACCTCACGCGCACAAGCAACC
	1725	TGCTTCGACCGATGAAACTCGAAG	CTTCGAGTTTCATCGGTCTGAAGCA
	1726	TGCCACCCATACTATGCCCAGTGG	CCACTGGGCATAGTATGGGTGGCA
10	1727	TGTGCGGCAACGCGTGAAGACGTT	AACGTCTTCACGCGTTGCCGCACA
	1728	TGAGAGAAGCTGGCCTCGGATCAG	CTGATCCGAGGCCAGCTTCTCTCA
	1729	TATTGCGAATTCGAGTACGTGCCC	GGGCACGTACTCGAATTCGCAATA
	1730	CGAGAGGGGTTCCCCAGTGATCGA	TCGATCACTGGGGAACCCCTCTCG
	1731	TGCCTGGGGTGTCTGTTCTAATTCT	AGAATTAGAACGACACCCAGGCA
	1732	GTGCGTCATTGTGGGTCATCCCAA	TTGGGATGACCCACAATGACGCAC
15	1733	AGGGCTCCCAGCATACCAACGTTG	CAACGTTGGTATGCTGGGAGCCCT
	1734	AACTAGCCGACCTTTGTGCAGAG	CTCTGCACAAAGGTGCGGCTAGTT
	1735	TTAGCCCAGCCCTTCAATGGGAAC	GTTCCCATTAAGGGCTGGGCTAA
	1736	CGGCCTCGGTTGTACGGGTAGTCT	AGACTACCCGTACAACCGAGGCCG
20	1737	TCTTTGAGGCGCGGACCCGCATAT	ATATGCGGGTCCGCGCCTCAAAGA
	1738	GATGGTTGCGCCTTGTGTGCGCAGC	GCTGCGACACAAGGGCGAACCATC
	1739	GAGATTCAATACAGGCCGCGGGTC	GACCCGCGGCCTGTATTGAATCTC
	1740	AGGGCGAAGGAAGGTTCCGTTTTT	AAAAACGGAACCTTCCTTCGCCCT
	1741	CTCGACCCCTGCCACTACTGGTTC	GAACCAGTAGTGGCAGGGGTCGAG
25	1742	TGTTCCGCGGTCTACGCATTACTG	CAGTAATGCGTAGACCGCGGAACA
	1743	GAGACGACGTCCTACACCCGCTAA	TTAGCGGGTGTAGGACGTCGTCTC
	1744	AGATTGCGACAGCGACACGTGATT	AATCACGTGTCGCTGTCGCAATCT
	1745	GATACCGTTGGGCATTTCTCGGTA	TACCGAGAAATGCCCAACGGTATC
	1746	GATTGGGAGGCATTACGCGACGGA	TCCGTCGCTGAATGCCTCCCAATC
	1747	AGGAGGAAACGAGGGCGTAGGTTT	GAACCTACGCCCTCGTTTCCTCCT
30	1748	GCCAAACAACGTCTGACGCCTAGC	GCTAGGCGTCAGACGTTGTTTGCC
	1749	TTTAATGCGGAAAGGATGCACGCG	CGCGTGATCCTTTCCGCATTAAA
	1750	TTATCGGCCGTTAAATGGGATGG	CCATCCCATTTTAACGGCCGATAA
	1751	CCTTGGATTGTTTCATCGCTAGCA	TGCTAGCGATGAACGAATCCAAGG
	1752	AAGTGAACGTGCAGTGGTCTTCGA	TCGAAGACCACTGCACGTTCACTT
35	1753	TCCTTACCCCTCGTTCAAACGCCT	AGGCGTTTGAACGAGGGGTAAGGA
	1754	ATTCCTGAACCATGCATGGCCTGT	ACAGGCCATGCATGGTTCAGGAAT
	1755	AGCGAGACGCTCGATCACGAACTA	TAGTTCGTGATCGAGCGTCTCGCT
	1756	GCTGGTCTGGCTCGCTGTTTAGAA	TTCTAAACAGCGAGCCAGACCAGC
	1757	CGTGCGCGGCATAAAGATAGGTCT	AGACCTATCTTTATGCCGCGCACG
40	1758	TCTGGCACTCACATCGGACAGTCT	AGACTGTCCGATGTGAGTGCCAGA
	1759	ACCATTGGAGGACCACAGAGCTCC	GGAGCTCTGTGGTCTCCAATGGT

	1760	TCCAGGGTCGGAGTACATGGCGGG	CCCGCCATGTACTCCGACCCTGGA
	1761	ATATGCCGTCGGATCGTACACGCA	TGCGTGACGATCCGACGGCATAT
	1762	TGCTGGCGTCAACACTTCCCGATT	AATCGGGAAGTGTTGACGCCAGCA
	1763	CAGGGCGGTGCGGTGAACTAGCCA	TGGCTAGTTCACCGCACCGCCCTG
5	1764	CATGGACTGCCGTACATCAGCTGG	CCAGCTGATGTACGGCAGTCCATG
	1765	CCGGCCATACGCTGGCAAGATTAC	GTAATCTTGCCAGCGTATGGCCGG
	1766	AGCGGACACCTGTACTCTCCTCCA	TGGAGGAGAGTACAGGTGTCCGCT
	1767	GGAGCCACACCAAGTCGAAGATGGT	ACCATCTTCGACTGGTGTGGCTCC
	1768	CGCCACCGGAAATTGAAAAGACTG	CAGTCTTTTCAATTTCCGGTGGCG
10	1769	TGAAACGGATGTTGCTTCTTGACG	CGTCAAGAAGCAACATCCGTTTCA
	1770	TTGAAGCGGTGAAGAGCCTGTCCT	AGGACAGGCTCTTCACCGCTTCAA
	1771	CGAACCAAGCTGCATTGTCACTGG	CCACTGACAATGCAGCTTGTTTCG
	1772	GAGTCTGCGCTTGCAATCTTTGCG	CGCAAAGATTGCAAGCGCAGACTC
	1773	GCTGGGTATAGTTGCCTGGCAATG	CATTGCCAGGCAACTATACCCAGC
15	1774	GCAGGCGTTCCATATTCGCAACCC	GGGTTGCGAATATGGAACGCCTGC
	1775	GCGCCAATAATACCTCCACCGCG	CGCGGTGGAGGTATTAGTTGGCGC
	1776	TGGCGTTCAGTGCAACGCTGGTTA	TAACCAGCGTTGCACTGAACGCCA
	1777	CAAACTGACGGGTATGGGAGCGC	GCGCTCCCATACCCGTCAGTTTG
	1778	AGGTGTCGCTGGAACCCGACTTGT	ACAAGTCGGGTTCCAGCGACACCT
20	1779	CTTCCAAAAGCGCAATTGGCTTTG	CAAAGCCAATTGCGCTTTTGGAAG
	1780	TCGGGCTTCTCGCAATTCTGTCAG	CTGACAGAATTGCGAGAAGCCCGA
	1781	GCCAAAAGAATGCGCTGGGTAGGT	ACCTACCCAGCGCATTCTTTTGGC
	1782	TGGTGCCCGCACCGAGAGACTGTA	TACAGTCTCTCGGTGCGGGCACCA
	1783	CGAGGCCGTAGTGGGGACTGCTCT	AGAGCAGTCCCCACTACGGCCTCG
25	1784	CGATCTGCGCATAGAGGGGACTTT	AAAGTCCCCTCTATGCGCAGATCG
	1785	TGTGCAATCGGCCTTCTCAGAGCC	GGCTCTGAGAAGGCCGATTGCACA
	1786	GATCACCTGGACCGCTACCGTTTT	AAAACGGTAGCGGTCCAGGTGATC
	1787	ATGGGGAGTTAAGGACCCTGCACC	GGTGCAGGGTCCTTAACTCCCCAT
	1788	CATTGTGGACAGCCAATGGTGGCT	AGCCACCATTGGCTGTCCACAATG
30	1789	CCATCACCATGCCACGGTAAGATC	GATCTTACCGTGGCATGGTGATGG
	1790	GCACCCGTGTCGTTGGTTAGCAAG	CTTGCTAACCAACGACACGGGTGC
	1791	GGAGTGGGTTCCGCGAATTCAGTG	CAGTGAATTCGCGGAACCCACTCC
	1792	GGGGATTTCCTTTCGACGGCTCGA	TCGAGCCTGCGAAAGGAAATCCCC
	1793	CATTGATCATGTGCACTTGACCA	TGGTGCAAGTGACATGATCAATG
35	1794	AGCAGCGCTGCGCTTGTTTCGGAT	ATCCGAAACAAGCGCAGCGCTGCT
	1795	CGAGTAACGCGGTTGCTTTGCGAA	TTGCGAAAGCAACCGCGTTACTCG
	1796	TGGCCTGGAACATAGGTGGAATC	GAGTTCACCTATGTTCCAGGCCA
	1797	CGCACACCAAGCGTTTATTGAGAA	TTCTCAATAAACGCTTGGTGTGCG
	1798	TCACCTTCACAGTGGGCATACAGC	GCTGTATGCCCACTGTGAAGGTGA
40	1799	CAAATATCCCTGAGCCCTCGAGCT	AGCTCGAGGGCTCAGGGATATTTG
	1800	GGGAGCTGGTGAGCAGATGTAACG	CGTTACATCTGCTCACCAGCTCCC

	1801	AGGATTGCTTTTGC GTTATGCGGA	TCCGCATAACGCAAAAGCAATCCT
	1802	ATCGTTTGGGCGCTACGCAATTGT	ACAATTGCGTAGCGCCCAAACGAT
	1803	CCGATTTGTCCCAAATGCAACGTT	AACGTTGCATTTGGGACAAATCGG
	1804	AAGGGTCAAGCTCATGGAGCGGAA	TTCCGCTCCATGAGCTTGACCCTT
5	1805	TCTGACGTCGTTCAAGGGCTCGCT	AGCGAGCCCTTGAACGACGTCAGA
	1806	CGCACCACTCCGAGGTATTTGTCT	AGACAAATACCTCGGAGTGGTGCG
	1807	AAGGGGTGAAAAAGGAGAAGCCGA	TCGGCTTCTCCTTTTTCACCCCTT
	1808	AAACCACGCAAATGGCGATACCAT	ATGGTATCGCCATTTGCGTGTTT
	1809	CAGAAGGGATGACGCCTTAAGTCG	CGACTTAAGGCGTCATCCCTTCTG
10	1810	CATGACGAGAGCGGACCTGAAGTG	CACTTCAGGTCCGCTCTCGTCATG
	1811	CTGGACATGTTTGTTCGCCACTG	CAGTGGCGAAACAAACATGTCCAG
	1812	AAGACCGACTCTCGTCGTTTGCAC	GTGCAAACGACGAGAGTCGGTCTT
	1813	GCGCGATTACATACCGTTTCCGTA	TACGGAAACGGTATGTAATCGCGC
	1814	CACTGACCGGACCCAACCTAACAT	ATGTTAGGTTGGGTCCGGTCAGTG
15	1815	AGTGCAAGTCTAGACACGCCCCGAG	CTCGGGCGTGTCTAGACTTGCACT
	1816	GGTTGGTGCGAGATCCTGGACTGT	ACAGTCCAGGATCTCGCACCAACC
	1817	GGTCGTCCCGAAACGTAAACGAGG	CCTCGTTTACGTTTCGGGACGACC
	1818	GACTAGTACGATCACGGGGCGGGT	ACCCGCCCGTGATCGTACTAGTC
	1819	CCGACCTGACCCTGTGTACAGGTT	AACCTGTACACAGGGTCAGGTCGG
20	1820	TGCTCACTGCCACACTGTTATGG	CCATAACAGTGTGGGCAGTGAGCA
	1821	CGAGGAAACACATTTCTTCGGGCC	GGCCCGAAGAAATGTGTTTCCTCG
	1822	TGGCACCGGGTGGATTCTTGTCTA	TAGACAAGAATCCACCCGGTGCCA
	1823	GAGGCACGGTGATAGTGGTTGTGC	GCACAACCACTATCACCGTGCCTC
	1824	ATGCAGATGGATCTTTTCGACGC	GCGTCGAAAAAGATCCATCTGCAT
25	1825	TGCGATAGCCAAAGAGTCGAGGAC	GTCTCGACTCTTTGGCTATCGCA
	1826	ATGGCGTGTGAGCGAACTGCCTGG	CCAGGCAGTTCGCTGACACGCCAT
	1827	CAATGCAGCTCGGAAGTCAGGTCG	CGACCTGACTTCGAGCTGCATTG
	1828	AGGATCAGTGCACATGTCCCTCA	TGAGGGGACATGTGCACTGATCCT
	1829	CACATCTTGGCTGTCACCCGAGAA	TTCTCGGGTGACAGCCAAGATGTG
30	1830	CGCATTATCACCTCAATGCCAGTG	CACTGGCATTGAGGTGATAATGCG
	1831	ACATCCGCAGACTCCCTATAGCCC	GGGCTATAGGGAGTCTGCGGATGT
	1832	GTGAACCCGAACGAGGGGAGTCTC	GAGACTCCCCTCGTTCGGGTTCAC
	1833	GCGTAGGGAATTTGCCTCACGACT	AGTCGTGAGGCAAATTCCTACGC
	1834	TTTACGCGTCGCTCGGTTGTAGTG	CACTACAACCGAGCGACGCGTAAA
35	1835	GAGAGGCGTCTAGGCGGTTCTAGC	GCTAGAACCGCCTAGACGCCTCTC
	1836	GCATGCTGATAACGAATGCTTCCC	GGGAAGCATTGTTATCAGCATGC
	1837	CTGAAGCTCGTGTGCGATGAGGGA	TCCCTCATCGCACACGAGCTTCAG
	1838	ACAACGGCATGAGGAGGCTTTTTC	GAAAAAGCCTCCTCATGCCGTTGT
	1839	TTTGGAGACGCCAGTACGCGTGGT	ACCACGCGTACTGGCGTCTCCAAA
40	1840	GCTATCATTTGGTGTAAGCCCGCC	GGCGGGCTTACACCAAATGATAGC
	1841	TCAACATCCAGGGCGGTGCTTGGT	ACCAAGCACCGCCCTGGATGTTGA

	1842	TTCGATGTAATCCCCAAAGATGCC	GGCATCTTTGGGGATTACATCGAA
	1843	GGACCTTCGGCAGGTTATCGCCGT	ACGGCGATAACCTGCCGAAGGTCC
	1844	AGTAAGAAGAGGCAGGCCCCACCT	AGGTGGGGCCTGCCTCTTCTTACT
5	1845	AACGGCTCCCCGTCGTA CTGCTTA	TAAGCAGTACGACGGGGAGCCGTT
	1846	CCTATACCGTCGTGGTTCACGTT	AACGTGGAACCACGACGGTATAGG
	1847	CCGCGCAGGCGCTAATACTCAAGG	CCTTGAGTATTAGCGCCTGCGCGG
	1848	AAATGGGCCAGTGAAATCCTTGGT	ACCAAGGATTTCACTGGCCCATTT
	1849	ACGGTTTCGAATACTGCTGGGCAG	CTGCCCAGCAGTATTCGAAACCGT
10	1850	CCGCTTGAGGTT CAGGTCAGAGCT	AGCTCTGACCTGAACCTCAAGCGG
	1851	ATCGTGCCCGAAGACACTTAAACG	CGTTTAAGTGTCTTCGGGCACGAT
	1852	ACCTGAACCAGGGCGATTGCTTTA	TAAAGCAATCGCCCTGGTTCAGGT
	1853	ACCCTATACGCTGGGCTAAGCGGG	CCCGCTTAGCCCAGCGTATAGGGT
	1854	TGTTTCGCGACTAGAAAGCCTTGC	GCAAAGGCTTCTAGTCGCGAAACA
15	1855	GAAGTTGGCGGCTCACCCGTATTA	TAATACGGGTGAGCCGCCAACTTC
	1856	TGGCTACACCGCTTAGGAGGAACC	GGTTCCTCCTAAGCGGTGTAGCCA
	1857	CCACAGTTGCGTGACTTACATCGC	GCGATGTAAGTCACGCAACTGTGG
	1858	ACTGCCACTGCGTCTGAAGAGTGG	CCACTCTTCAGACGCAGTGGCAGT
	1859	GCGCCAGCAAATTTCTGTGTGGTGT	ACACCACACGAAATTTGCTGGCGC
20	1860	TGCCTCCGTCGAGCCGAATAGCCA	TGGCTATTCGGCTCGACGGAGGCA
	1861	GTACAAACGGGCGCTATTTCTGCC	GGACGAAATAGCGCCCGTTGTAC
	1862	GCTTCCCTGGCTCTGAACGGAAAC	GTTTCCGTT CAGAGCCAGGGAAGC
	1863	CGGCTACCCAGGCAGATAAGCTGA	TCAGCTTATCTGCCTGGGTAGCCG
	1864	GGTTGGACCCGACAGGGAATTTCC	GGAAATTCCCTGTCGGGTCCAACC
25	1865	GGGGAATACCCGGCGTTTGTAATA	TATTACAAACGCCGGGTATTCCCC
	1866	TGGTTCGGTGAGGTTATGTTCCGT	ACCGAACATAACCTCACCGAACCA
	1867	TCGGTAGGGTTCAGTCGCTGAGGA	TCCTCAGCGACTGAACCCTACCGA
	1868	TTCGGAGTGTGCCGGTGCTAGTAC	GTA CTAGCACCGGCACACTCCGAA
	1869	TCGTA CTGGAATGATGGCCGGGCC	GGCCCGGCCATCATTCCAGTACGA
30	1870	TCCGTCGACCGTCCAGCGAAGTTT	AAACTTCGCTGGACGGTCGACGGA
	1871	AGGGAATATAACAACACCGCGCAC	GTGCGCGGTGTTGTTATATTCCCT
	1872	ATGTCCCGGAAACCAGCTACCTCA	TGAGGTAGCTGGTTTCCGGGACAT
	1873	ACCAGCGACTTAGATAGCCGTCCG	CGGACGGCTATCTAAGTCGCTGGT
	1874	GGAAAACCTCCTTTGCGTCAACCA	TGGTTGACGCAAAGGAGGTTTTCC
35	1875	ACGTGCGTG CATACCCAAGAGGAC	GTCCTCTTGGGTATGCACGCACGT
	1876	ACGCCACTTTCCCTAGAACCAACG	CGTTGGTTCTAGGGAAAGTGGCGT
	1877	CGAAGTACGCAATAGTGCCACCCCT	AGGGTGGCACTATTGCGTACTTCG
	1878	GATCCCGGCGGATCACCTATCAAT	ATTGATAGGTGATCCGCCGGGATC
	1879	AGAAAGCGACCGTTTCAGGCTAGC	GCTAGCCTGAAACGGTCGCTTTCT
40	1880	CGCTCCCTTTCATAGTCTCTCCG	CGGAGAGGACTATGAAAGGGAGCG
	1881	GTGGGTGGTCATAACGACAGCAGA	TCTGCTGTCGTTATGACCACCCAC
	1882	CTGGAGGCTGCATCGTTCGTAACA	TGTTACGAACGATGCAGCCTCCAG

1883	CACCATGAGTTTCGGAGCGAGGAT	ATCCTCGCTCCGAAACTCATGGTG
1884	CAAGCTGCGTTCGATGAGAGATTG	CAATCTCTCATCGAACGCAGCTTG
1885	CCTGGGAGCAATGACCGCTCTGGT	ACCAGAGCGGTCAATTGCTCCCAGG
1886	TCCGGCGCTCTACCAAGATGAGAC	GTCTCATCTTGGTAGAGCGCCGGA
1887	CGACCGCGTCGCGTATACTATCCG	CGGATAGTATACGCGACGCGGTCTG
1888	AACATTGCTAGTGGGGTCCAACA	TGTTGGACCCCACTAGCGAATGTT
1889	TGTATGATCATCCGACCGAGCAGC	GCTGCTCGGTCCGATGATCATACA
1890	AGTGCGCCGAGAGGGTGAATAGAC	GTCTATTCACCCTCTCGGCGCACT
1891	AGGCTTGTTCTGGACCAGCACCAT	ATGGTGCTGGTCCAGAACAAGCCT
1892	GGGGCCACATAAAGAATTCCGAAC	GTTCCGAATTCTTTATGTGGCCCC
1893	TGGTGAAGATAAATCCGCATGGCA	TGCCATGCGGATTTATCTTCACCA
1894	ATTTCCACCACGCTCTTGCCAAAT	ATTTGGCAAGAGCGTGGTGAAAT
1895	CGCGTAAAGCTGTCACCGATGACC	GGTCATCGGTGACAGCTTTACGCG
1896	TCCCCAACCGGTAACAACAGCGAC	GTCGCTGTTGTTACCGGTTGGGGA
1897	CCTCTGCTCGCCTTACACCCATGG	CCATGGGTGTAAGGCGAGCAGAGG
1898	CAAGCTGCTCCTGTGCTGAAGGGC	GCCCTTCAGCACAGGAGCAGCTTG
1899	AAACGAACGATGGTCGGTAGACCG	CGGTCTACCGACCATCGTTCGTTT
1900	TCAGTTCGATGGCTATTGCGCCTC	GAGGCGCAATAGCCATCGAACTGA
1901	GGCTCTCAACGACGCAAATCATA	TATGATTTGCGTCCGTTGAGAGCC
1902	AGTAGAGTGTTGCGGCTGCCGATC	GATCGGCAGCCGCAACACTCTACT
1903	AGACACTAGACCGCCGTGACCTGA	TCAGGTCACGGCGGTCTAGTGTCT
1904	ACCGAGCACCGAATTTCTTGTC	GGACAAGGAAATTCGGTGCTCGGT
1905	CCGTGGCCAAGATACGAACGAATT	AATTCGTTCTGATCTTGGCCACGG
1906	CCTCCTACAGCATCCACATGAGGG	CCCTCATGTGGATGCTGTAGGAGG
1907	CACTCGGCAAATACGTATGCGCAT	ATGCGCATACGTATTTGCCGAGTG
1908	ACCGAGTTGAAGCACGAATTTGGG	CCCAAATTCGTGCTTCAACTCGGT
1909	GACCACCTCGGAAGATCGTTCTGC	GCAGAACGATCTTCCGAGGTGGTC
1910	TCAACTGGGCAAACGAAGAGCACA	TGTGCTCTTCGTTTGCCAGTTGA
1911	GCTTAGCCTCACACGTGCATACCA	TGGTATGCACGTGTGAGGCTAAGC
1912	CTGCGGTCTCCAAGTACCATTTCG	CGAAATGGTACTTGGAGACCGCAG
1913	GTTCCGTATTACGGCGGCCATAAG	CTTATGGCCGCCGTAATACGGAAC
1914	ATCGACGCAACCGGATAGTCTCTG	CAGAGACTATCCGTTGCGTCGAT
1915	CGCAGATAAACCGGCATCTTTCAG	CTGAAAGATGCCGTTTATCTGCG
1916	ACCTGCCAATACGGGTCTACGGTT	AACCGTAGACCCGTATTGGCAGGT
1917	ACACCTGTTGCCATGCTGATCCGT	ACGGATCAGCATGGCAACAGGTGT
1918	AAACTGTCTACTGCGCAATTCCGC	GCGGAATTGCGCAGTAGACAGTTT
1919	GCAACTAGCCCGTGCTAGGATCGT	ACGATCCTAGCACGGGCTAGTTGC
1920	TCGTAGTGGTGGATTGTTGTGCGT	ACGCACAACAATCCACCACTACGA
1921	GGCTTACTCCTCAATTGCGACACG	CGTGTGCAATTGAGGAGTAAGCC
1922	CACGACTCCCTGCCAGATTTGATT	AATCAAATCTGGCAGGGAGTCGTG
1923	CTTAGACGTCGGCAATGTCACGTC	GACGTGACATTGCCGACGTCTAAG

1924	CTCAGAGCACAATCTGCCCTGCCCT	AGGCAGGGCAGATTGTGCTCTGAG
1925	GCTAGGAAAGTCGGCATTTCATGGG	CCCATGAATGCCGACTTTCCTAGC
1926	AAAGCCCCAAAATTCCGCCTAACC	GGTTAGGCGGAATTTTGGGGCTTT
1927	GCGCAACGCTAAGGGACTATCAAG	CTTGATAGTCCCTTAGCGTTGCGC
1928	CGTCCGCTGGGATGAGTCTCCTGC	GCAGGAGACTCATCCAGCGGACG
1929	ACAGGCCTCGTGATTGGTGTGGGT	ACCCACACCAATCACGAGGCCTGT
1930	CATTCTCCTTCCGGGACCACGCCT	AGGCGTGGTCCCGGAAGGAGAATG
1931	TCGGAGTTGACCAAGCTCAGTGCG	CGCACTGAGCTTGGTCAACTCCGA
1932	ACGCGCCACTGCAATTGCAAACAC	GTGTTTGCAATTGCAGTGGCGCGT
1933	AGTTCATGGAGCCGGCGTATTGTT	AACAATACGCCGGCTCCATGAACT
1934	ACGTTTAATGCGGGGCCCGCCTAC	GTAGGCGGGCCCCGCATTAAACGT
1935	TGAGGCTTTAGCCTACGCGCAGGT	ACCTGCGCGTAGGCTAAAGCCTCA
1936	CAGCGTTATGAGCGCGGAGTTTAT	ATAAACTCCGCGCTCATAACGCTG
1937	GTCCACGTGACCACGGATAGTTGG	CCAACATATCCGTGGTCACGTGGAC
1938	GATTATGCTCCTACGCCTGCTCCG	CGGAGCAGGCGTAGGAGCATAATC
1939	TCGTCAAGGGCATGATGTGTGGGA	TCCCACACATCATGCCCTTGACGA
1940	GATGGACCGCCAAAGACACCTTGA	TCAAGGTGTCTTTGGCGGTCCATC
1941	TACACGAGGATGGGGTCAAGCTTT	AAAGCTTGACCCCATCCTCGTGTA
1942	ACACGCACAAAACGTTTGAAAGGC	GCCTTTCAAACGTTTTGTGCGTGT
1943	GTTATCGTGGGCCGATGGTACTGA	TCAGTACCATCGGCCCACGATAAC
1944	ACATGACCGTATCCGCCTGCTTCG	CGAAGCAGGCGGATACGGTCATGT
1945	GAAGGCGAACCCTGAACTACGC	GCGTAGTTTCAGTGGTTCGCCTTC
1946	TGACTTTTGCAACGGGTGGAACCA	TGGTTCCACCCGTTGCAAAAGTCA
1947	TGAATTCGTAGGTTTTGGGTGCGG	CCGCACCCAAAACCTACGAATTCA
1948	AGCATTTATGAAGCGGCCATTGCG	CGCAATGGCCGCTTCATAAATGCT
1949	TGCTCCTCGCGTTGGTACCGTGAG	CTCACGGTACCAACGCGAGGAGCA
1950	CGCAGCAAGAAACAGCAACTGTTG	CAACAGTTGCTGTTTCTTGCTGCG
1951	AGACGCTTGAGTGAAAACCTCGGA	TCCGAGTTTTCACTCCAAGCGTCT
1952	CATTCGTAGAATGCCCCAATGGA	TCCATTTGGGGCATTCTACGAATG
1953	CCAGAAGGTTCTGGGACCCGTCGTG	CACGACGGGTCCCGAACCTTCTGG
1954	GAGAAGCCGTTCTCAGAGCACAT	ATGTGCTCTGAGAACC GGCTTCTC
1955	TTGCGTTGCAAGATATCTGGCCCG	CGGGCCAGATATCTTGCAACGCAA
1956	GGGTTGCATGTTCAAGCAAGACGA	TCGTCTTGCTGAACATGCAACCC
1957	CTCACGAAGGTGACATATCACGCC	GGCGTGATATGTCACCTTCGTGAG
1958	GCCCCAGATACGGGTTCAAAAAGA	TCTTTTGAACCCGTATCTCGGGC
1959	CATCTTCGCGCTTCTTCACTCCGC	GCGGAGTGAAGAAGCGCGAAGATG
1960	TTACACGGTAAGCGTACGGCCGCC	GGCGGCCGTACGCTTACCGTGTA
1961	ACCTTCGGACAATGTGGCGTTCGC	GCGAACGCCACATTGTCCGAAGGT
1962	TGAATGGTTCTGCTAGGCCACAC	GTGTGGGCTTAGCAGAACCATTCA
1963	CACGCCTGTCTGACATATGGATGC	GCATCCATATGTCAGACAGGCGTG
1964	CGCCTCAACCCAATCTGAGAACGT	ACGTTCTCAGATTGGGTTGAGGCG

	1965	TTACGCTTACTGCGAGCTGGGTCC	GGACCCAGCTCGCAGTAAGCGTAA
	1966	GGCTTGTGGGGCAATACGCATCTT	AAGATGCGTATTGCCCCACAAGCC
	1967	CACTCTCCTTTGGATGCGGAACAA	TTGTTCCGCATCCAAAGGAGAGTG
	1968	GACCAGCCATCACGTAACGGCCCT	AGGGCCGTTACGTGATGGCTGGTC
5	1969	AGGAACCGGATGTGGTTATGGAGC	GCTCCATAACCACATCCGGTTCCT
	1970	ATCCATGGGCAACTGAGCCTATGC	GCATAGGCTCAGTTGCCCATGGAT
	1971	GGAACAGCACTTGTTACCGCCAC	GTGGGCGGTAACAAGTGCTGTTCC
	1972	TGGCTCGCTTCAAGCCTGTTTGCT	AGCAAACAGGCTTGAAGCGAGCCA
	1973	CAAACGTGAGGTCATGACCACCAT	ATGGTGGTCATGACCTCACGTTTG
10	1974	ACCGATGTCTTGAAGTCCGGAGGT	ACCTCCGGACTTCAAGACATCGGT
	1975	CGAAAATGCATGATGATCTCCCCT	AGGGGAGATCATCATGCATTTTCG
	1976	TTTGGTATTCTCGCTGCACCGTTG	CAACGGTGCAGCGAGAATACCAAA
	1977	GCGTACTCAACCACATTCCCGACC	GGTCGGGAATGTGGTTGAGTACGC
	1978	AGCAAACAACAGCGGTCCGAGCAT	ATGCTCGGACCGCTGTTGTTTGCT
15	1979	GGACTAGGAGCGGGGATAGCTGAG	CTCAGCTATCCCCGCTCCTAGTCC
	1980	CCTTAACGAAAACCTGTGACCGC	GCGGTCGACAGGTTTTCGTTAAGG
	1981	CTCGATCGCATAAGCAAGAAACCG	CGGTTTCTTGCTTATGCGATCGAG
	1982	CCCGTTGTTTGGGCGACAAAAGT	ACTTTTGTGCCCCAAACAACGGG
	1983	CGGCGGCTCTCGCATGATCTCGTT	AACGAGATCATGCGAGAGCCGCCG
20	1984	CGGATGGAGAGGAGTCTACGTCCC	GGGACGTAGACTCCTCTCCATCCG
	1985	CAGAACAATATCGTGCGTCAACCG	CGGTTGACGCACGATATTGTTCTG
	1986	CCTTTGCGCGCTCCGAGTAAGGTA	TACCTTACTCGGAGCGCGCAAAGG
	1987	GGAAACGGCACCTATCTGTCGTGA	TCACGACAGATAGGTGCCGTTTCC
	1988	CGACCGACAAAACCAAATGCCGCC	GGCGGCATTTGGTTTTGTGCGTCCG
25	1989	CCAAGGGTGTGGGAGCTGAAGAGA	TCTCTTCAGCTCCCACACCCTTGG
	1990	TTAAGTGCGCATAGTCCTCGTGGG	CCCACGAGGACTATGCGCACTTAA
	1991	GCCTGGTGGGGTAAGTCATGATGC	GCATCATGACTTACCCACCAGGC
	1992	GAGCAGCAGATTGATGCGCTTATG	CATAAGCGCATCAATCTGCTGCTC
	1993	TGCGCCAACCTCCGGAATATTTGC	GCAAATATTCCGGAAGTTGGCGCA
30	1994	AACCCCATCATGAAATGCTCTCCG	CGGAGAGCATTTTCATGATGGGGTT
	1995	GTCCAACGGTACTGGCGTGATGTT	AACATCACGCCAGTACCGTTGGAC
	1996	ACTCGGCTGATCGTGAGATGGTGA	TCACCATCTCACGATCAGCCGAGT
	1997	ATTCGTGGGCGCATCTCGGAATGT	ACATTCCGAGATGCGCCACGAAT
	1998	TCCCGTCCTGTAATCCAGGGAACA	TGTTCCCTGGATTACAGGACGGGA
35	1999	CTTCGCTGCACCTACATTGCGCCA	TGGCGCAATGTAGGTGCAGCGAAG
	2000	GCGTGTAGATGACTGTGCTTTGGG	CCCAAAGCACAGTCATCTACACGC
	2001	CTATGGTATCGAGACATCGGCGGA	TCCGCCGATGTCTCGATACCATAG
	2002	CCTCGTACTCCGTCGTATGCACAA	TTGTGCATACGACGGAGTACGAGG
	2003	TGGTGCGTCCGTAGTGCCCTGCACT	AGTGCAGGCACTACGGACGCACCA
40	2004	CGCGATCCTAGTTGAAAGCTTTGC	GCAAAGCTTTCAACTAGGATCGCG
	2005	ACGATCCAGGTGTTGGGCACTAAG	CTTAGTGCCCAACACCTGGATCGT



	2006	CCAATCTAGGATACACCACGCCCG	CGGGCGTGGTGTATCCTAGATTGG
	2007	GATACGTGGGGTATAGGCGGGCCC	GGGCCCCGCTATACCCACGTATC
	2008	CATGGAACAAACCGTCGTAGGGGA	TCCCCTACGACGGTTTGTTCATG
	2009	AACTCGCGCAGTATTCGAGTCGT	ACGACTCGAATACTGCGCGAGTGT
5	2010	CTCAGTCTCGAAGGTGATCCGACC	GGTCGGATCACCTTCGAGACTGAG
	2011	TCCCAATCCCCGTGGTATCGTCGT	ACGACGATACCACGGGGATTGGGA
	2012	AATCAACGTAGTTCCGGTGGTCCG	CGGACCACCGGAACACTACGTTGATT
	2013	CTTAACAACCCAGGGGTTTGGGCT	AGCCCAAACCCCTGGGTTGTTAAG
	2014	CTACCGCTGCATGGCGTTAGATTG	CAATCTAACGCCATGCAGCGGTAG
10	2015	TTATTGGTGGCGGACGGAGTGAGT	ACTCACTCCGTCCGCCACCAATAA
	2016	TTAAGGGTGAACCTAACCGCGTGA	TCACGCGGTTGAGTTCACCCTTAA
	2017	TTTGATTGAAACGCTGCGCACTAC	GTAGTGCGCAGCGTTTCAATCAA
	2018	TCATGTGTAGGTCGCGGCCGTCAC	GTGACGGCCGCGACCTACACATGA
	2019	CTCCGAACCTTCTGGGCCTCTTTT	AAAAGAGGCCCCAGAAGGTTCCGGAG
15	2020	CTGTTGCCCATTTGGCCCCGACACTC	GAGTGTGCGGGCCAATGGGCAACAG
	2021	CACGATCGCTGAGCAACACATCAC	GTGATGTGTTGCTCAGCGATCGTG
	2022	CGGATCATAAGCGTCCGCCTTCGT	ACGAAGCGGACGCTTATGATCCG
	2023	AGGTTAACGCAACATGTGATCCGC	GCGGATCACATGTTGCGTTAACCT
	2024	GGGAAAAACAGCTAAGCCTTGCGA	TCGCAAGGCTTAGCTGTTTTTCCC
20	2025	ACTTATTGCCGGGATCCGTACACA	TGTGTACGGATCCCGGCAATAAGT
	2026	TGCGGTCTGGAAAGGAAGGGAGGG	CCCTCCCTTCCTTTCCAGACCGCA
	2027	GCTGCCACCTGGACATCGCATACA	TGTATGCGATGTCCAGGTGGCAGC
	2028	GCAGGCATGACAGTGGCGTAGTAC	GTAATAAGCACTGTCATGCCTGC
	2029	GCGGCCCTGATGGTTTGGCTGAGC	GCTCAGCCAAACCATCAGGGCCGC
25	2030	TCCCCATTTAGTCCCTCCATCAC	GTGATGGAGGGGACTAAATGGGGA
	2031	GCAACACAAATGCGAGCGTAGGAG	CTCCTACGCTCGCATTTGTGTTGC
	2032	GGCGTTTGTATTCGAGCCACGTAG	CTACGTGGCTCGAATACAAACGCC
	2033	GGTAACGTCGCACGTGGAATTCCG	CGGAATTCCACGTGCGACGTTACC
	2034	ACTTCACAACGCTCCGTTGGACAC	GTGTCCAACGGAGCGTTGTGAAGT
30	2035	CCGAATTATAAAGCGCAAGGCACA	TGTGCCTTGCGCTTTATAAATTCGG
	2036	GGACCCGATAAGACTCTGACGCCG	CGGCGTCAGAGTCTTATCGGGTCC
	2037	ACCCGTTTCTCGTAGGAACCTGCT	AGCAGGTTCTACGAGAAACGGGT
	2038	CACGTTGACTGTATCTGGTTGCC	GGCAACCAGATACAGTCGAACGTG
	2039	CCTCGGATGGGCCCATGACCTTGA	TCAAGGTCATGGGCCCATCCGAGG
35	2040	GGACGCCTGCTGTAGGGGTTTGAT	ATCAAACCCCTACAGCAGGCGTCC
	2041	CTCGAGCGTGGGCTAAAAGAGCAT	ATGCTCTTTTAGCCACGCTCGAG
	2042	TTTACTTCTTAGGGCGGTTTGGG	CCCAAACGCGCCCTAAGAAGTAAA
	2043	ACCACCAACATAGCGCGCACTAGT	ACTAGTGCGCGCTATGTTGGTGGT
	2044	TGGTTACACGGCAGCCCGCGTAAG	CTTACGCGGGCTGCCGTGTAACCA
40	2045	TTATGGTACGTTGCTGCGTGCGGG	CCCGCACGCAGCAACGTACCATAA
	2046	ACCGCGGATCTAACGAATCCCATT	AATGGGATTGTTAGATCCGCGGT

2047	CATGATCCCGCCCTTAGGTTAAGC	GCTTAACCTAAGGGCGGGATCATG
2048	TACCGCTTCAAAGGGTTGCCGAAT	ATTCGGCAACCCTTTGAAGCGGTA
2049	GCACCGCGTCAATATTACCGAGGA	TCCTCGGTAATATTGACGCGGTGC
2050	GTGTCGCGGCTTTACAGAAGGAGA	TCTCCTTCTGTAAAGCCGCGACAC
2051	GCAAGCCATACCGCAATAAACTCG	CGAGTTTATTGCGGTATGGCTTGC
2052	ATGAGGTCGTGCTGCGTTACGAG	CTCGTGAACGCAGCACGACCTCAT
2053	CGAGACTAGTGCCGATGCAGGGTA	TACCCTGCATCGGCACTAGTCTCG
2054	GCCTCATCATAGACGCTGGATGCA	TGCATCCAGCGTCTATGATGAGGC
2055	GACAGGCGTCGGTAAGCTCTCAAG	CTTGAGAGCTTACCGACGCCTGTC
2056	GCTACGAATCTTCCCTGTGCCAC	GTGGCGACAGGGAAGATTTCGTAGC
2057	TTTGGCAGAACGTACCAGTGGGGT	ACCCCACTGGTACGTTCTGCCAAA
2058	GGACAATAAGCACCGGAGAATGCG	CGCATTCTCCGGTGCTTATTGTCC
2059	TCATGAACCTTCTGATGCCGCGAA	TTCGCGGCATCAGAAGGTTTCATGA
2060	CGCCGCATTACCTTAAAAACGTGC	GCACGTTTTTAAGGTAATGCGGCG
2061	ACGAGTCCAACCGCCTCATTGATT	AATCAATGAGGCGGTTGGACTCGT
2062	GCGAAGAGTTGCTACTCTTCCGCC	GGCGGAAGAGTAGCAACTCTTCGC
2063	CGTCGGCAACAATCTTTTTCGTGA	TCACGAAAAAGATTGTTGCCGACG
2064	AATCCTGTGCACCCGTGAGACGCG	CGCGTCTACGGGTGCACAGGATT
2065	AACCTATATGCATCAACGCGAGCC	GGCTCGCGTTGATGCATATAGGTT
2066	GAAC TTGGCAAAACAGCCCGGAAA	TTTCCGGGCTGTTTGGCAAAGTTC
2067	CTCTATGGCCGTTTGCCGTCTGCA	TGCAGACGGCAAACGGCCATAGAG
2068	AGTGCACCGGGTTGTGGACACAAT	ATTGTGTCCACAACCCGGTGCACT
2069	CCTGGCTTTTCACACGCCAAGAAA	TTTCTTGGCGTGTGAAAAGCCAGG
2070	CACTCAGCGTAGCCTGAAGCCTGG	CCAGGCTTCAGGCTACGCTGAGTG
2071	GAATTATCGACCGCAGCGGTGTCG	CGACACCGCTGCGGTGATAATTC
2072	GTGACATCACATGGTGGCCGAGCG	CGCTCGGCCACCATGTGATGTCAC
2073	AGCACCTTGCCGAGTCACCAGTGA	TCACTGGTGACTCGGCAAGGTGCT
2074	TAGGTTGCAGGAATGGTGGGCACC	GGTGCCCAACCTTCCTGCAACCTA
2075	GTCCCATACGTGTGGTACGCGGAT	ATCCGCGTACCACACGTATGGGAC
2076	TCGGATACTCTCGCGTGCCACGGG	CCCGTGGCACGCGAGAGTATCCGA
2077	CAACGTTCCGCCCTAAGCCCAAAT	ATTTGGGCTTAGGGGCGAACGTTG
2078	GTTAGGTCACCGCGGCATATCCTA	TAGGATATGCCGCGGTGACCTAAC
2079	GTTACCGGCCTCTACTTGGGTTT	AAACCCAAGTAGAGGCCGGTGAAC
2080	AATCCGCGTCTAGGTCATGTGGTC	GACCACATGACCTAGACGCGGATT
2081	GCTACGCTCTGGAGGTGGTACCC	GGGTACCACCTCCAGAGGCGTAGC
2082	CAGGGAATGCTACAAAGGTTCCAA	TTGGACCCTTTGTAGCATTCCCTG
2083	AAGGGTTAGCTGCCCGGTTAACAG	CTGTTAACCAGGGCAGCTAACCTT
2084	CCTCGCAAGCGCGATATTTATGCC	GGCATAAATATCGCGCTTGCGAGG
2085	GCCTCCCGGTCATGGTCAAGGGAA	TTCCCTTGACCATGAACGGGAGGC
2086	GCTGTTGAGCGGCGACCTGTGCAC	GTGCACAGGTCGCCGCTCAACAGC
2087	CGCTGACTTAGCTCTGATGTGCCG	CGGCACATCAGAGCTAAGTCAGCG

2088	TTCATGGCATTTCATCACGAAGGAA	TTCCTTCGTGATGAATGCCATGAA
2089	TAGTGTTATGCCCGCGTGTGAATG	CATTACACGCGGGCATAACACTA
2090	CATGTAAGGGCACGGTCGTGGGCA	TGCCACGACCGTGCCCTTACATG
2091	CAGGAAGCTCGCTCCGTGATGCAC	GTGCATCACGGAGCGAGCTTCCTG
2092	CCTGCTGATAGCAACCTCACTGCA	TGCAGTGAGGTTGCTATCAGCAGG
2093	ACTACGAGGGGCAGGGTCTAGGCG	CGCCTAGACCCTGCCCTCGTAGT
2094	CATAATGTGGGTGCTGACGCCGAT	ATCGGCGTCAGCACCCACATTATG
2095	TAGCGAATCCACACAGAGCCGCTC	GAGCGGCTCTGTGTGGATTGCGTA
2096	TCGCGAAATCCCTAAATCCTGTGC	GCACAGGATTTAGGGATTTGCGCA
2097	TGGCACGAATCAAGCCACCAACTC	GAGTTGGTGGCTTGATTGCTGCCA
2098	GCGGACCGTCTTTGCTATCTGACG	CGTCAGATAGCAAAGACGGTCCGC
2099	AGGCCCCGCCTTGTAATTGGTCAT	ATGACCAATTACAAGGCGGGGCCT
2100	CTGGTCCCATACGCCGCTGACTAG	CTAGTCAGCGGCGTATGGGACCAG
2101	TGCTAACTGCGGCCCTACAGAGTC	GACTCTGTAGGGCCGAGTTAGCA
2102	TGGTTTTATGTTGCGGTAGCGTCCG	CGGACGCTACCGAACATAAAACCA
2103	AGCTCAAACCTTCTCCACGGGATG	CATCCCGTGGGAGAAGTTTGAGCT
2104	CGCGAAGATAGTGAAATCCGCATC	GATGCGGATTTCACTATCTTCGCG
2105	GAGTGAAACCTCTCGCGGGTTGCA	TGCAACCCGCGAGAGGTTTCACTC
2106	TCGAATGCTCTGCAGTGACGTCAA	TTGACGTCACTGCAGAGCATTGCA
2107	AGGTGGCAATGATCGACGACCCTG	CAGGGTCGTCGATCATTGCCACCT
2108	GTCCGAGCCGTGCAAAGCAATAA	TTATTGCTTTGCACGGCTCCGGAC
2109	CTTTTGGGGATTAGAGGCCGACAA	TTGTCGGCCTCTAATCCCCAAAAG
2110	GGCATAAAGGCTTCCGTTCTGTGC	GACAGGAACGGAAGCCTTTATGCC
2111	GCGGACCGTAAAGCGGGCAGATAG	CTATCTGCCCGCTTTACGGTCCGC
2112	TTTCAAGAGTGCATCGAATCCACG	CGTGGATTGATGCACTCTTGAAA
2113	CCGGCATCCCTTCTCGCTGTTGCC	GGCAACAGCGAGAAGGGATGCCGG
2114	ACACAGAGACGCGAACGGAGTGCA	TGCACTCCGTTGCGCTCTCTGTGT
2115	AGCGGCATTCTCCCACTCGTTACT	AGTAACGAGTGGGAGAATGCCGCT
2116	GGAGCGTACTGCGCCTCGCAAGTC	GACTTGCGAGGCGCAGTACGCTCC
2117	AAACCCGAATGACACGGCAGATAA	TTATCTGCCGTGTCATTGCGGTTT
2118	AACCAGCGGATCGATAAACGACA	TGTCGTTTTATCGATCCGCTGGTT
2119	GGTGTCCACCCGTTAACGCCGGTA	TACCGGCGTTAACGGGTGGACACC
2120	AGCGCGACGTGGCTTGCCGTTAAA	TTTAACGGCAAGCCACGTCGCGCT
2121	TCCCACGGCTATAGGTCCAACGAC	GTCGTTGGACCTATAGCCGTGGGA
2122	ATCAACGAACGATGCCGTTAGGTG	CACCTAACGGCATCGTTCGTTGAT
2123	GAGGCTAAGCCGTATGGCCGAGGC	GCCTCGGCCATACGGCTTAGCCTC
2124	ACGGTCCGAAATGGTTAGAGGCAC	GTGCCTCTAACCATTTGCGACCGT
2125	ACGCAAACCATTCCTCGAGTAGGC	GCCTACTCGAGGAATGGTTTGCCT
2126	TTACACGCTCGCTATTGGGCCATA	TATGGCCCAATAGCGAGCGTGTA
2127	CTCGGCACGGGTTTAGAACGCCGG	CCGGCGTTCTAAACCCGTGCCGAG
2128	ATTGCGTAAGGTATCGGGCTAGCG	CGCTAGCCCGATACCTTACCGAAT

	2129	AGCACACCGTTATACATGACGGCG	CGCCGTCATGTATAACGGTGTGCT
	2130	AGTCCCTGCCGTTGCTCATGGAA	TTCCATGAGCGAACGGCAGGGACT
	2131	GGGCTTATGACCAGTCAGGTTGGA	TCCAACCTGACTGGTCATAAGCCC
5	2132	GGTCACCACACGAGTGCCTGGTCT	AGACCAGGCACTCGTGTGGTGACC
	2133	TTGATCGTGTCTCCCGAAACCCTC	GAGGGTTTCGGGAGACACGATCAA
	2134	ATTGTGCGGATCGGCATTTCTTAA	TTAAGAAATGCCGATCGCGACAAT
	2135	GGGTCCAACGACTTCTCGCTGCTG	CAGCAGCGAGAAGTCGTTGGACCC
	2136	CAAATTCCTTGGGGGCCATAGTGG	CCACTATGGCCCCAAGGAATTTG
10	2137	CCAGAGTATCCGCCGTTAGACGGT	ACCGTCTAACGGCGGATACTCTGG
	2138	TCCTGCAGATCATCTCGTGTCTGG	CCAGACACGAGATGATCTGCAGGA
	2139	TGCGGGAGATTTGAACAAGCTGTA	TACAGCTTGTTCAAATCTCCCGCA
	2140	TTAGACGCCGAGCTAGGCAACGTC	GACGTTGCCTAGCTCGGCGTCTAA
	2141	TTTCGGCAGAATCTCCGATTCAAC	GTTGAATCGGAGATTCTGCCGAAA
	2142	TGGCGAGCAGACCTACAAGACAGA	TCTGTCTTGTAGGTCTGCTCGCCA
15	2143	GGCGACAGACCGGTACATCGGCCA	TGGCCGATGTACCGGTCTGTGCGCC
	2144	TCTAGACCTGCGTTTCGTGGGACC	GGTCCACGAAACGCAGGTCTAGA
	2145	GCCGAGCGTGGTACCATACGTTCA	TGAACGTATGGTACCACGCTCGGC
	2146	TAATCACACCCGCTTTCTGTGGCT	AGCCACAGAAAGCGGGTGTGATTA
	2147	GGCCGGAGCCATTGGACACTTCTT	AAGAAGTGTCCAATGGCTCCGGCC
20	2148	CCTGTAGACCTGCATGGATCGCTG	CAGCGATCCATGCAGGTCTACAGG
	2149	ATCGCCGTTCCCGCAAAATAAGCA	TGCTTATTTTGCGGGAACGGCGAT
	2150	TGGATCAACGGGGTAGTGAAAACG	CGTTTTCACTACCCCGTTGATCCA
	2151	AAGCGACGATGCTTTCTTGAGCTG	CAGCTCAAGAAAGCATCGTCGCTT
	2152	CACGGGCACGTGTTCTACGCTTGC	GCAAGCGTAGAACACGTGCCCGTG
25	2153	ACGGGCTGGGACAAGAGCTAGAAA	TTTCTAGCTCTTGTCAGCCCGT
	2154	GGTAACTGGCTCCGCTCTCACATC	GATGTGAGAGCGGAGCCAGTTACC
	2155	ACTCTGGCTGTTGGCGAACGTGAC	GTCACGTTCCGCAACAGCCAGAGT
	2156	GACCGAGGACCAGTCCTTGCTCTC	GAGAGCAAGGACTGGTCCTCGGTC
	2157	AGTAGCTCTTGCGGCCTAACGGCA	TGCCGTTAGGCCGCAAGAGCTACT
30	2158	TTCTTGTCCTGGGGGAGAGCAGTG	CACTGCTCTCCCCAGGACAAGAA
	2159	TTAGCAGGGAGGTTGTGCGCTCAT	ATGAGCCGACAACCTCCCTGCTAA
	2160	AGAACGTGGATTGTACGCTCCGCC	GGCGGAGCGTACAATCCACGTTCT
	2161	CTTCACAGCCTGGAGCCACCAATG	CATTGGTGGCTCCAGGCTGTGAAG
	2162	GAGATCGATGAAACGCACCAGCGG	CCGCTGGTGCCTTTCATCGATCTC
35	2163	GGGTCCAGAGTTGGTGTGGGATAA	TTATCCACACCAACTCTGGACCC
	2164	CCGTCCACCCCAGATAGGAATCAC	GTGATTCTATCTGGGGTGGACGG
	2165	TGCCTCGCTTCTGTGAATCTACGA	TCGTAGATTACAGAAGCGAGGCA
	2166	GATCACAGCGTCCGCGCATAACGG	CCGTTATGCGCGGACGCTGTGATC
	2167	ATGACGCCTTACATGACGCACCTT	AAGGTGCGTCATGTAAGGCGTCAT
40	2168	GCGTGGAATAACGCCCTTAGTTCA	TGAACTAAGGGCGTTATTCCACGC
	2169	GGTCTACCATTCTCGCCCCGACCG	CGGTGCGGCGAGAAATGGTAGACC

5	2170	ACACCTCTCTGGCGTAGACGCTCA	TGAGCGTCTACGCCAGAGAGGTGT
	2171	GTAGAGGTGCTCAGGACTCGTCGC	GCGACGAGTCGTGAGCACCTCTAC
	2172	GTAAGCAGGAGGCGAAGGCGCGAA	TTCGCGCCTTCGCTCCTGCTTAC
	2173	TCTAAGGGCCGTTTCAATCGACCT	AGGTCGATTGAAACGGCCCTTAGA
	2174	AACCTGATTTCAGGGTCAGCCCGA	TCGGGCTGACCCTGAAATCAGGTT
	2175	GTCACGCGATTGGCCACCTATTA	TAATAGGTGGGCCAATCGCGTGAC
	2176	ACGATGCCGCGCATGTAACCTAGT	ACTAGGTTACATGCGCGGCATCGT
	2177	TGAGAGATGTCTCGTCAACGCCTG	CAGGCGTTGACGAGACATCTCTCA
10	2178	GCATATCTCGCGGTGACAGACGAA	TTCGTCTGTCACCGCGAGATATGC
	2179	GACCCAACGTCGAAATTGTGCGAT	ATCGCACAATTTGACGTTGGGTC
	2180	TGAAAATCGGGGCATCTAGTTTGG	CCAAACTAGATGCCCCGATTTTCA
	2181	CCGCGAAAAGGATTTGTGTACGCA	TGCGTACACAAATCCTTTTCGCGG
	2182	CATTCCATTTATCCGCAGTTCGCT	AGCGAACTGCGGATAAATGGAATG
	2183	CCTGTCTGTGAGGCCAGCGTCTAT	ATAGACGCTGGCTCGACAGACAGG
15	2184	TCAGCGCGGCTAAACAAGTTATGC	GCATAACTTGTTTAGCCGCGCTGA
	2185	ACGCCTACGAACGACCCAAGAGAG	CTCTCTTGGGTGTTTCGTAGGCGT
	2186	TGCGCATCTACCATTGTGTGGATC	GATCCACACAATGGTAGATGCGCA
	2187	AAGTCCGCGCTCGTCTCTGTAATA	TATTACAGGAGCGAGCGCGGACTT
	2188	GCTGGGTCATTGCTCGAGTAACCA	TGGTACTCGAGCAATGACCCAGC
20	2189	TGGAGCGTTCTGGCAATGACCGAC	GTCGGTCATTGCCAGAACGCTCCA
	2190	CAAGTCAATTCTTGGCCAATTCGG	CCGAATTGGCCAAGAATTGACTTG
	2191	CGTTCATGCAAGGATCCCAGGTTA	TAACCTGGGATCCTTGCATGAACG
	2192	ATGCCAATAGAAGCTGGGGATGCT	AGCATCCCCAGCTTCTATTGGCAT
	2193	CCTAACTCTCCCTTGAGGCCGTTT	GAACGGCCTCAAGGGAGAGTTAGG
25	2194	ATCTCGGCGAAGGTTCCAAACATT	AATGTTTGGAACCTTCGCCGAGAT
	2195	GCGACAGATTACGCTGCGGTTTTT	GAAAACCGCAGCGTAATCTGTGCG
	2196	AAGCCCAGACGGCCAACACGTTAC	GTAACGTGTTGGCCGTCTGGGCTT
	2197	TCAAGTTCAAATCACATCCCGTGG	CCACGGGATGTGATTTGAACCTGA
	2198	GATTGTCGTTCTGTCTGTGAGGCG	CGCCTCACAGACAGAACGACAATC
30	2199	ACCGAACTATGTTCCGGCATGGCA	TGCCATGCCGGAACATAGTTCGGT
	2200	CGTCATCGGGTGTGCAATGCCGTT	AACGGCATTGCACACCCGATGACG
	2201	CGGACGGAGTCACGTTTGTGCACT	AGTGCACAAACGTGACTCCGTCCG
	2202	TAAACAAGTCGTGTGCCTTTGCCG	CGGCAAAGGCACACGACTTGTTTA
	2203	TAATTACTGGCCTGTGGAGCAGGC	GCCTGCTCCACAGGCCAGTAATTA
35	2204	GGAGCGGCCCGAATGGTGCTCTTA	TAAGAGCACCATTGGGGCCGCTCC
	2205	ACTAAGCAAGGCTTGATGTGCGT	ACGCACATCCAAGCCTTGCTTAGT
	2206	GGCAGCTCAGCGGCAGTACGCTAC	GTAGCGTACTGCCGCTGAGCTGCC
	2207	GCGAGGCGAATTATCCGCGGATTT	AAATCCGCGGATAATTCGCCTCGC
	2208	CATACGACACACCTTGGGGTGCTA	TAGCACCCCAAGGTGTGTGCTATG
40	2209	TGCTTGGGCTTTAAACCCGTTTT	AAAACGGGGTTTAAAGCCCAAGCA
	2210	CCGGTTGAAAACGCAAATATCGG	CCGATATTTGCGTTTTCCAACCGG

	2211	AAACTAGCTAGCCGCACCCGCAAG	CTTGCGGGTGCGGCTAGCTAGTTT
	2212	GTTGTTCCACCAGTGATCACGCAG	CTGCGTGATCACTGGTGGAACAAC
	2213	GCCGCTGACAAGATGATCATCGTT	AACGATGATCATCTTGTCAGCGGC
5	2214	CTTTCATAAAGCCAACCGATGCCC	GGGCATCGGTTGGCTTTATGAAAG
	2215	CTGACTGCATCTCGAAAGCGGGTG	CACCCGCTTTCGAGATGCAGTCAG
	2216	ATTTCTTCGGAGAATCGGCCACGT	ACGTGGCCGATTCTCCGAAGAAAT
	2217	CATTTGCGGCCCTAGCTACTGCGC	GCGCAGTAGCTAGGGCCCGAAATG
	2218	CCGATCCCGCACATCCGTATCCTG	CAGGATACGGATGTGCGGGATCGG
10	2219	TATCACCGGGAGCGTCTTATCGTG	CACGATAAGACGCTCCCGGTGATA
	2220	TAGGGCTCGTGACCGATTAGAGG	CCTCTAATCGGTGCACGAGCCCTA
	2221	GCGTGGCACTCGCTTGTCTAGGTA	TACCTAGACAAGCGAGTGCCACGC
	2222	CTCAACGAACCTCAAGGGCCGCTAC	GTAGCGGCCCTTGAGTTCGTTGAG
	2223	AGCCTGGTATCGACCAATCCTGCA	TGCAGGATTGGTCGATACCAGGCT
	2224	TACGCGTTCTAGTTGGCCGGATCC	GGATCCGGCCAACTAGAACGCGTA
15	2225	TTTATGGGTTTGTGCCTGATGGGT	ACCCATCAGGCACAAACCCATAAA
	2226	GGGACCCCTAGCAACGTCACTTA	TAAGGTGACGTTGCTAGGGGTCCC
	2227	CTGCCTCCCCAGGAGTCATTGGAT	ATCCAATGACTCCTGGGGAGGCAG
	2228	AACCCCGCAAGACCAGTACCAATC	GATTGGTACTGGTCTTGCGGGGTT
	2229	GGTCACATACGCGCTAAAAAGCGC	GCGCTTTTTAGCGCGTATGTGACC
20	2230	AAATGGCTCCGACCAGTTAGGGAC	GTCCCTAACTGGTCGGAGCCATTT
	2231	AACGCGGCACGCTTAAAGGTGCAT	ATGCACCTTTAAGCGTGCCGCGTT
	2232	GATCGCACGCCGATTAACCTTACA	TGTAAGGTTAATCGGCGTGCGATC
	2233	CCTCCTGATTGGGAGTGCGGAATT	AATTCGCACTCCCAATCAGGAGG
25	2234	CGGAGGGTAATAGGCTCCTCTGCG	CGCAGAGGAGCCTATTACCCTCCG
	2235	ACAAGAAGTGGACATTACCGCGGG	CCCGCGGTAATGTCCAGTTCCTGT
	2236	TGTCGTCTTAAAGGCCCTTTGTGCG	CGCACAAAGGCCTTTAAGACGACA
	2237	GGTGACCATGTGGCGTTTTAGCTT	AAGCTAAAACGCCACATGGTCACC
	2238	CACGTTGCGCACGGTACCAGAAC	GTTCTGGTACCGTGCGCAACCGTG
	2239	CCTTTATTGTTTGGTCCCCTGCCC	GGGCAGGGGACCAACAATAAAGG
30	2240	GTGCGCCTGCATTCTACCGTCAAT	ATTGACGGTAGAATGCAGGCGCAC
	2241	GTTTACGTTGATGGCTTGCCGCCG	CGGCGGCAAGCCATCAACGTAAAC
	2242	CCGTGCGGTGGTAGGACGTGAATGT	ACATTCACGTCCTACCACCGACGG
	2243	TGATCGCCCCAGAATCCCTGTGCT	AGCACAGGGATTCTGGGGCGATCA
35	2244	AAGCAGCCAAAAATCGGTTGCTTT	AAAGCAACCGATTTTGGCTGCTT
	2245	CGACGGGACTTAGTAGCAGGGCCT	AGGCCCTGCTACTAAGTCCCGTCG
	2246	CCGATTCGCGAAACGACCAAGTAG	CTACTTGGTCGTTTCGCGAATCGG
	2247	CCACCCCAACTCCAATCTTCTCA	TGAGAAAGATTGGAGTTGGGGTGG
	2248	GTGCAGTAGACGACTACCGGCGTC	GACGCCGGTAGTCGTCTACTGCAC
	2249	TTCGCCCATCGTATCAAGCAATTC	GAATTGCTTGATACGATGGGCGAA
40	2250	GAATCGCGACTACCCGTGCGGTCA	TGACCCGACGGGTAGTCGCGATTTC
	2251	CCAGCACTCGCCATCGGTTATAAT	ATTATAACCGATGGCGAGTGCTGG

5	2252	CGAACCGTAGAACTCCGGTCGGTG	CACCGACCGGAGTTCTACGGTTCG
	2253	GCACCATGACAGAGCCCCAGGATG	CATCCTGGGGCTCTGTCATGGTGC
	2254	TGGGCTACCGCAGAATAAGGGTGA	TCACCCTTATTCTGCGGTAGCCCA
	2255	TGGCCTGTCGTGTCGAAGGAAACA	TGTTTCCTTCGACACGACAGGCCA
	2256	GCCTCACCGATAGCGAGCGTTTGC	GCAAACGCTCGCTATCGGTGAGGC
	2257	GTGCGCGCCGGCTAAAACGAGACA	TGTCTCGTTTTAGCCGGCGCGCAC
	2258	CCGCAGACGAGTTTCTTGTCAGAG	CTGTCACAAGAACTCGTCTGCGG
	2259	GTTTCGAATCGCGTGCTAGGAAGC	GCTTCCTAGCACGCGATTGCGAAC
10	2260	TGTTGTACACATGCATCCGGTGAA	TTCACCGGATGCATGTGTACAACA
	2261	CACTGAACACGATATAAGGGCGCG	CGCGCCCTTATATCGTGTTCAAGT
	2262	CGCGATGGTTCTTAGCAAGACGAT	ATCGTCTTGCTAAGAACCATCGCG
	2263	TACACCAAGGAAGAAATGGGGACG	CGTCCCCATTTCTTCCTTGGTGTA
	2264	CGTGCCCTGCGTTTTAGGTGCAGC	GCTGCACCTAAAACGCAAGGCACG
	2265	GTCGTTTGTCTGGGCATTAACGGC	GCCGTTAATGCCAGACAAACGAC
15	2266	CAGGCTCTCGTTCGGTACAAACGT	ACGTTTGTACCGAACGAGAGCCTG
	2267	CGGACACTGTTTCACCAGAACCCA	TGGGTTCTGGTGAAACAGTGTCCG
	2268	TACCCATGATGCGGAAGAAGCGTA	TACGCTTCTTCGCGATCATGGGTA
	2269	CTGTCCCTAAGCGGATGAGAACCG	CGGTTCTCATCCGCTTAAGGACAG
	2270	CGGGAGATGAGAACGGTTTTGTGC	GCACAAAACCGTTCTCATCTCCCG
20	2271	TAGATCGCGACTGTACTCAGGCCG	CGGCCTGAGTACAGTCGCGATCTA
	2272	TAAAACAGTTCGCGCGACTGTCGT	ACGACAGTCGCGCGAACTGTTTTA
	2273	CGAGGAGCTCCACATAAGCCCAAT	ATTGGGCTTATGTGGAGCTCCTCG
	2274	TGGCTAGGGATGGGGAATCATCTT	AAGATGATTCCCCATCCCTAGCCA
	2275	AGGATTGGGTGCCTGGATGCATTG	CAATGCATCCAGGCACCCAATCCT
25	2276	TGTATCTACCGGCCCTGAAGCAGGT	ACCTGCTTCAGGCCGGTAGATACA
	2277	TCCCTACGCGCATGACTCGCTTAC	GTAAGCGAGTCATGCGCGTAGGGA
	2278	TGGTCGATCACCTGTGACAGACGC	GCGTCTGTCACAGGTGATCGACCA
	2279	TGGGGGTAGTCCATGCATCAATTG	CAATTGATGCATGGACTACCCCA
	2280	CCCTGCCAGGATTACTATTCCGGA	TCCGGAATAGTAATCCTGGCAGGG
30	2281	TCCCGCACGGGGAATTTAAGTAGA	TCTACTTAAATCCCCGTGCGGGA
	2282	GTGATGTGCAGGAACTTCTGTGCG	GCGACAGAAAGTTCCTGCACATCAC
	2283	ATTAGGCATGCATGCGCTTCTCA	TGAGAAGCGCATGCATGCCTAAAT
	2284	TTCGGCGCTAGTGGACGCCGTCAA	TTGACGGCGTCCACTAGCGCCGAA
	2285	GAGCTTCATCTCATCAGTTCCGCG	CGCGGAACTGATGAGATGAAGCTC
35	2286	GACAACTCCACTGCTCCAATCGCA	TGCGATTGGAGCAGTGGAGTTGTC
	2287	GGCCAAGGATGGACCTTACGATGG	CCATCGTAAGGTCCATCCTTGCC
	2288	GGTTCCGGAATTTGTCACCGCTTC	GAAGCGGTGACAAATCCGGAACC
	2289	GCGCTGGATAGTCTGCGAGAAGCC	GGCTTCTCGCAGACTATCCAGCGC
	2290	TGAGTCCAGTGCTGCCACCATGAA	TTCATGGTGGCAGCACTGGACTCA
40	2291	TTGAATTGGGTGTGCGAGCGTTCT	AGAACGCTCCGACACCCAATTCAA
	2292	CGGCGGGCAGACAATGCTTTGAAC	GTTCAAAGCATTGTCTGCCCGCCG

5

0

5

10

25

30

35

40

2293	GGGTCTGTCAAAGAGGGTGTCTGG	CCAGACACCCTCTTTGACAGACCC
2294	CTTTGTGCAAGACGAAGCACCCCTT	AAGGGTGCTTCGTCTTGACAAAAG
2295	ATCGAATTCCGAGGAGGTCTCCAT	ATGGAGACCTCCTCGGAATTCGAT
2296	TCCGACCCTCAGAGTCGACTCATT	AATGAGTCGACTCTGAGGGTCGGA
2297	ATCAACGGCCACCTCCTCGCCGAG	CTCGGCGAGGAGGTGGCCGTTGAT
2298	AGCCACGGAATAATTCCGTCCACC	GGTGGACGGAATTATTCCGTGGCT
2299	GATCGCTTGCATATCGCAAAGACT	AGTCTTTGCGATACGCAAGCGATC
2300	TCCACGCCTTACCATCAACTGCAA	TTGCAGTTGATGGTAAGGCGTGGA
2301	GCCAAGCGATAGGCCAGAACTCAG	CTGAGTTCTGGCCTATCGCTTGGC
2302	AGCGTGTGGGTCAATTTAGCACGA	TCGTGCTAAAATGACCCACACGCT
2303	GTTATGCGCGGCTTACGAGTTCTGA	TCGAACTCGTAAGCCGCGCATAAC
2304	TCTGTCCACGTAACCTGCCTGCAG	CTGCAGGCAAGTTACGTGGACAGA
2305	TCGGCAGCCAATGATCATACCTCT	AGAGGTATGATCATTGGCTGCCGA
2306	TAAGCCCGATCCGGTCTGTGTTT	AAACACAGGACCGGATCGGGCTTA
2307	ACATGGCAGACTAACAGGCCTCGC	GCGAGGCCTGTAGTCTGCCATGT
2308	CATGGCTGCACTCTAAGTCGAACG	CGTTGCACTTAGAGTGCAGCCATG
2309	TCTTCAACCCACGCGGAACGATTG	CAATCGTTCCGCGTGGGTTGAAGA
2310	CTCGTGTCTCCAGAGGATTGTCCC	GGGACAATCCTCTGGAGACACGAG
2311	TGAAGGCATCAACCCAGAGGATTT	AAATCCTCTGGGTTGATGCCTTCA
2312	ACAGCTCGAAGGCAGCCACATTGG	CCAATGTGGCTGCCTTCGAGCTGT
2313	ACAACGAGTACCGCGACAGAAGGG	CCCTTCTGTGCGGGTACTCGTTGT
2314	ATAACCGAAAAACCAGCCTGCGAT	ATCGCAGGCTGGTTTTTCGGTTAT
2315	ACAACCTCAGCACTTTCGACGTCCA	TGGACGTCGAAAGTGCTGAGTTGT
2316	CGGGTTACTGGGTATCACCAATGC	GCATTGGTGATACCCAGTAACCCG
2317	CATCGGTTATCGCTGCACGCGCGT	ACGCGCGTGCAGCGATAACCGATG
2318	GAAGGAATCCCGGATAGTCCGTGG	CCACGGACTATCCGGGATTCCTTC
2319	GCATGGTCTCAGCCAAAGAACCTG	CAGGTTCTTTGGCTGAGACCATGC
2320	AGCCTGCGACGTTTTCCCGACAGAC	GTCTGTGCGGAAACGTGCGAGGCT
2321	AAGAAAGGCGCACGGGATCGATAT	ATATCGATCCCGTGCGCCTTTCTT
2322	TGTCGCGAAGCCAACCTTCAGTAA	TACTGAAAGTTGGCTTCGCGACA
2323	GCGGCATGCAAGGTAGGTCTGGAT	ATCCAGACCTACCTTGATGCCGC
2324	GGTGGCCATCTCCTCGAATTGCAT	ATGCAATTCGAGGAGATGGCCACC
2325	GCGTGCATAAGTTGCACATTGTGC	GCACAATGTGCAACTTATGCACGC
2326	TTGAGGTAGCGTTTTTCGCGCATAT	ATATGCGCGAAAACGCTACCTCAA
2327	ATCCCACTTGTGAGAGGGCGCATT	AATGCGCCCTCTCACAAGTGGGAT
2328	CGGTCAGCGAGCAGACATCAACCT	AGGTTGATGTCTGCTCGCTGACCG
2329	GCGTATCTTCGGGTGCAACACTTG	CAAGTGTTGACCCGAAGATACGC
2330	ATGCCATTGAACTCGCACTTTGCG	CGCAAAGTGCAGATTCAATGGCAT
2331	CGATTCCCATCATAATGTGGGTCC	GGACCCACATTATGATGGGAATCG
2332	CAATTTGGATAATCCAGCCACGCC	GGCGTGGCTGGATTATCCAAATTG
2333	CGGCTTACCCTATGATTCCGTGCA	TGCACGGAATCATAGGGTAAGCCG



5	2334	GGTGGACCATGCGCTGTGGTATGA	TCATACCACAGCGCATGGTCCACC
	2335	TATTTGTCTGAAGATCGCAAGCGCC	GGCGCTTGCGATCTTCGACAAATA
	2336	GTCAGTGGGTTTTGAGAGCCCGCA	TGCGGGCTCTCAAACCCACTGAC
	2337	AGGGGGTCGGGAAATCTGACAAAA	TTTTGTCAGATTTCCCGACCCCT
	2338	TGCTTGCTATCCGAAAAAAGCAGG	CCTGCTTTTTTCGGATAGCAAGCA
	2339	TTATCGGATCAAATTCGGCTTCGG	CCGAAGCCGAATTTGATCCGATAA
	2340	TGCAGCAACGAGTTACCCGGACTT	AAGTCCGGGTAAGTCTGTTGCTGCA
	2341	TATACATGTCCGAGGGGCACCCA	TGGGTGCCCTCCCGACATGTATA
10	2342	TGCAAAACCGGAGGATGAACCCTT	AAGGGTTCATCCTCCGGTTTTGCA
	2343	TGGTCTAATGTCCACGCAGACAC	GTGTCTGCGTGGACATTAGACCGA
	2344	ATGTGTTTGCCACGCGCTCCTATT	AATAGGAGCGCGTGGCAAACACAT
	2345	TGGCGAGGCACGGCTCTAATTCGG	CCGAATTAGAGCCGTGCCTCGCCA
	2346	GCGACGACCCGAGCGACTTTTACA	TGTAAAAGTCGCTCGGGTCGTCGC
	2347	CTCAGAGAGTCTATCCGGCGCCCT	AGGGCGCCGGATAGACTCTCTGAG
15	2348	GGAACATCTCCTGGGTCCCTCAGA	TCTGAGGGACCCAGGAGATGTTCC
	2349	GCAACGCAGGGAAGTACTTAGCGA	TCGCTAAGTACTTCCCTGCGTTGC
	2350	TGACTTGGCGGACAAAGAAACGC	GCGTTTCTTTGTCCGCCCAAGTCA
	2351	AGATCATCGGGACGCTTCATGCTA	TAGCATGAAGCGTCCCGATGATCT
20	2352	CCCTTCTGACCGCTAAGGCCATAA	TTATGGCCTTAGCGGTCAGAAGGG
	2353	CGTGAGCCGTGGGGTGTCTCTGTA	TACAGAGACACCCACGGCTCACG
	2354	TACCTTGTCGTCTCCGCTTTTGT	ACAAAAGCGGAGACGACCAAGGTA
	2355	TCGCCGCAAAATGCTACGTGAAAA	TTTTCACGTAGCATTTTGCGGCGA
	2356	GAGTGACCTAATGGCTGCCCGACT	AGTCGGGCAGCCATTAGGTCCTC
	2357	AAAGGAACTTGGCCAACCTATGG	CCATAGGGTTGGCCAAGTTCCTTT
25	2358	TGTTTTCGCACTCCACCTAATCGC	GCGATTAGGTGGAGTGCGAAAACA
	2359	CAATGGGTTTCATAAGGGCAGGCA	TGCCTGCCCTTATGAAACCCATTG
	2360	GCCTAACACACAAGGGTCCCTCTG	CAGAGGGACCCCTGTGTGTTAGGC
	2361	CGTCATGCGGTCCGAGGATCGATC	GATCGATCCTCGGACCGCATGACG
	2362	CCACACGGGCACGGAGTAATATCT	AGATATTACTCCGTGCCCGTGTGG
30	2363	CATCAGACATAGGTGCGGTGCCGA	TCGGCACGCGACCTATGTCTGATG
	2364	AGATGAAACCAAGGGAGGACGCAG	CTGCGTCCTCCCTTGGTTTCATCT
	2365	GGCTACCCATAGGCTCAGCAGCAC	GTGCTGCTGAGCCTATGGGTAGCC
	2366	GGCTTGTGAGGGTGTGTTCTCGAC	GTCGAGAACACACCCTCACAAGCC
	2367	TGTGTTACGGCGAATGCAACAGTC	GACTGTTGCATTGCGCGTAACACA
35	2368	CGATAACAGGTCGCGCCGTTACTA	TAGTAACGGCGCGACCTGTTATCG
	2369	TGATAAAGTGAGGCTCCAGCGCGA	TCGCGCTGGAGCCTCACTTTATCA
	2370	AATTGTGCACGGATCTGCACGGCG	CGCCGTGCAGATCCGTGCACAATT
	2371	GCAATGTACTGTCACCAAGTGCGA	TCGCCACTGGTGACAGTACATTGC
	2372	GGCATATCGGTAACACTTGGTCGG	CCGACCAAGTGTTACCGATATGCC
40	2373	GGGTCTCAAACCAGCGTGGCCGCT	AGCGGCCACGCTGGTTTGAGACCC
	2374	GTCTCCGGGACCATTGAGCTGGAG	CTCCAGCTCAATGGTCCCGGAGAC

5	2375	GGCCTTCGGCATTGAGACGGGTTG	CAACCCGTCTGAATGCCGAAGGCC
	2376	CGTGATAGGCCACAGCGCTCAATT	AATTGAGCGCTGTGGCCTATCACG
	2377	GGCAGGCCCGCGAGGATGATTAAC	GTTAATCATCCTCGCGGGCCTGCC
	2378	CGGGTATGGTTGATAACAGCGTGG	CCACGCTGTTATCAACCATAACCCG
	2379	ACGACGTCCTTGGGACCGTATTGT	ACAATACGGTCCCAAGGACGTCGT
	2380	CTGATATCGAGCCTGAGCCTTTCG	CGAAAGGCTCAGGCTCGATATCAG
	2381	TCCCATTGGCCTGTATGCTGGCCT	AGGCCAGCATACAGGCCAATGGGA
	2382	GTGTCGTGCGATTGTTTCATCGACG	CGTCGATGAAACAATCGACGACAC
10	2383	CGAAAGCCAGTAGCCGATTGCGTG	CACGCAATCGGCTACTGGCTTTTCG
	2384	GGTTCGGCTTATTCCACTGCGACA	TGTCGCAGTGGAATAAGCCGAACC
	2385	AGCGAGGGCTAACTTTTTAACGCG	CGCGTTAAAAAGTTAGCCCTCGCT
	2386	CGGCGCTGATGACGGGACTCGATT	AATCGAGTCCCGTCATCAGCGCCG
	2387	TCACAGTGCTCGGCGTAAGGACTA	TAGTCCTTACGCCGAGCACTGTGA
	2388	CCCATTACGAGCACACACCATGGC	GCCATGGTGTGTGCTCGTAATGGG
15	2389	GGCCGCTAATCTTTACGCATCACG	CGTGATGCGTAAAGATTAGCGGCC
	2390	ACGGCTTCCTAGTGTCCAGCCCTT	AAGGGCTGGACACTAGGAAGCCGT
	2391	CTGTCAGGTCCTACCCAATGGCTC	GAGCCATTGGGTAGGACCTGACAG
	2392	CACAGCCCATCCCCTGAAGTGT	AGCAGTTCAGTGGGATGGGCTGTG
	2393	ACAAACGATACACGCAACGCTGTG	CACAGCGTTGCGTGTATCGTTTGT
20	2394	TGGCGGCCAGCTAGCAGGCGAAGT	ACTTCGCTGCTAGCTGGCCGCCA
	2395	ATCTCGAAACGATGCGTGCCTAAA	TTTAGGCACGCATCGTTTCGAGAT
	2396	ATCTCGAGAACAGCGTGCGTGCGG	CCGCACGCACGCTGTTCTCGAGAT
	2397	GAAGAAATCCGCCGACATCTACGG	CCGTAGATGTCGGCGGATTTCCTC
	2398	GCGGAGCAACCTTGGCTGTTTCTA	TAGAAACAGCCAAGGTTGCTCCGC
25	2399	CGCGTTCGGAAGACTTGTTGTTTG	CAAACAACAAGTCTTCGGAACGCG
	2400	TGACCTGAAGCCCATCCATAAGCA	TGCTTATGGATGGGCTTCAGGTCA
	2401	TGGTATTCATTCCGGATAAGCGGG	CCCGCTTATCCGGAATGAATACCA
	2402	GCGTTGCGGGTCATTGATGCAAC	GTTTGCATCAATGACCCGCAACGC
	2403	ACCGCTTCTGTGTAGAGCCCTGA	TCAGGGCTCTACACAGAAAGCGGT
30	2404	CAAATAGACAATCGCAGCTTCGGG	CCCGAAGCTGCGATTGTCTATTTG
	2405	TGTCCTGACAAATCAAGGTGCAGG	CCTGCACCTTGATTTGTCAGGACA
	2406	AAATTGCACTCGCGGAGATTTCTT	AGGAAATCTCCGCGAGTGCAATTT
	2407	TGACGCCCATTCTATATGGTGCA	TGCACCATATAGAAATGGGCGTCA
	2408	TGTTCCGACAGGGCACTGCTAGAC	GTCTAGCAGTGCCCTGTGGAACA
35	2409	TCGCTGGCTTGGGAAGGCCTTCGT	ACGAAGGCCTTCCCAAGCCAGCGA
	2410	GTGCACCTCCGTTGGCGTAGAATG	CATTCTACGCCAACGAGGTGCAC
	2411	CTCATTTGGGACCGATCGGGTTGC	GCAACCCGATCGGTCCCAAATGAG
	2412	GCCAGTGTCTGTCAATGGATGGGA	TCCCATCCATTGACAGACACTGGC
	2413	TTGCCCGGCAGGTTCTGTGTAATG	CATTACACAGAACCTGCCGGGCAA
40	2414	ACCCGCGAACCAGAGACGCACTTCT	AGAAGTGCGTCTCGGTTCCGGGGT
	2415	TCCGTGCGATTGGTCAAGGTTGAT	ATCAACCTTGACCAATCGCACGGA

	2416	AGGGCGTCTCGGTTGAACCTCGGT	ACCGAGGTTCAACCGAGACGCCCT
	2417	TGACCGTTCAAAGAGCAAGCCAAC	GTTGGCTTGCTCTTTGAACGGTCA
	2418	ACACTCACCTGCTGTCCCTGCTGA	TCAGCAGGGACAGCAGGTGAGTGT
5	2419	GCGTTTAACTCCTTGGGTGGTGGT	ACCACCACCCAAGGAGTTAAACGC
	2420	CGCCTGCGCAGGTAACCTCTCCGCA	TGCGGAGAGTTACCTGCGCAGGCG
	2421	AATCGAATTTCCAGCGGCTGTTT	AAACAGCCGCTGGGAAATTCGATT
	2422	AAGCAGGTGGGATCCTGGGGATCA	TGATCCCCAGGATCCACCTGCTT
	2423	AATCCCAGACTCGCTCTTCGTGCT	AGCACGAAGAGCGAGTCTGGGATT
10	2424	ACGGTTATAAGGGCCGGCTGCGAC	GTCGCAGCCGGCCCTTATAACCGT
	2425	TACGAGAGCGGGCTTAGACGTCGC	GCGACGTCTAAGCCCCTCTCGTA
	2426	GCGATTTTGACCCACGGTTATCGA	TCGATAACCGTGGGTCAAATCGC
	2427	AGCTGTATAATTTGGATGGCGCGA	TCGCGCCATCCAAATTATACAGCT
	2428	TCCGCGAGTCTTAGCCGATTGAAC	GTTCAATCGGCTAAGACTCGCGGA
15	2429	GGCATCAGCTCCGTAAGCCGATAG	CTATCGGCTTACGGAGCTGATGCC
	2430	TGTTATTGGCAGTTCGAGCGACAG	CTGTGCTCGAACTGCCAATAACA
	2431	GCGAGCCTTTTTGCTTGGGAAGAG	CTCTTCCAAGCAAAAAGGCTCGC
	2432	AGAAGAAAAGGTCAGCGTCGACGA	TCGTGACGCTGACCTTTTCTTCT
	2433	CGGGTCGACCCTTGAAGCATAACC	GGTTATGCTTCAAGGGTCGACCCG
20	2434	CTCGGTTTTACAACTTACCGCG	CGCGGTAAGTTTGTGAAAACCGAG
	2435	GCAGTCCTATCCGGAGCCTGACAA	TTGTCAGGCTCCGGATAGGACTGC
	2436	AAGGTGCGCTATTTGTTGTCGGTC	GACCGACAACAAATAGCGCACCTT
	2437	AGTGGAATCCATGCCGACACCTGA	TCAGGTGTCGGCATGGATTCCACT
	2438	TACAGGCGTAATTCCTGCGAGGGA	TCCCTCGCAGGAATTACGCCTGTA
	2439	CCGAAGTGCGAGAAGCACGTTGTT	AACAACGTGCTTCTCGCACTTCGG
25	2440	AAGGACTGGTATGGCCGGAGCTTT	AAAGCTCCGGCCATACCAGTCCTT
	2441	GGACACCGCCAACCTCATAGTTGC	GCAACTATGAGGTTGGCGGTGTCC
	2442	AATGGTGTTTCGCTGGACTACCAC	GTGGTAGTCCAGGCGAACACCATT
	2443	TAGGAAAGCGTACACGGGAATCCG	CGGATTCCCGTGTACGCTTTCCTA
	2444	TCTCACCCCAATGATGAGGACGTC	GACGTCCTCATCATTGGGGTGAGA
30	2445	CGTGTCGGTGTGACACTGTCCATG	CATGGACAGTGTACACGGACACG
	2446	TCCAGGCTGTTGCGGATACGGTAG	CTACCGTATCCGCAACAGCCTGGA
	2447	GTAGGCAAAATGGTCGCGATCAAT	ATTGATCGCGACCATTTTGCCTAC
	2448	ATCTCCGTGGACCCGATTGTGACA	TGTCACAATCGGGTCCACGGAGAT
	2449	GAATATGCCGTCAACGCTATGGGC	GCCCATAGCGTTGACGGCATATTC
35	2450	TTCCGGAAGCGTTTGGTAACTTTG	CAAAGTTACCAAACGCTTCCGGAA
	2451	TTCGATAGGAATACCAGGGCCTGG	CCAGGCCCTGGTATTCCTATCGAA
	2452	GGCCATTTGAGGAGGATTATGCAA	TTGCATAATCCTCCTCAAATGGCC
	2453	ACCTTCTGACCTGGACTTTTGGCG	CGCCAAAAGTCCAGGTCAGAAGGT
	2454	GACCAATCCGCAGTTGAGCAACAG	CTGTTGCTCAACTGCGGATTGGTC
40	2455	TCGGCCACTCACCATGAGTGTAGG	CCTACACTCATGGTGAGTGCCGA
	2456	AGCGCTCACATGTTCGAAAACGGG	CCCGTTTTCGAACATGTGAGCGCT

	2457	TAACGCAAAGGCGCGATCCTCGCT	AGCGAGGATCGCGCCTTTGCGTTA
	2458	TGGGTGGGCCAAATATTACTGCAA	TTGCAGTAATATTTGGCCCACCCA
	2459	GTCCTCGAAAGGGGCATCCAAACA	TGTTTGATGCCCTTTTCGAGGAC
5	2460	CCCATCTGGTGGGAGGCGTTATCA	TGATAACGCCTCCCACCAGATGGG
	2461	GTGCGCGGTCTGCAAACCTCGCCAT	ATGGCGAGTTTGCAGACCGCGCAC
	2462	TGTGTTGCCAACCCTAGGTCATCA	TGATGACCTAGGGTTGGCAACACA
	2463	CTGATGCTGTTCTCGTCGGTTGAC	GTCAACCGACGAGAACAGCATCAG
	2464	AAGCTGCAAAAGGTGAGCGTGGCA	TGCCACGCTCACCTTTTGCAGCTT
10	2465	TCTGACGCGTGCTTGGGAGTCTAT	ATAGACTCCCAAGCACGCGTCAGA
	2466	GAATTACTTGAGAGCGCCGTGCAA	TTGCACGGCGCCTCCAAGTAATTC
	2467	GATTCTTCCCGACCTAGGTTGGCC	GGCCAACCTAGGTCGGGAAGAATC
	2468	CGCAGCGTATCCCATGTTGCTTGA	TCAAGCAACATGGGATACGCTGCG
	2469	GAGATGGAATTGTTGCCCAAAGA	TCTTTGGGCGAACAATTCATCTC
15	2470	GATGCCTGGATCGGTCTAGCGTCA	TGACGCTAGACCGATCCAGGCATC
	2471	GCAGCGACTGCTAAGCTATCTCGG	CCGAGATAGCTTAGCAGTCGCTGC
	2472	AGGGCTAATTTACATCGCCTTGCC	GGCAAGGCGATGTAAATTAGCCCT
	2473	AAGTGACATCCTCACGAAGCGAT	ATCGCTTCGTGAGGATGTGCACTT
	2474	TCAGGCAGCCGTAATTAATGCGC	GCGCATTTAATTACGGCTGCCTGA
	2475	CCACTGGGAAATCGCACTGTTGG	CCAACAGTGCGATTTCCCCAGTGG
20	2476	TTGTCAAAGCCACCTACGACAGA	TCTGTCTAGGTGGCTTTGGACAA
	2477	TGGGCGGAATAGATTGGGTGTCTT	AAGACACCCAATCTATTCCGCCCA
	2478	TAGAATTCGCCTCTTCTAGCCGCC	GGCGGCTAGAAGAGGCGAATTCTA
	2479	CATTACTTCCTGCAGATGCGATGC	GCATCGCATCTGCAGGAAGTAATG
	2480	GGAAATGCTAGCTGGGGTAATCGC	GCGATTACCCAGCTAGCATTTCC
25	2481	GCCGCCACTTGCGAATCTACATCT	AGATGTAGATTGCAAGTGCGGCGC
	2482	ACAATAGCGGACAGCTCGCCAGAT	ATCTGGCGAGCTGTCCGCTATTGT
	2483	AGTTAGGCTCTCGGTGCGGTCCAT	ATGGACCGCACCGAGAGCCTAACT
	2484	TGGGCCTGAGAAGCGGTTAATAGG	CCTATTAACCGCTTCTCAGGCCCA
	2485	ACGCTCTGAGCGACGCTATCGTA	TACGATAGGCGTCGCTCAGAGCGT
30	2486	CCTGGTGATCGTGTCCCAGACTCA	TGAGTCTGGGACACGATCACCAGG
	2487	GCGTGTCCATTGCTTGAGGTTTC	GAAACCTCAAGCGAATGGACACGC
	2488	ATCCTGAACGGCGATGACCACCAC	GTGGTGGTCATCGCCGTTTCAGGAT
	2489	TTACGTTTCTCACCGATCAACGCC	GGCGTTGATCGGTGAGAAACGTAA
	2490	GCCGTCTTGAGTGGCTAAAAGGCA	TGCCTTTTAGCCACTCAAGACGGC
35	2491	ATCTACGATGCGGCTCGAAGTGTT	AACACTTCGAGCCGCATCGTAGAT
	2492	AACCAAGACTCGTCCCCAAACGAA	TTCGTTTGGGGACGAGTCTTGTTT
	2493	AACTGCGGTGGTGGAGGCAGGTGC	GCACCTGCCTCCACCACCGCAGTT
	2494	TGCGATCTTCTCCACCTACAGCGC	GCGCTGTAGGTGGAGAAGATCGCA
	2495	AGGCGCTTAGAACCGTGAAGGCAG	CTGCCTTCACGGTTCTAAGCGCCT
40	2496	TGGAAAATTTTGGGAAACGCTGGA	TCCAGCGTTTCCCAAATTTTCCA
	2497	CCAGCGCCGCACCTTCTCCAATAG	CTATTGGAGAAGGTGCGGCGCTGG

	2498	TAGACGGCTGGCGAATCTTACGGT	ACCGTAAGATTGCCAGCCGTCTA
	2499	TACCATACAAGAGAACGAGCCGCA	TGCGGCTCGTTCTCTTGTATGTA
	2500	GTAGCCGAGAGCAATTTTACCCGC	GCGGTGAAAATTGCTCTCGGCTAC
5	2501	GCAAACCTCCCCTGCCCTTTAGCCT	AGGCTAAAGGGCAGGGGAGTTTGC
	2502	ATCCCGCTGATAACCGCCAGGATA	TATCCTGGCGGTTATCAGCGGGAT
	2503	AGTCTCAGTTCGGCGCAACGGTAG	CTACCGTTGCGCCGAACTGAGACT
	2504	AACCTACAGTCGCCGCAATGCATT	AATGCATTGCGGCGACTGTAGGTT
	2505	ATACACGTTTCAGCCGGCAACAAT	ATTGTTGCCGGCTGAAACGTGTAT
10	2506	ACGACGGGACGTGCCCTCGTTGAT	ATCAACGAGGGCACGTCCCGTCGT
	2507	AAGTCCAACTCGAATGGGGCAGT	ACTGCCCCATTGAGTTTGGACTT
	2508	GATTTATTGGCGCGGTAACGACCT	AGGTCGTTACCGCGCCAATAAATC
	2509	TGTTTTAGAGGGCTACCCTGCCAT	ATGGCAGGGTAGCCTCTGAAAACA
	2510	ACGGTCTCAGGGAAATGCGATCTC	GAGATCGCATTTCCCTGAGACCGT
	2511	GACTTGAAACCGCCTATGCCACACA	TGTGGGCATAGGCGGTTTCAAGTC
15	2512	CGATCGGTTGTGTGCTGTCTTACC	GGTAAGACAGCACACAACCGATCG
	2513	AGTAGCACAATGCCTCATTTCCGC	GCGGAAATGAGGCATTGTGCTACT
	2514	CTCGCTATCTACGCGTCTCCGAAA	TTTCGAGACGCGTAGATAGCGAG
	2515	AGCCCGTTACGGCATCTAGGATTC	GAATCCTAGATGCCGTAACGGGGCT
20	2516	TCGCGATGGCGAGAGTTCAGAATA	TATTCTGAACTCTCGCCATCGCGA
	2517	TTACAGGATTCCTAAAACCCGCAAA	TTTGCGGGTTTTGGAATCCTGTAA
	2518	CGGTACCAACGCGCGGGCATATGA	TCATATGCCCGCGCGTTGGTACCG
	2519	TGCCAGTATTATCCGTGCCAGCCG	CGGCTGGCACGGATAATACTGGCA
	2520	ATTTTCAGACCTCGGGACAACCTGG	CCAGGTTGTCCCGAGGTCTGAAAT
	2521	GAAGTGCGCGTAACTTAGGGAGCC	GGCTCCCTAAGTTACGCGCACTTC
25	2522	TTGGCCAGGTCATCACTCTGCCAT	ATGGCAGAGTGATGACCTGGCCAA
	2523	ATCGGCCGGTATTAGCTGCCCTCC	GGAGGGCAGCTAATACCGGCCGAT
	2524	CGCAGGTAAGGCCGAGCAATGTTT	AAACATTGCTCGGCCTTACCTGCG
	2525	TTGGGAACGTGCTAGGCGGCCCTC	GAGGGCCGCCTAGCACGTTCCCAA
	2526	CATCTCGGCACACTGGTGCTGTAT	ATACAGCACCAGTGTGCCGAGATG
30	2527	ACGCGTAAATCAACGACGTGGTCG	CGACCACGTCGTTGATTACGCGT
	2528	CGTAGGTGGTAAATGTTGGCCCAG	CTGGGCCAACATTTACCACCTACG
	2529	TTCGAGCCAGAATAAAACGGTTGG	CCAACCGTTTTATTCTGGCTCGAA
	2530	AGAGATATTCGGCCTCGGTCGAGA	TCTCGACCGAGGCCGAATATCTCT
	2531	CGACAAAGTTTCTCGCGAGCAACT	AGTTGCTCGCGAGAACTTTGTCTG
35	2532	ATTGCCGCGTCTCGTATCAAAAGA	TCTTTTGATACGAGACGCGGCAAT
	2533	CGGAGAATGGATGCAGGTTCTTCG	CGAAGAACCTGCATCCATTCTCCG
	2534	TATAATCATTTGCGACTCGCCCCA	TGGGGCGAGTCGCAAATGATTATA
	2535	AATTTTCCCCGATTTGAAGAAGCG	CGCTTCTTCAAATCGGGGAAAATT
	2536	TCGCATACTTCGTGCGCGAGTATT	AATACTCGCCGACGAAGTATGCGA
40	2537	CGTGAGCCGTTCTCATCCAAGCGG	CCGCTTGGATGAGAACGGCTCACG
	2538	GCAGAATCGAATTGGGGTGGGTTT	AAACCCACCCCAATTGATTCTGC

	2539	CTCTCGGTTTCTCAACCGAGCTCG	CGAGCTCGGTTGAGAAACCGAGAG
	2540	GACCAGTTAGTGCAATGGTTGGCG	CGCCAACCATTGCACTAACTGGTC
	2541	TTCTCGCACAGCTAGTCAGCCGAT	ATCGGCTGACTAGCTGTGCGAGAA
	2542	CCAAGTCTTGCGTGAGCGATCCTG	CAGGATCGCTCACGCAAGACTTGG
5	2543	GCGAAAGTGGCTCGTATTTCTCCA	TGGAGAAATACGAGCCACTTTTCGC
	2544	CCTCGGGACTGTCCGACTGAAAAA	TTTTTCAGTCGGACAGTCCCGAGG
	2545	AGGCGAGTGACGGCTCATCCATG	CATGGATGAGCCGTACACTCGCCT
	2546	GCGGCTCTGCCTACGATATTCACA	TGTGAATATCGTAGGCAGAGCCGC
	2547	TGCACCTGTCTGTAGATTTGCGGT	ACCGCAAATCTACAGACAGGTGCA
10	2548	CATAAAGCACGGACGCGACTTGAT	ATCAAGTCGCGTCCGTGCTTTATG
	2549	CCCTCAACGTAGGGCGTGACTTTC	GAAAGTCACGCCCTACGTTGAGGG
	2550	GGGTCATCGTGCAATTATGCCGTA	TACGGCATAACTGCACGATGACCC
	2551	CCCGGATAATCCTTTGTCCAGCCG	CGGCTGGACAAAGGATTATCCGGG
	2552	TCCGATAAGCGAACTCACATGGGT	ACCCATGTGAGTTCGCTTATCGGA
15	2553	CCTGCTGGTTCGGTCGTAAGCGAA	TTCGCTTACGACCGAACCAGCAGG
	2554	GAGGCACCAATCGGTCTGAAAATG	CATTTTCAGACCGATTGGTGCCTC
	2555	TACGAAAATGGTTGCGCCGGGTCT	AGACCCGCGCGCAACCATTTTCGTA
	2556	AATTGCCGGAAGCAGTCAGAATCG	CGATTCTGACTGCTCCGGCAATT
	2557	CCGAATCAGCCGATTTTGCTGGAA	TTCCAGCAAATACGGCTGATTCGG
20	2558	CCCGCTTATCTGTACTCGATCGCA	TGCGATCGAGTACAGATAAGCGGG
	2559	TTTTGGGGATCCCTATTAGGCGCA	TGCGCCTAATAGGGATCCCCAAA
	2560	AGTGACAGCGCTCACCACGGTCCC	GGGACCGTGGTGAGCGCTGTCACT
	2561	CCATGAGTGTTTCGGGACATCGTA	TACGATGTCCCGAAACACTCATGG
	2562	GCCACATTCTGCTACCTCCGTGTT	AACACGGAGGTAGCAGAATGTGGC
25	2563	TCCTGTGCTTTGTGACGTGCTAGG	CCTAGCACGTCACAAAGCACAGGA
	2564	GACCGCATATACACCTGATGGGCC	GGCCCATCAGGTGTATATGCGGTC
	2565	GTAGGCCCGTCGTTAACCATCTCA	TGAGATGGTTAACGACGGGCCTAC
	2566	CGGCTCGCGAAATGGAGTTTAGCG	CGCTAAACTCCATTTTCGCGAGCCG
	2567	GCTGATCGGCTTTTACCGCTATA	TATAGCGGTGAAAAGCCGATCAGC
30	2568	TATCAAATCGTTGGCACGCGACTA	TAGTCGCGTGCCAACGATTTGATA
	2569	TTGGCGAGGATCCCTAGGCGTACT	AGTACGCCTAGGGATCCTCGCCAA
	2570	AAGTCCTGAGGCCGTTTCGGTTTCT	AGAAACCGAACGGCCTCAGGACTT
	2571	ACTCCGGACATCTCGGCCAGAGAT	ATCTCTGGCCGAGATGTCCGGAGT
	2572	CCAAGGGGAACACAGGATCGTAGA	TCTACGATCCTGTGTTCCCTTGG
35	2573	GTGGCCTAAATCCGCCTTCTCAAC	GTTGAGAAGGCGGATTTAGGCCAC
	2574	CACTCCGTCTCGTCCATTAATGCG	CGCATTAAATGGACGAGACGGAGTG
	2575	TCAAGAACCCAGTGCCGGTCAGCA	TGCTGACCGGCACTGGGTTCTTGA
	2576	GAATCAATTTTCCAGGGACGGGAC	GTCCCGTCCCTGGAAAATTGATTC
	2577	ATCGGTGTGCTGGAGCGCCAGAGT	ACTCTGGCGCTCCAGCACACCGAT
40	2578	GCCTCTCCTATGACGATGACCCAC	GTGGGTCATCGTCATAGGAGAGGC
	2579	TGGGCGCGCTTTTAAGACTACATC	GATGTAGTCTTAAAAGCGCGCCCA

	2580	CGTTGGGTACCGTTCTATCAACCG	CGGTTGATAGAACGGTACCCAACG
	2581	GCAGTGAGCTGGGTTCAATGCTTC	GAAGCATTGAACCCAGCTCACTGC
	2582	CATCATCCACACAGGCAGGTGTGT	ACACACCTGCCTGTGTGGATGATG
5	2583	AGACAAAGGTCCCCATTGCGAAAT	ATTTGCAATGGGGACCTTTGTCT
	2584	ATACTCGTCGACGAGAAGCGGAAA	TTCCGCTTCTCGTCGACGAGTAT
	2585	GCAGAATGTGTTGTCTTCGAGCC	GGCTGCGAAGACAACACATTCTGC
	2586	CACCATGCCTTCATCTTGGCCTAG	CTAGGCCAAGATGAAGGCATGGTG
	2587	ACTCTTCAACGCCAGGTTAAGCCA	TGGCTTAACCTGGCGTTGAAGAGT
	2588	GCGACCTGCGGCGTGTGTATTCTC	GAGAATACACACGCCGCGAGGTCCG
10	2589	TCGGTGTATGCACCCTTTCTCCAT	ATGGAGAAAGGGTGCATACACCGA
	2590	ACCGTCGAATCTTGGCGCAATGT	ACATTGGCCGCAAGATTCGACGGT
	2591	TAATGCATGCTCCCGGCTCACGTT	AACGTGAGCCGGGAGCATGCATTA
	2592	TCTGTACACACCACGTCGTGCACA	TGTGCACGACGTGGTGTGTACAGA
	2593	CATGGGGTTGTGACGACACCTA	TAGGTGTCGTCTGACAACCCCATG
15	2594	AATCTGATGCTCGCTGTAGGACGG	CCGTCTACAGCGAGCATCAGATT
	2595	TCGAAACCGCGGGAAAGGGTAAAA	TTTTACCCTTTCCGCGGTTTCGA
	2596	TGGGGGACGGGCGTCTAATCCTCC	GGAGGATTAGACGCCCGTCCCCCA
	2597	AGGCATGCACCCATGCTGCCAGAG	CTCTGGCAGCATGGGTGCATGCCT
	2598	TCCCAATGGCCTGTCAAGCATAAA	TTTATGCTTGACAGGCCATTGGGA
20	2599	GAACCTGAGCCTTTGCTAGCACGA	TCGTGCTAGCAAAGGCTCAGGTTT
	2600	CGAATTGATAGCGTTACGGGCGAA	TTGCCCCGTAAACGCTATCAATTG
	2601	TTGCACGCGCGCGAACGACTATTC	GAATAGTCGTTGCGCGCGGTGCAA
	2602	TGCGGTGAAGCAGTCCAAGGTCAG	CTGACCTTGGACTGCTTACCCGCA
	2603	TGAGGACCATCCAATGGATCGGTT	AACCGATCCATTGGATGGTCTCTCA
25	2604	TCGGTGATTGGTAATTTGGATCCG	CGGATCCAAATTACCAATCACCGA
	2605	GCGGGCAGGTAGTTTGAAGTGGATG	CATCCAGTCAAACCTACCTGCCCGC
	2606	CAAGCACAAGCCCATGAAATTTCA	TGAAATTTGATGGGCTTGTGCTTG
	2607	CGGTACAGCGGATAGCCAAGGATA	TATCCTTGGCTATCCGCTGTACCG
	2608	CCATGCTCTTCGCTGCAGCATACT	AGTATGCTGCAGCGAAGAGCATGG
30	2609	CGCGGCAAAGATTAATTTCCCGCG	CGCCGGGAATTAATCTTTGCCGCG
	2610	GAAGACCCGTCCGGGTTCCATAC	GTATGGAAACCCGGACGGGTCTTC
	2611	CTGGCAAGGAGGATGTGGCTCGTG	CACGAGCCACATCCTCCTTGCCAG
	2612	CTGTGCAGGGGGTGGCTCTGTTGA	TCAACAGAGCCACCCCTGCACAG
	2613	TTCAATAATGATCACGAGGCCCCA	TGGGGCCTCGTGATCATTATTGAA
35	2614	TGGTGATGCGAAGCCTTACCTTTG	CAAAGGTAAGGCTTCGCATCACCA
	2615	CTGCCACCATCTACGGCGCAGTCT	AGACTGCGCCGTAGATGGTGGCAG
	2616	TTTGCCAGCTCTCGCAGAAGTTA	TAACTTCTGCGAGAGCTGGGCAAA
	2617	AATTCAGACGCCACATCGACGGTC	GACCGTCGATGTGGCGTCTGAATT
	2618	CCGTGGTCTGCCTCGATTACCTAC	GTAGGTAATCGAGGCAGACCACGG
40	2619	GGCGAGGAATTTCCGAACCTTATG	CATAAGGTTCCGAAATTCCTCGCC
	2620	ATCCGATGATCAGATACCGGCTGG	CCAGCCGGTATCTGATCATCGGAT

	2621	CCATAGACTAGCGCCAGAGTGCCC	GGGCACTCTGGCGCTAGTCTATGG
	2622	TGTGGACCTAGAAAATTGCCAGCC	GGCTGGCAATTTTCTAGGTCCACA
	2623	GAATAATCATCGCGGTCCTCATGG	CCATGAGGACCGCGATGATTATTC
5	2624	GGGATTGGCTCTTGGTTGGAAGAA	TTCTTCCAACCAAGAGCCAATCCC
	2625	ATTGTGCTTCCTCGAACTGGGAAA	TTTCCCAGTTCGAGGAAGCACAAAT
	2626	TGCCCCACCCCGTAAGTCAATAAT	ATTATTGACTTACGGGGTGGGGCA
	2627	TCAGGACCGACGGTGCACTTAGTG	CACTAAGTGCACCGTCGGTCCTGA
	2628	CCAGCCGTCACAGTGCAATTTCCG	CGGAAATTGCACTGTGACGGCTGG
10	2629	CTTAAAGAGGCGCGAAGCACAACA	TGTTGTGCTTCGCGCCTCTTTAAG
	2630	TACCGCTCGTCGCGATCACAATGA	TCATTGTGATCGCGACGAGCGGTA
	2631	CCGAGTGCGCGAAGTGTCTATGTG	CACATAGACACTTCGCGCACTCGG
	2632	GCACCAAGTCCCCGATCAAAACGTA	TACGTTTTGATCGGGCACTGGTGC
	2633	TGCAGGCTTCTCAACGGCTGGGAG	CTCCCAGCCGTTGAGAAGCCTGCA
15	2634	CTCCGTACGTATCCCGCGTGATAC	GTATCACGCGGGATACGTACGGAG
	2635	GGAAGTGCAACTTAAAGCCCCGCC	GGCGGGGCTTTAAGTTGCACTTCC
	2636	CGAACCGGCAGTCGATCGTTGCAT	ATGCAACGATCGACTGCCGGTTCCG
	2637	CCGTTAGTGGTCGACAGTTCGGTT	AACCGAACTGTCGACCACTAACGG
	2638	TCAGGCTACGCCCTCAGCACTACA	TGTAGTGCTGAGGGCGTAGCCTGA
20	2639	TATACGGGCCGAGGTCCGTATTCCG	CGAATACGGACCTCGGCCCGTATA
	2640	CCAACGTGTGACGAAGGGCCATTG	CAATGGCCCTTCGTCACACGTTGG
	2641	CTGCTCAGCGGTGCTTGAAAGACA	TGTCTTTCAAGCACCGCTGAGCAG
	2642	GGAGATTGACTTCGCGTTTCACCA	TGGTGAAACGCGAAGTCAATCTCC
	2643	ATGGTTCAGAAGGTTTCGTCCGGTT	AACCCGACGAACCTTCTGAACCAT
25	2644	GAGTGGAGCATTCTCGGCCCTCAA	TTGAGGGCCGAGAATGCTCCACTC
	2645	TGGATTGGAACCAATCCCGCACAA	TTGTGCGGGATTGGTTCCAATCCA
	2646	TGCTCTTGTGGTCACTCGAGAGGA	TCCTCTCGAGTGACCACAAGAGCA
	2647	TTGGGAGCACGGTTACCGCCTGTG	CACAGGCGGTAACCGTGCTCCCAA
	2648	CAACGCGAGCTAACGGTAGTTTCG	CGAAACTACCGTTAGCTCGCGTTG
	2649	AACGCTGAGCGCTCACCTTCACCT	AGGTGAAGGTGAGCGCTCAGCGTT
30	2650	CCGTCGTAGATCTGGAGGCTTCAA	TTGAAGCCTCCAGATCTACGACGG
	2651	GGATGGCATGGGCACACTGTAACC	GGTTACAGTGTGCCCATGCCATCC
	2652	TCGCTCGTAGATATCCTTCACGCC	GGCGTGAAGGATATCTACGAGCGA
	2653	GGAGCAATACCGCGTCCAAAACAC	GTGTTTTGGACGCGGTATTGCTCC
35	2654	TTGTTTCAGACTTAGGCGCTGCCCA	TGGGCAGCGCCTAAGTCTGAACAA
	2655	CGGCGGTACTCTTTCCACTGTCCT	AGGACAGTGGAAGAGTACCGCCG
	2656	AAGACGATTGCCACGTGCCAGAG	CTCTGGCACGTGGGCAATCGTCTT
	2657	AGGTGAGCGCAGGCATATTGCAGT	ACTGCAATATGCCTGCGCTCACCT
	2658	CTCGGGCCTGTACAGCAAAGCCGT	ACGGCTTTGCTGTACAGGCCCGAG
40	2659	TGCGCGCTAGTGCTGCCTATGATC	GATCATAGGCAGCACTAGCGCGCA
	2660	CCATCCTTTGCCTTGAGGGTAAGG	CCTTACCCTCAAGGCAAAGGATGG
	2661	AACAACAGCGTAAGACGGACAGGG	CCCTGTCCGTCTTACGCTGTTGTT



	2662	GAGGCGGTCTGAGGCTCACAATATT	AATATTGTGAGCCTCGACCGCCTC
	2663	CGAGGTTAGACGCCTATGACCCAC	GTGGGTCATAGGCGTCTAACCTCG
	2664	AAC TTGCTATACCGGGCGCAGCAA	TTGCTGCGCCCGGTATAGCAAGTT
5	2665	CGCGGTGAATCGCATACACAGCGC	GCGCTGTGTATGCGATTCAACGCG
	2666	CACCGAATCAAGCCATATGGCTCT	AGAGCCATATGGCTTGATTGCGTG
	2667	TTACAGCTATCCTAGGCGCTGCC	GGCAGCGCTTAGGATAGCTGTGAA
	2668	AGAAGCGCGAAGTGTACCCCGCAT	ATGCGGGGTACACTTCGCGCTTCT
	2669	TGCATGGTATTTGCGTGCGATAGG	CCTATCGCACGCAAATACCATGCA
10	2670	GGCCGGACCTATGTGAGATGAAAA	TTTCCATCTCACATAGGTCCGGCC
	2671	TCAACCTGAGTCCTGATCCCAAGC	GCTTGGGATCAGGACTCAGGTTGA
	2672	TGCTTACCGTTCAGGGAGGCGTGT	ACACGCCTCCCTGAACGGTAAGCA
	2673	GGAGAGTTACGCGATGAGCCACCT	AGGTGGCTCATCGCGTAACTCTCC
	2674	CGGTATGCGGTGTACAGCTTTCGT	ACGAAAGCTGTACACCGCATACCG
15	2675	GTAAGCCGGGTCTCGTGCGCCGT	ACGGCGACACGAGACCCGGCTTAC
	2676	GCGTAGTGCGAACGCCCGACCTA	TAGGTGCGGGCGTTTCGCACTACGC
	2677	TCCTCGCGGCTTACGTCAAATTCG	CGAATTTGACGTAAGCCGCGAGGA
	2678	CGACGTTCAAAGCGGGAGAGGAGG	CCTCCTCTCCCGCTTTGAACGTCG
	2679	CGAGGCACCCCGACATGTTGAGAT	ATCTCAACATGTCGGGGTGCCCTCG
20	2680	CTATTTCTGTGCCGCTCGGACAAG	CTTGTCGACGCGGCACGAAATAG
	2681	GGCTGCTCAGTGACGTGTCAACTG	CAGTTGACACGTCACTGAGCAGCC
	2682	ATCACTCGTGCGTACCCGACCGTC	GACGGTCGGGTACGCACGAGTGAT
	2683	CGAGATGTCCTATACCGTGCGGAA	TTCCGCCACGGTATAGGACATCTCG
	2684	TCACACCGAGCCCCATAAATGAAA	TTTCATTTATGGGGCTCGGTGTGA
25	2685	AGCTACGTGTCTCGAGCAAAAGCG	CGCTTTTGCTCGAGACACGTAGCT
	2686	TCAGGGCGAGTTTTTTCAGCGGCG	CGCCGCTGAAAAAACTCGCCCTGA
	2687	TTGTTCTGTCTATTTTGCCCCG	CGGGGCAAAAATAGACAGAACGAA
	2688	TGGTATGCCAGGATCCAGCCTAC	GTAGGCTGGATCCTGGGCATACCA
	2689	TCTCAGTCGTTAGGCCAATGGCGG	CCGCCATTGGCCTAACGACTGAGA
30	2690	AAAGATCACCGTGAGCGATCGGC	GCCGATCGCTCCACGGTGATCTTT
	2691	TAGCAGGACTTGCACTCGTGATGC	GCATCACGAGTGCAAGTCCTGCTA
	2692	TGCCACCGGTACCGTTCAAGGCTG	CAGCCTTGAACGGTACCGTGGGCA
	2693	TGAGGTGCGTCGCCCTAAGTAATG	CATTACTTAGGGCGACGCACCTCA
	2694	AGCAAGGGTTACAACCCGCAACCC	GGGTTGCGGGTTGTAACCCTTGCT
35	2695	CACAACAGCCAGTATTCGCCACAA	TTGTGGCGAATACTGGCTGTTGTG
	2696	GGCAACACCATACTCGACGAGCTC	GAGCTCGTCGAGTATGGTGTTGCC
	2697	GGCTGGATTGACAATTTAGCCCCT	AGGGGCTAAATTGTCAATCCAGCC
	2698	CGTGAGAAATGCTACACGCGTCAG	CTGACGCGTGATGATTTCTCACG
	2699	CGCATCTGCCCCATTTGTTCCCT	AAGGAACAAAATGGGGCAGATGCG
40	2700	GTCGGCCTAGTCGGCAGAACGGTG	CACCGTTCTGCCGACTAGGCCGAC
	2701	TCCCTCACCTTCCAAAAATGTGCT	AGCACATTTTGGGAAGGTGAGGGA
	2702	GGGCAAGAACATGAGAACAGACCG	CGGTCTGTTCTCATGTTCTTGCCC

	2703	TCGTCCTGGTACGACTTGCGTAGA	TCTACGCAAGTCGTACCAGGACGA
	2704	TGGCGGTTGCATGTGATGATCAAG	CTTGATCATCACATGCAACCGCCA
	2705	CCTCGCGTGAGTAAAAACCGTCCG	CGGACGGTTTTTTACTCACGCGAGG
	2706	ACTTCCGCCACAGAATGCGGCCAG	CTGGCCGCATTCTGTGGCGGAAGT
5	2707	GTGTAGAGCTTGGGTAGCCCCGTT	AACGGGGCTACCCAAGCTCTACAC
	2708	CGCAGCATCCGAGTTAACACACAT	ATGTGTGTTAACTCGGATGCTGCG
	2709	ATGAGCCTGGGATGATCCGCTGGT	ACCAGCGGATCATCCCAGGCTCAT
	2710	CCTGGCATAAGTGCCGACATGCTT	AAGCATGTCGGCACTTATGCCAGG
	2711	GCGCATGAAAACTACGACGGACG	CGTCCGTCGTAGTTTTTCATGCGC
10	2712	AAAGATGGGTCGATGGGAGCGTCT	AGACGCTCCCATCGACCCATCTTT
	2713	ATCCTGGGCACGAGCGGATTTATC	GATAAATCCGCTCGTGCCCAGGAT
	2714	TCACCGCATTTGATAGTTACGCGA	TCGCGTAACTATCAAATGCGGTGA
	2715	TGGTGGAGCGGACTCTGGTGTTAT	ATAACACCAGAGTCCGCTCCACCA
	2716	CACAATGAAAAACAATGGCCCCA	TGGGGCCATTGTTTTTTCATTGTG
15	2717	CCTTGCCGCGCTTGTGGTACCAAC	GTTGGTACCACAAGCGCGGCAAGG
	2718	CCGAGACCTTTGCCACACGAAAGA	TCTTTCGTGTGGCAAAGGTCTCGG
	2719	ACCGCGGTGTACACCTGAGCAGGC	GCCTGCTCAGGTGTACACCGCGGT
	2720	GTCGTACGCTTACCGCAGCGGAGA	TCTCCGCTGCGGTAAGCGTACGAC
	2721	TCGTAATTTGACCGACACACGCAG	CTGCGTGTGTCGGTCAAATTACGA
20	2722	CCTAGACGGATACCCTGAGCGGAA	TTCCGCTCAGGGTATCCGTCTAGG
	2723	AAGCGACAGCAGAGGTTCAAGTCGC	GCGACTGAACCTCTGCTGTCGCTT
	2724	GCGTGGACGATATCACCTGGGCGT	ACGCCCAGGTGATATCGTCCACGC
	2725	GTCGGAGAGCCAGTGGTACGGCTT	AAGCCGTACCACTGGCTCTCCGAC
	2726	TATCCGCACGGTATAGCAGTTGCA	TGCAACTGCTATACCGTGCGGATA
25	2727	CATCAGTCGGGCTACCTTCAGCCT	AGGCTGAAGGTAGCCCGACTGATG
	2728	CGGATTAATGCCTTTCCTCGGAAT	ATTCCGAGGAAAGGCATTAATCCG
	2729	TTCGTCGTGCCAAGCTAATGCAAG	CTTGCAATTAGCTTGGCAGCAGAA
	2730	GGCCGAGACCACAGTAACAGGTT	AACCTGTTACTGGTGGTCTCGGCC
	2731	CGCGCGGAAGCATTGAAGTTACTA	TAGTAACTTCAATGCTTCCGCGCG
30	2732	TCGGCTTACCGCTTCGTCTGACTT	AAGTCAGACGAAGCGGTAAGCCGA
	2733	GA CTGACGTCAAGGCAAGCAACAC	GTGTTGCTTGCTTGACGTCAGTC
	2734	AGAGGAAGGAGGGGCTGTGACAGA	TCTGTACAGCCCCTCCTTCCTCT
	2735	TTCCAATGCGAGAGATGGCAGGCT	AGCCTGCCATCTCTCGCATTGGAA
	2736	AAATGGGGTGCTTCGAATATGTCG	CGACATATTGAAGCACCCCATTT
35	2737	GCTGTGCGATTATTGCACGCCTGT	ACAGGCGTGCAATAATCCGACAGC
	2738	CCGACTTTGTTTATGTTGCTGGCG	CGCCAGCAACATAAACAAGTCGG
	2739	GCTGCGATATAACCCGTCCCAGAA	TTCTGGGACGGGTATATCGCAGC
	2740	TGAGCTGGGCGTCAACTCCGAAGA	TCTTCGGAGTTGACGCCAGCTCA
	2741	CCCAAGCATCCTAAATCTCCCTCG	CGAGGGAGATTTAGGATGCTTGGG
40	2742	CGACAGCAATCCACATGCATTCTT	AAGAATGCATGTGGATTGCTGTGCG
	2743	TGAATGGTCGGGAAACCAATGCAT	ATGCATTGGTTTCCCGACCATTC

	2744	CTTTGCATCGAGATGCGGGGTAGC	GCTACCCCGCATCTCGATGCAAAG
	2745	TCCATTTCTCCGCAACTCTCAGG	CCTGAGAGTTGCGGAGGAAATGGA
	2746	CCACTACGCCATCCTGACAACGAG	CTCGTTGTCAGGATGGCGTAGTGG
5	2747	TAGTAAGGCCAATGTACGCCGTCC	GGACGGCGTACATTGGCCTTACTA
	2748	GTCATGCATATGGGGCCTGTTTTTC	GAAAACAGGCCCCATATGCATGAC
	2749	ACCGGTAGACGTTAGCGGGTCAA	TTGAACCCGCTAACGTCTACCGGT
	2750	TTGGTTCAAACGGCCACACGTCTC	GAGACGTGTGGCCGTTTGAACCAA
	2751	GACACAACTGCAAGGGAGGCATG	CATGCCTCCCTTGACGTTTGTGTC
10	2752	CTCGAGCGCTGTCATCATATCGGC	GCCGATATGATGACAGCGCTCGAG
	2753	GCGGCTAAGGCACAAGTAGACGTG	CACGTCTACTTGTGCCTTAGCCGC
	2754	ACAGCCTAAATGGCGCAAGACCGA	TCGGTCTTGCGCCATTTAGGCTGT
	2755	CCGATGATGTAAGCCGTCGGCCCT	AGGGCCGACGGCTTACATCATCGG
	2756	AGGAGCAAACAAACGCCAGTGACA	TGTCACTGGCGTTTGTGCTCCT
	2757	ACGAATTGGGTAGCCGGACTGAGA	TCTCAGTCCGGCTACCCAATTCGT
15	2758	CTGTTCCAGTTCGGCAAGTGCGGC	GCCGCACTTGCCGAAGTGAACAG
	2759	AGACAAGTCAGGAACGCGTTTCCG	CGGAAACGCGTTCCTGACTTGCT
	2760	AGACGACGCCAGATACGCTGCCA	TGGCAGCGTATCTGGCCGTCGTCT
	2761	AGGAAGCGCTTCTCCGGTTCTTC	GAAGAACCGGAAGAAGCGCTTCCT
	2762	GATGGACGCAACACAAGGCGATC	GATCGCCTTGTGTTGCGTCCATC
20	2763	CGCATAGCAGTCTCCGCATCTTGG	CCAAGATGCGGAGACTGCTATGCG
	2764	TGGTTCCGGTGTGCAACAGATAAA	TTTATCTGTTGCACACCGGAACCA
	2765	CCGTATGCCACCTCCAGAACTCAA	TTGAGTTCTGGAGGTGGCATAACGG
	2766	GTAAAGGAACCCCTCGGGAATCCT	AGGATTCCCGAGGGGTTCCTTTAC
	2767	GCCTGATGCTCGTTAAATTCGT	ACGCAATTTTAACGAGCATCAGGC
25	2768	TCGCACTTGGACCATGAGATCTGA	TCAGATCTCATGGTCCAAGTGCGA
	2769	TTCTCAGGCTGGGCAAGAGTCTGT	ACAGACTCTTGCCAGCCTGAGAA
	2770	CGGACCTGGGGATGCTGGGATTAC	GTAATCCCAGCATCCCCAGGTCCG
	2771	TCGAGCCGATAGGGTTGGCATTGC	GCAATGCCAACCCCTATCGGCTCGA
	2772	TACGTGTGTCCCACACACGTCGTA	TACGACGTGTGTGGGACACACGTA
30	2773	TGTGAAATTCGCGTTTCGCATCTT	AAGATGCGAAACGCGAATTTACA
	2774	TTGCAATGCTCCAAAAAACTGCC	GGCAGTTTTTTTGGAGCATTGCAA
	2775	TCTCATCATGGCTGTGGCTTTGAC	GTCAAAGCCACAGCCATGATGAGA
	2776	ATTACACCGCTTGGTTTGGAGTGG	CCACTCCAAACCAAGCGGTGTAAT
	2777	GCCGTGCAATGCACAGAGTTCAAG	CTTGAACCTCTGTGCATTGCACGGC
35	2778	GAGATCAGACCGTGTCCGATGCTG	CAGCATCCGACACGGTCTGATCTC
	2779	CCACCTATCTTGATGCGACCTGGA	TCCAGGTGCGATCAAGATAGGTGG
	2780	CCGATCGCCGTTTATGTCTACGGC	GCCGTAGACATAAACGGCGATCGG
	2781	GAAAATCACGGTAAGGCACGTTTCG	CGAACGTGCCCTTACCGTGATTTTC
	2782	GATTCTCGCTTCCCAACGAGCATA	TATGCTCGTTGGGAAGCGAGAATC
40	2783	TGTGAAATGTGGCAGTCTCAGGGA	TCCCTGAGACTGCCACATTTACA
	2784	CGATCCTGCGTGCCTCATCCAGGC	GCCTGGATGAGGCACGCAGGATCG

	2785	CCCTCAAGTGGGCGAGGGTTTTCA	TGAAAACCCTCGCCCACTTGAGGG
	2786	TCGCCTCCGCCTCGTGTGTAGAAG	CTTCTACACACGAGGCGGAGGCGA
	2787	TTCGCTTTCAGCTCATTGGAACGA	TCGTTCCAATGAGCTGAAAGCGAA
5	2788	TGTAATCTGAACAAGCGGACCCCT	AGGGGTCCGCTTGTTTCAGATTACA
	2789	TGGAATCTTCTTGAGCGCCGTGA	TCACGGCGCTCAAGAAAGATTCCA
	2790	GGCTTTCATCTTTAACCGCTCGGT	ACCGAGCGGTTAAAGATGAAAGCC
	2791	TGATCCGAGCCATTCTAATCACC	GGTGATTAGGAATGGCTCGGATCA
	2792	TGGTAGGCGTGATGTCTACGCAA	TTGCGTAGGACATCACGCCTACCA
10	2793	AGGCATCGGTAAGAAGGCCCTATG	CATAGGGCCTTCTTACCGATGCCT
	2794	CGCCGCGAGACGATCCTTATTATT	AATAATAAGGATCGTCTCGCGGCG
	2795	ACATGGACGAAATTACGCCCCGTCA	TGACGGGCGTAATTCGTCCATGT
	2796	ACAGAAAGGTGGGGAGCCTAGCGT	ACGCTAGGCTCCCCACCTTTCTGT
	2797	AGGCTTGCGAACATGGGTAGTGAC	GTCACTACCCATGTTTCAAGCCT
	2798	GCGTGGGCCTTGCTCCTGTTTAAC	GTTAAACAGGAGCAAGGCCACGC
15	2799	GAATACAGAGCGTCCGATGTGCCC	GGGCACATCGGACGCTCTGTATTC
	2800	GCGACTCTGTAGGGAGCGCGATAT	ATATCGCGCTCCCTACAGAGTCGC
	2801	GGTGCACTCATATGCGTCGCATCG	CGATGCGACGCATATGAGTGCACC
	2802	CTGTCCACGGGGAAACCTTACTT	AAGTAAGGTTTCCCCGTGGGACAG
	2803	TGGCTTACTGTGCAATCTAGGCC	GGCCTAGATTGCGACAGTAAGCCA
20	2804	GCACTCAGTTTCCGGTATCCCATG	CATGGGATACCGGAACTGAGTGC
	2805	GTGAGGTTACGTAAGGCACAGCG	CGCTGTGCCTTACGTGAACCTCAC
	2806	GTAACGCCTTTGTCCCAGCGTAT	ATACGCTGGGGACAAAGGCGTTAC
	2807	GCATTGATATGGTCGGTCTCGCCT	AGGCGAGACCGACCATATCAATGC
	2808	GTGGGTTTAAGTGACAACGGACGC	GCGTCCGTTGTCACTTAAACCCAC
25	2809	CAAAACCCTGCCGAAGATGTTGGT	ACCAACATCTTCGGCAGGGTTTTG
	2810	TCCGAGGAGACTGAACCTGCTACC	GGTAGCAGGTTCACTCTCTCGGA
	2811	CGGGGAAGAACGGATTGCTAAAT	ATTTAGCGAATCCGTTCTTCCCCG
	2812	TGGTTAGCTTATGTGCGAGCCACC	GGTGGCTCCGACATAAGCTAACCA
	2813	ACGCGTCGATGAACTAAGGCTCGC	GCGAGCCTTAGTTCATCGACGCGT
30	2814	TTCTCCTGACGAGTACGCAGTGGG	CCCACTGCGTACTCGTCAGGAGAA
	2815	TCCGCGGTTGCCGTTTGTAGGA	TCCTAACAACCGGCAACCGCGGA
	2816	TGGCGCATCTTTCAGGGGATGATG	CATCATCCCCTGAAAGATGCGCCA
	2817	TCTTTGGTCCTTGGTGTTACGCG	CGCGTAAACACCAAGGACCAAAGA
	2818	GAGAACTCCCGCTACAAAGGAGCC	GGCTCCTTTGTAGCGGGAGTTCTC
35	2819	TTAACGTGGGAACCGTTGGTGAAT	ATTCACCAACGGTCCACGTTAA
	2820	GGGACACCATCCTTGGGTTTGTTA	TAACAAACCCAAGGATGGTGTCCC
	2821	CAACAAACCGCCTTGGAAGTGAC	GTCACCTCCCAAGGCGGTTTGTTG
	2822	TTGAAGGCCACCGATACTGATCGC	GCGATCAGTATCGGTGGCCTTCAA
	2823	TCGTAATAGAAGTGCGCCCAATGC	GCATTGGGCGCAGTTCTATTACGA
40	2824	GGCACGTTGCCCAAGTTGGATCCA	TGGATCCAACCTTGGGCAACGTGCC
	2825	ACATAGCTTGCCCGGACACCCACC	GGTGGGTGTCCGGCCAAGCTATGT

	2826	CTTGCCGCCTTGCGAGTGGCTAAA	TTTAGCCACTCGCAAGGCGGCAAG
	2827	AATGGCTCGCCAGATACCGCAGCC	GGCTGCGGTATCTGGCGAGCCATT
	2828	CAAAAGGCGTGTCCGAACTTTTCA	TGAAAAGTTTCGGACACGCCTTTTG
	2829	CGTCCACTTAGGTGGAGATACGCC	GGCGTATCTCCACCTAAGTGGACG
5	2830	GAGCCTCTTCGTCCTGAAGACCGA	TCGGTCTTCAGGACGAAGAGGCTC
	2831	AACATCAAGCGGCAATCTCCCTTC	GAAGGGAGATTGCCGCTTGATGTT
	2832	CGTCCTGACATTATTAGCGCGTGC	GCACGCGCTAATAATGTCAGGACG
	2833	TGTGCAGACCCTAACGACCTACGG	CCGTAGGTCGTTAGGGTCTGCACA
	2834	TTAGGTCGGCCTAGACCCTCGTA	TACGGAGGGTCTAGGCCGACCTAA
10	2835	TCACATCGCTTAAGTACGCGCATT	AATGCGCTCAGTTAAGCGATGTGA
	2836	AGACCTTCCCACGCGAGATGCTAC	GTAGCATCTCGCGTGGGAAGGTCT
	2837	TTCTTGCCAAAATGTGTCCAACCA	TGTTGGACACATTTTGGAAGAA
	2838	CAGTTTTCAATTGCAGCGAAAGCAA	TTGCTTTCGCTGCAATGAAAAGT
	2839	GTGCGGATCCCGAGACAAGTTCCG	CGGAACTTGTCTCGGGATCGGCAC
15	2840	CATCCGGCCTCAGTGATTCTTACC	GGTAAGAATCACTGAGGCCGATG
	2841	TGCTGGAAGCCACAAACGTTACGT	ACGTAACGTTTGTGGCTTCCAGCA
	2842	GAACGGCCAGGGGACAACTATCGT	ACGATAGTTGTCCCCTGGCCGTTT
	2843	TCATCTAGGTGGAAGCGCAAGACA	TGTCTTGCCTTCGACCTAGATGA
	2844	TTTGGTTACCAGCACCCATGTTCC	GGAACATGGGTGCTGGTAACCAAA
20	2845	GACAACAGTCTGTCCGCCACATCC	GGATGTGGCGGACAGACTGTTGTC
	2846	GCCAACAGGAGATGCTTGACCAT	ATGGTGCAAGCATCTCCTGTTGGC
	2847	CTAAGGACGCATTGACCCCTGAAC	GTTCAAGGGTCAATGCGTCCTTAG
	2848	GGTCGCGTAGTGAGTCAGAGGCGT	ACGCCTCTGACTCACTACGCGACC
	2849	TTACCTCATGAACCTTCGCGGCG	CGCCGCGAAGGGTTCATGAGGTAA
25	2850	TATACAGCATCGTCGCCGGGCATA	TATGCCCGGCGACGATGCTGTATA
	2851	GCTTAGTGCGCTTTCGTCGTAGG	CCTACGACGAAGACGCCACTAAGC
	2852	TGCACTCCGCAACCTTGTGAAATC	GATTTACAAGGTTGCGGAGTGCA
	2853	AACCCGTCATGCCGACTCCATCTA	TAGATGGAGTCGGCATGACGGGTT
	2854	AGCACTAGTGGCGTGCGACTTTGC	GCAAAGTCGCACGCCACTAGTGCT
30	2855	TAAAAAGTGCCGCTAACCCAGGAG	CTCCGTGGTTAGCGGCACTTTTAA
	2856	CGCGGAATATTTGTCGTCCGATTC	GAATCGGACGACAAATATTCCGCG
	2857	TTCTGCTATGCGTATGGGGGCCCCG	CGGGCCCCCATACGCATAGCAGAA
	2858	CGAACTACTGCGTCAGCCTCTCCC	GGGAGAGGCTGACGCAGTAGTTCG
	2859	AGATGACGAATTAGCGGGGTTGGG	CCCAACCCCGCTAATTCGTCATCT
35	2860	AATAACAGTGGCAATGAGCGGGAA	TTCCCGCTCATTGCCACTGTTATT
	2861	ATATGTTGATTCCCGTGCTGCACA	TGTGCAGCACGGGAATCAACATAT
	2862	AGAGTGGGCACCACCAGGCAGACA	TGTCTGCCTGGTGGTGCCCACTCT
	2863	AGGCCTGGGTTTCTGCGTCTTAGT	ACTAAGACGCAGAAACCCAGGCCT
	2864	CGGACGTGACAAACGGACATACCC	GGGTATGTCCGTTTGTACGTCCG
40	2865	CAAGTGTTCGGCCCACTCTCGA	TCGAGAGTTGGGCCGAAACACTTG
	2866	GAACCCTTATCGGGATAGGCCCAA	TTGGGCCTATCCCGATAAGGGTTC

	2867	CAGGACGATACCAAGCAGAACGCC	GGCGTTCTGCTTGGTATCGTCCTG
	2868	GCGTCTTGTGATTCTGCCCTAACC	GGTTAGGGCAGAATCACAAGACGC
	2869	AAACAACCATCAATGTCGGGTCCA	TGGACCCGACATTGATGGTTGTTT
5	2870	TGTAAAGACCAGTTGGCGGCTCTC	GAGAGCCGCCAACTGGTCTTTACA
	2871	GCGTTTTGACTCGGTGGTCAGTCC	GGACTGACCACCGAGTCAAAACGC
	2872	TGTATGGAGGCACGGCAAAGTCTT	AAGACTTTGCCGTGCCTCCATACA
	2873	TTACCTAGGTTCCCGCTGACACGC	GCGTGTCAGCGGGAACCTAGGTAA
	2874	CGGCTCGTGGAATCCTCTGAAGA	TCTTCAGAGGATTCCCACGAGCCG
10	2875	CCGGCTCGGGCATTCTTGACCT	AGGTCCAAGAAATGCCCGAGCCGG
	2876	CAACGATGGAATTGTCTCCTTGGG	CCCAAGGAGACAATTCCATCGTTG
	2877	CGGGCTATTATCGGGATTATGGGG	CCCCATAATCCCGATAATAGCCCG
	2878	ACGTACCTGAAGATGCAACGGCGG	CCGCCGTTGCATCTTCAGGTACGT
	2879	CATGGTGCAGCACGCACAAGTAAC	GTTACTTGTGCGTGCTGCACCATG
	2880	CGTCGATATGTGGGCTATTGCCT	AGGCAATAGCCCGACATATCGACG
15	2881	AAATGCAGGGTTAAGAGGAGGCC	GGGCCTCCTCTTAACCCTGCATTT
	2882	TGCAAGGACTGATTCTCCCGCTGT	ACAGCGGGAGAATCAGTCTTGCA
	2883	GTTTTCGGAACGCCGAGAGTTCA	TGAACTCTGCGCGTTCCGAAAC
	2884	CCCTCGATGGTTCATTGGGAAGAC	GTCTTCCCAATGAACCATCGAGGG
	2885	CCTGTTGCTCATAATGGTGGGGT	ACCCCAACATTATGAGCGAACAGG
20	2886	GAAAGAACGATCGCGGAATAGCTG	CAGCTATTCCGCGATCGTCTTTC
	2887	TCCACCTGTGTGCCTTTATCCTCA	TGAGGATAAAGGCACACAGGTGGA
	2888	TCCTCCGTGAACCGCTGTAGCGCA	TGCGCTACAGCGGTTACGGAGGA
	2889	TTGAGATTTTACGGTTTCCCCGC	GCGGGGAAACCGTAAAAATCTCAA
	2890	CGATAGGACGTGGGCATGTCCAG	CTGGGACATGCCACGTCTATCG
25	2891	CCCGAACTTTGAGATCCGAGAACA	TGTTCTCGGATCTCAAAGTTCGGG
	2892	TCACGCAGCTAGAGTCGCGTTACC	GGTAACGCGACTCTAGCTGCGTGA
	2893	AGATAACGCCCACTGACGACATGC	GCATGTCGTGAGTGGGCGTTATCT
	2894	ACGCTTAGAGCTCCGATGCCGAAT	ATTCGGCATCGGAGCTCTAAGCGT
	2895	GGGCGATAACTTAAATTGTGCCGC	GCGGCACAATTTAAGTTATCGCCC
30	2896	AGGACGTTGATGCGTCTTTGCA	TGCAAAGAGACGCATGAACGTCT
	2897	CGGCTGGTAGAACTGTGCATCGTA	TACGATGCACAGTTCTACCAGCCG
	2898	TTCGAAATGTACTTCCACGCGGA	TCCGCGTGGGAAGTACATTTGAA
	2899	GCAGGTTGGCTGTCTTGTGGAGTC	GACTCCACAAGACAGCCAACCTGC
	2900	CGTTTGGTTGCTTCAAGAACCGGT	ACCGGTTCTTGAAGCAACCAAACG
35	2901	CATACTTGTTGTTGTGCCACGC	GCGTGGGCACAACAACCAAGTATG
	2902	GGGGTCGGCTGAAGTGTTTTATCC	GGATAAAACACTTCAGCCGACCCC
	2903	GTGACGGTTGATTAACGACCGTGG	CCACGGTCGTTAATCAACCGTCAC
	2904	CTTATGGCAGCGCCAGGGGCACTC	GAGTGCCCCTGGCGCTGCCATAAG
	2905	GTTAGGGGACCCACCTCGTTTGAT	ATCAAACGAGGTGGGTCCCCTAAC
40	2906	CAATATAAATGCCGCGCATCGAGT	ACTCGATGCGCGGCATTTATATTG
	2907	TTCTTCATCAGCAGTCCCCGAGAA	TTCTCGGGGACTGCTGATGAAGAA

	2908	AGTTGCGTCCCTTGATGGCATTIT	AAAATGCCATCAAGGGACGCAACT
	2909	CCGACTTTCGTCCACGATTCCTCT	AGAGGAATCGTGGACGAAAGTCGG
	2910	ACTTGCCCGGACGACAGCAAAGAC	GTCTTTGCTGTCGTCCGGCCAAAGT
	2911	CACCGCGGTAGATGTATCCCTTCC	GGAAGGGATACATCTACCGCGGTG
5	2912	GTTAGCTTTAGCTCGGCACGCCTG	CAGGCGTGCCGAGCTAAAGCTAAC
	2913	GCGCATAAGAAGGTCCGCTAAAGC	GCTTTAGCGGACCTTCTTATGCGC
	2914	ACATCATCACGCCTGGCGTGACCA	TGGTCACGCCAGGCGTGATGATGT
	2915	CCGGCGAAGTTTGGTGTGATTAGA	TCTAATCACACCAAACCTCGCCGG
	2916	TGCACCGCCAGATTGTGCTGAGTC	GACTCAGCACAATCTGGCGGTGCA
10	2917	ACATGTGAAGTGAGTGCCGTCCAA	TTGGACGGCACTCACTTCACATGT
	2918	CCTCTGGAGGGGATTAGCCACGCT	AGCGTGGCTAATCCCCTCCAGAGG
	2919	CAATAGCCATGTCACTGGCAACGG	CCGTTGCCAGTGACATGGCTATTG
	2920	ACCCATGGTTCCAACGTTCTTTCG	CGAAAGAACGTTGGAACCATGGGT
	2921	AATCTGGTCTTGGCATCCTCCAAA	TTTGGAGGATGCCAAGACCAGATT
15	2922	GTATACCGGTGCATGCTGAAGCAA	TTGCTTCAGCATGCACCGGTATAC
	2923	AGTGTTCTGGTTCGAGTCGACCCG	CGGGTCGACTCGAACCAGAACACT
	2924	CGGGTATTCGACACACACGAGGAC	GTCCTCGTGTGTGTCGAATACCCG
	2925	AGTGCAACAGAGCGCTTGGTCACG	CGTGACCAAGCGCTCTGTTGCACT
	2926	TGCACCTATAGTTTGGTGCCGGTG	CACCGGCACCAAACCTATAGGTGCA
20	2927	TGCTCACGTACCAGGACACTCGAG	CTCGAGTGTCTTGGTACGTGAGCA
	2928	AGTCCACACCTCGAACGACAGGCG	CGCCTGTCGTTGAGGTGTGGACT
	2929	CGCCGACCTGGTCAAAGAGCGCTA	TAGCGCTCTTTGACCAGGTGCGCG
	2930	GCCTAAGGGCCTGTGCTTTCCGA	TCGGAAAACGACAGGCCCTTAGGC
	2931	TGTGCGTGCTTATGTTCCGGTCTC	GAGACCGGAACATAAGCACGCACA
25	2932	CAACCGTTGGCCGTAACAAAATC	GATTTTTGTTACGGCCAACGGTTG
	2933	CGAGAATCAAGGCGTACCATCTCG	CGAGATGGTACGCCTTGATTCTCG
	2934	GCGTAGGCAGCCTCCAGGGAATGG	CCATTCCCTGGAGGCTGCCTACGC
	2935	GATGGTGTTTTGCGCAAGACCAAT	ATTGGTCTTGCGCAAAACACCATC
	2936	CAAGCTAGGGACAGAATTGCCAC	GTGGGCAATTCTGTCCCTAGCTTG
30	2937	TAAATAGGCGAAACCGTTTCGTGGC	GCCACGAACGGTTTCGCCTATTTA
	2938	TCAAGACCCGCAATGTGTTTATGT	ACATGAACACATTGCGGGTCTTGA
	2939	GCGGCTGGTAGACTCTTTCACAA	TTGTGCAAAGAGTCTACCAGCCGC
	2940	CAGGCGTAAACCTGAACCAAACGG	CCGTTTGGTTCAGGTTTACGCCTG
	2941	GCCGATCTGTGCTGAGGTTTATCA	TGATGAACCTCAGCACAGATCGGC
35	2942	GATATCGCGTCGCAATATCACGCG	CGCGTGATATTGCGACGCGATATC
	2943	CCCTGCACGATTAAGCCACCTGTA	TACAGGTGGCTTAATCGTGCAAGG
	2944	TGACATACAGATTTGTGTGGCCCC	GGGGCCACACAAATCTGTATGTCA
	2945	GTTTGCGGCCGGTATTACGATGT	ACATCGTGAATACCGGCCGCAAAAC
	2946	TTTTACCTGGCCATTGGTGAGCTC	GAGCTACCAATGGCCAGGTAAAA
40	2947	CTCTACTCAATCAGGGTGGGAGCG	CGCTCCCACCCTGATTGAGTAGAG
	2948	GGGTTGGAGGGAGTCTTGACCATT	AATGGTCAAGACTCCCTCCAACCC

	2949	CGAGGTCGGTAAGGAAAAGCTTGC	GCAAGCTTTTCCTTACCGACCTCG
	2950	CTTTACGCAGGCACCTCCGAGCTG	CAGCTCGGAGGTGCCTGCGTAAAG
	2951	CATTGTATGGCCACGTGATTGACG	CGTCAATCACGTGGCCATACAATG
	2952	GTACGGTGCGAGAGCGCCTAAGCG	CGCTTAGGCGCTCTCGCACCCTAC
5	2953	TTCCATATGCCGAAATGGACACAA	TTGTGTCCATTTCCGGCATATGAA
	2954	TACGCCTTCCGCTATAGCTCGTGA	TCACGAGCTATAGCGGAAGGCGTA
	2955	CTGTACGCCACGCATGAAGGGTGA	TCACCCTTCATGCGTGGCGTACAG
	2956	CTTACGCGTCCAATGACTGCCACC	GGTGGCAGTCATTGGACGCGTAAAG
	2957	CACATGGTAGAACTCGATCGGCAG	CTGCCGATCGAGTTCTACCATGTG
10	2958	CGCACCGGAACTAGTGGATGTGT	ACACATCCACTAGTTTCCGGTGCG
	2959	ACTATGGCAACCGACACTTGGTCC	GGACCAAGTGTGCGTTGCCATAGT
	2960	CTAGTTTGCGCTACCCACCTGCAA	TTGCAGGTGGGTAGCGCAAACCTAG
	2961	TAGTATCGCCCGACAATAGCCTGG	CCAGGCTATTGTGCGGGCGATACTA
	2962	CCAATATTTACGGCCTGATCAGCG	CGCTGATCAGGCCGTAATATTGG
15	2963	ATGGCTATCCCTTACTGGCTCGCC	GGCGAGCCAGTAAGGGATAGCCAT
	2964	CAAACTTGGCAGGCTTGGGACTT	AAGTCCCAAGCCTGCCAAGTTTTG
	2965	AATGACCGAGGCTGCAAGATTGAC	GTCAATCTTGCAACCTCGGTCATT
	2966	ATCATCTTTCGCCACCAGACATGG	CCATGTCTGGTGGCGAAAGATGAT
	2967	CGTTATTACCGATGCACACGTTGC	GCAACGTGTGCATCGGTAATAACG
20	2968	CACACTGGCAATCGCCTCCCTCGT	ACGAGGGAGGCGATTGCCAGTGTG
	2969	AGGTTGGTAGGAAATCGGAGCGCT	AGCGCTCCGATTTCTACCAACCT
	2970	GCTGAACCACTGTGGTCAAGATGC	GCATCTTGACCACAGTGGTTCAGC
	2971	CGTTGAGTACGACACGGTCGAGGT	ACCTCGACCGTGTCTACTCAACG
	2972	TTTTTCCGCCGCAATGTGATCTAA	TTAGATCACATTGCGGCGGAAAAA
25	2973	ACAATACCTCGACCGCTCAGCATC	GATGCTGAGCGGTGAGGTATTGT
	2974	AGTATCCCTGCTGGCATACACGGG	CCCGTGTATGCCAGCAGGGATACT
	2975	TCTTGGGCTCGGTAGTTCAGCACT	AGTGCTGAACTACCGAGCCCAAGA
	2976	CCCTATATCGAGCCCATAGGGCGA	TCGCCCTATGGGCTCGATATAGGG
	2977	CACGAGTGGCATCAACGGCCTACT	AGTAGGCCGTTGATGCCACTCGTG
30	2978	TGCAGGGTCCGATGTGTTCAAGTA	TACTTGAACACATCGGACCCTGCA
	2979	GCTTGACCGCTGCTAACCTCGTAC	GTACGAGGTTAGCAGCGGTCAAGC
	2980	TTTTGCATCTCTCCACCATCCAGA	TCTGGATGGTGGAGAGATGCAAAA
	2981	AGAATGTGCACCGGCTTCCATCTT	AAGATGGAAGCCGGTGCACATTCT
	2982	TGTTATGACCCGCTCTGTGGCGTG	CACGCCACAGAGCGGGTCATAACA
35	2983	GGAGCTCCTGTTTCATCGAGGCTA	TAGCCTCGATGAAACAGGAGCTCC
	2984	CATTTTGCTGTTTGGGGTCCCAT	ATGGGACCCCCAAACAGCAAAATG
	2985	CCCGCTCCTTCACGTGAGACGAGA	TCTCGTCTCACGTGAAGGAGCGGG
	2986	GCGCTCAAGTCGATTGCCACAACC	GGTTGTGGCAATCGACTTGAGCGC
	2987	CGGTTGACGGAGACCGCAGTACTT	AAGTACTGCGGTCTCCGTCAACCG
40	2988	ACTCAAGACCGGTGCACCTCCAGC	GCTGGAGGTGCACCGGTCTTGAGT
	2989	TTTCGTGTGCATGCAAGTAATGGC	GCCATTACTTGCATGCACACGAAA



2990	GCGGCGTTAGCTCGAGCTAACAAA	TTTGTTAGCTCGAGCTAACGCCGC
2991	GGGTATCCTGCCCCGAGCAGTAATT	AATTACTGCTCGGGCAGGATACCC
2992	GGCTCCGAATCTCTTGTCGGGTCT	AGACCGGACAAGAGATTCGGAGCC
2993	AGGATGGCCACGCCGAATCAAAGT	ACTTTGATTGGCGTGGCCATCCT
2994	GTGCGGGGACGTTTACATAACGAG	CTCGTTATGTAAACGTCCCCGCAC
2995	ACTTTTGACCTGAGGCCGCTTGCA	TGCAAGCGGCCTCAGGTCAAAGT
2996	ACTCCGCTTCAATGGAGACCGTTG	CAACGGTCTCCATTGAAGCGGAGT
2997	GATCGGAATTCGCCGCCATATTGA	TCAATATGGCGGCGAATTCCGATC
2998	ATGCGTGCCCATGGAATGACTTTT	AAAAGTCATTCCATGGGCACGCAT
2999	CCGCATCGCACGAAGGCAGGTCAT	ATGACCTGCCTTCGTGCGATGCGG
3000	CACCCTATGCGTCTCCAATTCCTG	CAGGAATTGGAGACGCATAGGGTG
3001	TGATATGCATCGCTGAGCCTCTGT	ACAGAGGCTCAGCGATGCATATCA
3002	AGCTTCACACGCTCACTGAACCTG	CAGGTTCAGTGAGCGTGTGAAGCT
3003	AACCCGGAACCTCCTCTCACTCGG	CCGAGTGAGAGGAGGTTCCGGGTT
3004	CTCGTCAAACCTTGCCGAGGAGTC	GACTCCTCGGCCAAGTTTGACGAG
3005	GTAGCTGGCAACAGGCAATCAGGA	TCCTGATTGCCTGTTGCCAGCTAC
3006	CTTGTCACGAATATTCGCCAAGCG	CGCTTGCGAATATTCGTGACAAG
3007	CAGTATCTGAAACACGGGGTGCTG	CAGCACCCCGTGTTTCAGATACTG
3008	GGCTAAAATGGGCGCCACGTGTA	TACACGTGGGCGCCCATTTTAGCC
3009	ATGAGAGCCAAGCGCCTCAACTCC	GGAGTTGAGGCGCTTGCTCTCAT
3010	TATTGTTAGGCACCGCTTCGCGCT	AGCGCGAAGCGGTGCCTAACAATA
3011	GGAAGTAGATTGCCAGTGCTCGCC	GGCGAGCACTGGCAATCTAGTTCC
3012	AGTCGACCCCAAGGCAACTGGGTC	GACCCAGTTGCCTTGGGGTCGACT
3013	GGTACTGTTAGCTCGACGATGGCC	GGCCATCGTCGAGCTAACAGTACC
3014	CCGCAATACTTGACGGTAACAGGG	CCCTGTTACCGTCAAGTATTGCGG
3015	AATTCCGGGTTTGAACGGTTGGAA	TTCCAACCGTTCAAACCCGGAATT
3016	GACACGCAATCGGGTCTATGCGAA	TTCGCATAGACCCGATTGCGTGTC
3017	GATTTTGGCGTCTCATTGCGTGAT	ATCACGCAATGAGACGCCAAAATC
3018	TGCCATAGGGAGGAAACGCAATTA	TAATTGCGTTTCCTCCCTATGGCA
3019	GAGGTGCCCATGTTAGTGGTGTC	GGACACCACTAACATGGGCACCTC
3020	GCTTTAGCGGTCATACGACCACCA	TGGTGGTCGTATGACCGCTAAAGC
3021	CCGCTACCAACAATCCGATTAAACG	CGTTAATCGGATTGTTGGTAGCGG
3022	GAGGATCTGGCCACATCGAGAAAG	CTTTCTCGATGTGGCCAGATCCTC
3023	CTCGTTTGGTACCACGTTTTGCCG	CGGCAAAACGTGGTACCAAACGAG
3024	AATACACGCGGCGTAAACAGACGA	TCGTCTGTTTACGCCGCGTGATT
3025	TGTCATGGGCCAAATGACAGTGGC	GCCACTGTCAATTTGGCCATGACA
3026	ACAGCACTTCGACCCGTGTACGA	TCGTACACGGGTCGGAAGTGCTGT
3027	CTCCGTAAAGAGCACAGCTTTGCC	GGCAAAGCTGTGCTCTTTACGGAG
3028	ACGAACAGGTAGGGATCGGTCCTC	GAGGACCGATCCCTACCTGTTCTG
3029	TGGATCCACCTTACCGCGCCATCG	CGATGGCGCGGTAAGGTGGATCCA
3030	AGTATCAAATAGCGGCGCGCAAG	CTTGCCGCGCCGCTATTTGATACT

	3031	GAATTACATTGTGGATGGAGGCGG	CCGCCTCCATCCACAATGTAATTC
	3032	CTCCTCGGGGAGTCGAGGAGTACG	CGTACTCCTCGACTCCCCGAGGAG
	3033	AGTGTGAGCCAACTCCCACCAAT	ATTGGTGGGAGTTGGCTCGACACT
	3034	AAATGACATCCGTTTGGCCACAGC	GCTGTGGCCAAACGGATGTCATTT
5	3035	CGAATCATATCGCCATCGAACTGG	CCAGTTCGATGGCGATATGATTGG
	3036	TATAATGCACTCGCTTGGTGCGCA	TGCGCACCAAGCGAGTGCATTATA
	3037	GCCAAGCAGATGGTAATTATGGCG	CGCCATAATTACCATCTGCTTGGC
	3038	CACGCGGGAAGAGCACGTAGAACT	AGTTCTACGTGCTCTTCCCGCGTG
	3039	TACCCGAGAATTTGGAGAACAGCG	CGCTGTTCTCAAATTCTCGGGTA
10	3040	TGACGGCAAACGTGGCATCTATC	GATAGATGCCACAGTTTGCCGTCA
	3041	CACAGTGTTCAGCCCTTGACGAT	ATCGTCAAGGGCTGGAACACTGTG
	3042	TACCCGCCCACACATGAAAGTTGG	CCAACTTTCATGTGTGGGCGGGTA
	3043	TGGCATATTTAAGATTCGGCGACG	CGTCGCCGAATCTTAAATATGCCA
	3044	ACTGAAAAAAGAACGGGTAGCGGG	CCCGCTACCCGTTCTTTTTCAGT
15	3045	TCTGACCGCAATAGGTGGTCATTG	CAATGACCACCTATTGCGGTCAGA
	3046	ACTTTTGGCGGGCCCTCTCTCGT	ACGAGAGAGGGCCCGCCAAAAAGT
	3047	CTGCCCAGATCATTGCGCGATCCG	CGGATCGCGCAATGATCTGGGCAG
	3048	CGGAGGTTAAATGCTTTAACCGGC	GCCGGTTAAAGCATTAAACCTCCG
	3049	AGGCGTCTCCAAACGTCCTTCTGT	ACAGAAGGACGTTTGGAGACGCCCT
20	3050	AGATGCTATCCTGAGTGGGCCTGC	GCAGGCCCACTCAGGATAGCATCT
	3051	ACAGGGTGAAGAGACCGTGGGATG	CATCCACGGTCTCTTACCCTGT
	3052	GACTGTCTAACGGACGACACGACG	CGTCGTGTCGTCCGTTAGACAGTC
	3053	AGCTGTTAGGACCCGACAACCGGT	ACCGGTTGTGCGGTCTTAACAGCT
	3054	TTGCGTAGTGTGGGCATTTCCTCT	AGAGGAAATGCCACACTACGCAA
25	3055	ATGCGCGCTTCTTTCTTGATGTA	TACATCAAGGAAAGAAGCGCGCAT
	3056	TTAAGGGCGTCCGCGTCTATTCAG	CTGAATAGACGCGGACGCCCTTAA
	3057	ACCTTTAACTTGTACCGCGGCCC	GGGCCGCGGTACAAGTTAAAGGT
	3058	AGGGATGCAGAGGCACCACATGTT	AACATGTGGTGCCTCTGCATCCCT
	3059	CGGTTGACGTATGAGCATCCGCA	TGCGGATGCTCATACGTCGAACCG
30	3060	CAGGGCGATAGTCACATGGAGGTT	AACCTCCATGTGACTATCGCCCTG
	3061	GCTTGACTGCCCCGTTTCATATGT	ACATATGAAACGGGGCAGTCAAGC
	3062	CGAAGGGGTTGTGCAATTACCCGA	TCGGGTAATTGCACAACCCCTTCG
	3063	AAAACGCACCGCAATGACAAAATT	AATTTTGTGATTGCGGTGCGTTTT
	3064	ATTCCTGGACAAGACCCTCAACCG	CGGTTGAGGGTCTTGTCCAGGAAT
35	3065	CCTACCTGCCTGCTAGCGGTGAGG	CCTACCGCTAGCAGGCAGGTAGG
	3066	GCTCGTAAATGGGGAGGAATTGGA	TCCAATTCCTCCCCATTTACGAGC
	3067	ACATGAAAACAGGCTCAATTGGGG	CCCCAATTGAGCCTGTTTTCATGT
	3068	GTTCCGCACATGGATTGAGGTCTC	GAGACCTCAATCCATGTGCGGAAC
	3069	GGCACCCAATACCACGAAGAAGAA	TTCTTCTTCGTGGTATTGGGTGCC
40	3070	AGGGGCATTTGAACTCCATCTTT	AAAGATGGAGTTCGAAATGCCCT
	3071	CATCATCACAAGGAACGTCGGTG	CACCGACGTTCCCTTTGTGATGATG

	3072	TAAAGACCCACCGTCAGCAGCAGC	GCTGCTGCTGACGGTGGGTCTTTA
	3073	CCCCAGGCGTAATGCACCACATAG	CTATGTGGTGCATTACGCCTGGGG
	3074	GCAGGTCTGAACGCTAGTGGTTGAA	TTCAACCACTAGCGTTCGACCTGC
5	3075	GGAACCTTAGGAGTTCACGTCGCCA	TGGCGACGTGAACTCCTAAGTTCC
	3076	GCAGATACGGCTAGCTGAGGTGGC	GCCACCTCAGCTAGCCGTATCTGC
	3077	CACAGGCCTAGAGCCTCGGCGTTC	GAACGCCGAGGCTCTAGGCCTGTG
	3078	GTTTTGCGCGCATGAGGTTCAATTA	TAATGAACCTCATGCGCGCAAAAC
	3079	TTGCGCCTGATGCCAGCAGTACTA	TAGTACTGCTGGCATCAGGCGCAA
10	3080	GATATCAGGCTTTCCCACTGCCGC	GCGGCAGTGGGAAAGCCTGATATC
	3081	TGCGCGGAGACGGAGATCTATGAA	TTCATAGATCTCCGTCTCCGCGCA
	3082	CATTGGTGTGGCTGAGAGTGGAC	GTCCACTCTCAGCCAACACCAATG
	3083	GTCGGCACTTGGGCACCATTAAATA	TATTAATGGTGCCCAAGTGCCGAC
	3084	ATCGATCGGTGTCTCACCACGGAG	CTCCGTGGTGAGACACCGATCGAT
	3085	CGTAGCCTTCCACCGTGTGATAG	CTATCGACACGGTGGAAAGGCTACG
15	3086	CGCTCTCCGTCTGAGGAAAAGGGG	CCCCTTTTCCTCAGACGGAGAGCG
	3087	TCGCCCCAGCCAAGGATATATTGC	GCAATATATCCTTGCGTGGGGCGA
	3088	TCTCTTGCAAGGAACTCTGCCGTC	GACGGCAGAGTTCCTTGCAAGAGA
	3089	GTCCTGGACAGACGGAGGGTGTTA	TAACACCCTCCGTCTGTCCAGGAC
	3090	GCCAAATTAAGCGGGCTCGTAATC	GATTACGAGCCCCTTAATTTGGC
20	3091	CCATTTGTTGACCGATGGGAGGGG	CCCCTCCCATCGGTCAACAAATGG
	3092	TGGTCAAAAGAGCACGATCCAGGA	TCCTGGATCGTGCTCTTTTGACCA
	3093	CGCTACTAAGACGCCCTGTCCAC	GTGGACAGGGGCGTCTTAGTAGCG
	3094	CATACCTCCCGCTTGGAATCACTG	CAGTGAATCCAAGCGGGAGGTATG
	3095	CCGCGGAAGGAATGTCATCTACAA	TTGTAGATGACATTCTTCCGCGG
25	3096	CACGGGACATTCATTACAGGACG	CGTCCTGTGAATGAATGTCCCGTG
	3097	AGGAGTCACCACTCCGCACAAAA	TTTTGTGCGGAGTGGGTGACTCCT
	3098	TCATGACAGCGCACCCCATACCAT	ATGGTATGGGGTGCGCTGTCATGA
	3099	GGTAGGGGACTATCGATCGTGCTG	CAGCACGATCGATAGTCCCTACC
	3100	ATGTCTCACTACCGCACGTAGCGG	CCGCTACGTGCGGTAGTGAGACAT
30	3101	ACGGAGGAGCGACTCGTTCGCTGC	GCAGCGAACGAGTCGCTCCTCCGT
	3102	GAAGTCTGTGCGCGGTGGACGGAC	GTCCGTCCACCGGCGACAGACTTC
	3103	CCGTAACGTGTATTTCGGACGAGCG	CGCTCGTCCGAATACACGTTACGG
	3104	CGTGGAAGCGACTTAACCAATCGT	ACGATTGGTTAAGTCGCTTCCACG
	3105	GGCATGGGCTATGCCTCACACTAG	CTAGTGTGAGGCATAGCCCATGCC
35	3106	GGGTCGTATTTACGATCGTTTCGT	ACGAACGATGCTGAAATACGACCC
	3107	AATGGTCGCGCAAACCGTAAGAAT	ATTCTTACGGTTTTCGCGACCAAT
	3108	CTGGATTTCGGTACGTCCAACGTTT	AAACGTTGGACGTACCGAATCCAG
	3109	CGCAAAAACACCCGTAGCCAAGAA	TTCTTGGCTACGGGTGTTTTGCG
	3110	TATGGATACGCTTTTGGACTGGGC	GCCCAGTCCAAAAGCGTATCCATA
40	3111	GCTTCAAACGCGCTTACGCTGGT	ACCAGCGTGAAGCGCGTTTGAAGC
	3112	TACAGCCCGCTCTACCTCGCCACC	GGTGGCGAGGTAGAGCGGGCTGTA

	3113	TCAACCGATGTCAAAATGCACGTT	AACGTGCATTTTGACATCGGTTGA
	3114	AGCTCTCTCCGAAGTAGGGCGGTA	TACCGCCCTACTTCGGAGAGAGCT
	3115	ACGCACACATGGAGACTTGGCTCC	GGAGCCAAGTCTCCATGTGTGCGT
5	3116	TTCTTGAAAGCTAGTGGGGCGCTA	TAGCGCCCCACTAGCTTTCAAGAA
	3117	CAATCACGGCTGGGCTATTCTGTG	CACAGAATAGCCCAGCCGTGATTG
	3118	GTGGCGACCCGTCGGTGAAAGAGT	ACTCTTTACCGACGGGTCGCCAC
	3119	CGTCGAATGCCGAACCAAGTTAAGT	ACTTAAGTGGTTCGGCATTTCGACG
	3120	TGCGTATTTGCATGCTCACAGCTG	CAGCTGTGAGCATGCAAAACGCA
10	3121	CGCAGTTGGTTTGTGCACGGCTGC	GCAGCCGTGCACAAACCAACTGCG
	3122	GTTTTTCCGTGAAAAGTGGCATCG	CGATGCCAGTTTTACGGAAAAAC
	3123	ACAGGTTCTCCACCACGATTTGA	TCAAATCGTGGTGGAGGAACCTGT
	3124	CTAGCGCGCTTTTAGGTCCTTGCG	CGCAAGGACCTAAAAGCGCGCTAG
	3125	CAAAATCAAAGGGATCAACCGGTG	CACCGGTTGATCCCTTTGATTTTG
	3126	AACGTAACCCAGTGAGTCAGGCA	TGCCTGACTCACTGGGGTTACGTT
15	3127	TCAACCGGTGCACCTTTAGAAGGCC	GGCGTTCTAAAGTGCACCGGTTGA
	3128	ATCGCAAAGTTGCAGGCGAATACT	AGTATTGCGCTGCAACTTTGCGAT
	3129	ATATGTCCCTGGGTGCTGCACAAC	GTTGTGCAGCACCCAGGGACATAT
	3130	TGGCACTTTGTAGTGCTGCGGTGG	CCACCGCAGCACTACAAAGTGCCA
20	3131	ACGCACGACGTCCTTCTAAGCTCG	CGAGCTTAGAAGGACGTCGTGCGT
	3132	CCCACGTGCACTATAGGGATTTTCG	CGAAATCCCTATAGTGCACGTGGG
	3133	CCGCGCTTGGTCAGTCATCCTTGC	GCAAGGATGACTGACCAAGCGCGG
	3134	AGCGGCTCAGGGAATAACAACAGG	CCTGTTGTTATTCCCTGAGCCGCT
	3135	ACAACGCGATCGGAGGCAACCAGT	ACTGGTTGCCTCCGATCGCGTTGT
	3136	AGCAATTGCCTCCGTAGAAACCCA	TGGGTTTCTACGGAGGCAATTGCT
25	3137	GAGTCGTGGCATCGCCTGCTATCG	CGATAGCAGGCGATGCCACGACTC
	3138	TCTATGCAAATACTGCGCTTGCGA	TCGCAAGCGCAGTATTTGCATAGA
	3139	TCAGCTTAAGTTACGGTGTGGCCG	CGGCCACACCGTAACTTAAGCTGA
	3140	TCCAAGGTCGAACAGGGATCAGAA	TTCTGATCCCTGTTGACCTTGGA
	3141	GTTAGGCTGGCGTCAATAGCGCTT	AAGCGCTATTGACGCCAGCCTAAC
30	3142	GGTGTGATAAGGAAGAGGGCATCG	CGATGCCCTCTTCCTTATGACACC
	3143	CCGGCGGGCTAGATCAATATTTCT	AGAAATATTGATCTAGCCCGCCGG
	3144	CTAACGTCAAGTTTTACGCCCGGA	TCGGGGCGTAAAAGTTGACGTTAG
	3145	GCAGCACAGTTTTCCGATTTGCGG	CCGCAAATCGGAAAAGTGTGCTGC
	3146	CGCACGCAAGGGGAGGGATGACTG	CAGTCATCCCTCCCCTTGCGTGCG
35	3147	CGGGGCCGAAAAGGACGTCACAAG	CTTGTGACGTCTTTTCGGCCCCG
	3148	TTCTCCAACACGGCTAACCGGTAG	CTACCGGTTAGCCGTGTTGGAGAA
	3149	TTACAGCCTGGCCCCGAGGTAGTTG	CAACTACCTCGGGCCAGGCTGTAA
	3150	TTTCGGGCAGCATGAGTTATCGAA	TTGATAACTCATGCTGCCCGAAA
	3151	CTACTGGACGCCCTGCTTCGAAGT	ACTTCGAAGCAGGGCGTCCAGTAG
40	3152	GGTCGTCCGACGTGAAAAGACCAA	TTGGTCTTTTCACGTCCGACGACC
	3153	GTTTTCGAGCTCTTTCTCCGCAGG	CCTGCGGAGAAAGAGCTCGAAAAC

5

10

15

3154	GCGTGAAGGTACCCAGTGTCACAG	CTGTGACACTGGGTACCTTCACGC
3155	TTTCTGAACGCTTCGACGCAACAC	GTGTTGCGTCGAAGCGTTCAGAAA
3156	TGCTAATAAGCACGCCTAGCCCGT	ACGGGCTAGGCGTGCTTATTAGCA
3157	AAATTAATTGTGGTGGCTCCGGCG	CGCCGGAGCCACCACAATTAATTT
3158	TTACAATCCTCGGGCTCACTGACA	TGTCAGTGAGCCCGAGGATTGTAA
3159	GCTGAAGGACAAGGCGTGGGCAAC	GTTGCCACGCTTGTCCTTCAGC
3160	GGGATAGGAGACCCTCGCAATGGT	ACCATTGCGAGGGTCTCCTATCCC
3161	TTGCAGTACGTCCTTGCGCATGAA	TTCATGCGCAAGGACGTACTGCAA
3162	TTGATCACTGGATTGGGTGCGAAC	GTTGCGACCCAATCCAGTGATCAA
3163	TCTGCAGACGTTGCGAGAGATGAT	ATCATCTCTCGCAACGTCTGCAGA
3164	AGTCTAGCAGGGATCGAAGCGGAT	ATCCGCTTCGATCCCTGCTAGACT
3165	GGGGTCCCGCAACAATAATGAAG	CTTCATTAGTTGTTGCGGGACCCC
3166	CAACCTCTTATGTGGTGTGCGCGA	TCGCGCACACCACATAAGAGGTTG
3167	CTCGCTGGGTTGCTGGAGTAGCAC	GTGCTACTCCAGCAACCCAGCGAG
3168	CGTTGTATTGTGCAACGCGAAGTT	AACTTCGCGTTGCACAATACAACG
3169	GGGCTCAAAGTGCCTGAGTCGAAA	TTTCGACTCAGGCACCTTTGAGCCC
3170	CTGCTGTGCCCTCTCAGTGAGAGC	GCTCTCACTGAGAGGGCACAGCAG
3171	CGGACGTA CTGTTGCGAGTCCTCA	TGAGGACTCCGAACAGTACGTCCG
3172	GTATACCACCATACCGGGACCGCA	TGCGGTCCCGGTATGGTGGTATAC

TABLE 3

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
17	TTCGCCGTCGTGTAGGCTTTTCAA	TTGAAAAGCCTACACGACGGCGAA
18	GTTCCCAAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTTCAAGGACACCGGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGGTTCATTGACCGTTC
22	GCGGCCTTGGTTCAATATGAATCG	CGATTCATATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTCTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TTCGTCACTGCCGGAAGTGTCCA
25	ATAAACTACCCAGGACGGGCGGAA	TTCCGCCCGTCTGGGTAGTTTAT
26	CATCGGTTGCGCCAATCCAGATA	TATCTGGATTGGCGCAACCGATG
27	GTCGGGCATAGAGCCGACCACCT	AGGGTGGTGGGCTCTATGCCCGAC
28	CTTGGGTCATGATTACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTGGAGGCGTCCCACT	AGTGTGGGACGCCTCAAACAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTCTTGGTCA
34	GACATCGCTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTTT
36	TGTCATGAATGATTGATCGCGCGA	TCGCGCGATCAATCATTATGACA
37	ATATCGGGATTTCGTTCCCGGTGAA	TTCACCGGGAACGAATCCCGATAT
38	GCGAGCGTACCGAAGGGCCTAGAA	TTCTAGGCCCTTCGGTACGCTCGC
39	TTACCGGCAGCGGACTTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAACCTATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGCGCGTAGTGATGTACC
44	AATTCATCTCGGACTCCCGCGGTA	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCCTGCCAATCCAGATTTGGC
46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
51	CCAACAACCTGGAACGGGAACCCGC	GCGGGTTCCCGTTCCAGTTGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC

54	TCACATCCAAATATGGTCCGCGAA	TTCGCGGACCATATTTGGATGTGA
55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTACACCGGCAGAC
56	CATCGCAGAGCATAAACACCCTCA	TGAGGGTGTATGCTCTGCGATG
57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
62	CACCGCGGTGTTCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
64	TTAACCTGCGTCTGCCCCTTTCCT	AGGAAAGGGGCAGACGCAGGTTAA
65	AGGCGCGTTCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
67	TGCATAGAGCCAAAGTCGGCGATG	CATCGCCGACTTTGGCTCTATGCA
68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCTCTCAA
69	TCCGCATTGTGAGAAAAACGAGC	GCTCGTTTTTCTCACAATGCGGA
70	GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAACCGCC
71	GGTGAAAATTCGTAGCCACGGGC	GCCCGTGGCTACGAAATTTTACC
72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCTCCGTGCG
73	CCAGTTTGGCCCAATTCGCCAAAA	TTTTGGCGAATTGGGCCAAACTGG
74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCCTAATAGATCC
75	CGGATGTCACCGTTTGGACTTTCA	TGAAAGTCCAAACGGTGACATCCG
76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTTGCGAT
77	CAGGGCATGCAATAATCGAGGTTT	GAACCTCGATTATTGCATGCCCTG
78	CATGCGTTGATATATGGGCCCAAG	CTTGGGCCCATATATCAACGCATG
79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
80	TTGTATGTCTGCCGACCGGCGACC	GGTCGCCGGTCGGCAGACATACAA
81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
82	ATGAGAATCGCCGGCAATCTGCTA	TAGCAGATTGCCGGCGATTCTCAT
83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTCAGTGCAAAT
84	CAGGGAGAACGGTTAAGTTCCCGT	ACGGGAACCTTAACCGTTCTCCCTG
85	AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACCTCTCGATCGCCGGCCT
86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCTCGGCGTTGCAC
88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
89	TGAAATACCACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTTCA
90	GCATCGTGTACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
91	CAGTGTCTAACGGCGCGCGTGAA	TTCACGCGCGCCGTTAGAACACTG
92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
93	CGAAAACTAGTGGGCTCGCCGCG	CGCGGCGAGCCCACTAGTTTTTCG
94	CTTTCAGGGGAAC TGCCGGAGTCG	CGACTCCGGCAGTTCCCCTGAAAG

5	95	TTGTGGCCTTCTTGTAAGGCACG	CGTGCCTTTACAAGAAGGCCACAA
	96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTCGCCGTTTCGTGGA
	97	CGACCTTGCACGAAACCTAACGAG	CTCGTTAGGTTTCGTGCAAGGTCG
	98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
	99	CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTTCGCACGAAAGCG
	100	TGCGCTTACAGGCTCCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
	101	CACGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAAGCGCGTG
	102	CGGAGGGAGGGAGCTAGCCTTCGA	TCGAAGGCTAGCTCCCTCCCTCCG
10	103	GCATCCGGCCTGTTGATGACGCCT	AGGCGTCATCAACAGGCCGGATGC
	104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
	105	CCTTCCAATGATTGCATACGCCA	TGGGCGTATGCAATCATTGGAAGG
	106	AACACTTGATCAGGCGGGTCGTCT	AGACGACCCGCTGATCAAGTGTT
	107	TGGAATCAAGGCCGTAAAGGACAG	CTGTCCTTTACGGCCTTGATTCCA
	108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
15	109	AGTGGTGAATGGCCGCTACCCTGA	TCAGGGTAGCGGCCATTCACTACT
	110	TGTTGAAGCGAGCTAAAACGGCCA	TGGCCGTTTTAGCTCGCTTCAACA
	111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
	2	TTCGAAGCGCACGTCCCTTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
	3	AACGCGTGGGGAATGGGACATCAA	TTGATGTCCATTCCCCACGCGTT
20	114	CACGAGATACCGGCGTAAGGGTGG	CCACCCTTACGCCGGTATCTCGTG
	115	CTACGGCAAACGTGTGGAATGGGT	ACCCATTCCACACGTTTGCCGTAG
	116	GTAGGGCGATGACGGGCGAAGTAC	GTAGTTCGCCCGTCATCGCCCTAC
	117	AATCGACCTCCGCACACATTTCGA	TGCGAATGTGTGCGGAGGTTCGATT
	118	GAGTCAGCATGGCGGCGGAGATTC	GAATCTCCGCCGCCATGCTGACTC
25	119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTTGCCAGCGTCTTTATCT
	120	GGTACCTCAACGCGAACCCTTGT	ACAAGTGGTTCGCGTTGAGGTACC
	121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
	122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
	123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCTGCGTGAGACCGAT
30	124	TAGGTTGCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
	125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
	126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGCAAATTTTCATCA
	127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
	128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
35	129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC
	130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTACGGGGACCAGCTCGA
	131	GTCTTGGGGGCCGCTTAGTGAAAA	TTTTCACTAAGCGGCCCCCAAGAC
	132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
	133	AGGACCATTGGAAGGCGAAGATA	TATCTTCGCCTTCCGAATGGTCCT
40	134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
	135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCGGTTTATT



5	136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
	137	CGCACCAAAGTGAAGTTTCCAGAC	GTCTGGGAAAGTCAAGTTTGGTGCG
	138	ACCTGATCGTTCCCTATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
	139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCCTCGCCTCTGTTCC
	140	CCCTGCCTTGGCGTGTGCGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGAGATTGGCGTGTGAGAGT
	142	CTGACGGTTTTTCATTGCGCGTGCC	GGCACGCCGAATGAAAACCGTCAG
	143	TGCGGTGGTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
10	144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
	145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTGCTTTACGGCCT
	146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTG
	147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
	148	GGACGGTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
15	149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
	150	GATGGCCTATTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
	151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
	152	AATAACTCGCGCGGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
	153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
	154	CTTTGGTATGGCACATGCTGCCCC	CGGGCAGCATGTGCCATACCAAAG
20	155	AGAAAGGCTCGAGCAACGGGAACT	AGTTCCCGTTGCTCGAGCCTTTCT
	156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAGTGCGGTAGATT
	157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAAGTGTGGCCGCCACG
	158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
	159	GGCCCAAAGCCCCAGACCATTTTA	TAAATGGTCTGGGGCTTTGGGCC
25	160	CGCCTGTCTTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG
	161	TGAGGCAACAGGGGCCAAAAGTAA	TAGTTTTTGGCCCCTGTTGCCTCA
	162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
	163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
	164	GCACGTGAAGTTTAAACCGCATTC	GAATCGCGGTTAAACTTCACGTGC
30	165	AGCGGCAGAAACGTTCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
	166	TCGTCGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
	167	TCTTTGCCGCGTAAGTACTGCTT	AAGCAGTCAGTTACGCGCAAAGA
	168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCTTGGCACATAAA
	169	TGTTACTGTGGTTCACGGCAGTCC	GGAAGTCCGTGAACCACAGTAACA
35	170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
	171	ACAAATGCGTGAGAGCTCCCAACT	AGTTGGGAGCTCTCACGCATTTGT
	172	CGCGCAGATTATAGACCCGAATGT	ACATTCGGGTCTATAATCTGCGCG
	173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTACGCGCGTATTG
	174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
40	175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTGCTCGTGTTC
	176	CAGCAGATCCTTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG

	177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACTCACCAGGTTCC
	178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTGCGTTATGA
	179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
	180	TGTCAGAGCCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
5	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182	CTCAGAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
	183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCGCGGAGTAGATAAAAGGAT
	184	AGGCGTGACGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
	185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
10	186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
	187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCGAGTTATAGTGGA
	188	GCCCAGTCGGCTCTAACAAGTTCG	CGAACTTGTTAGAGCCGACTGGGC
	189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
	190	TAAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
15	191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
	192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAAC
	193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
	194	TTCGCAGCACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTGCTGCGAA
	195	TAACCCGATTTTTGCGACTCTGCC	GGCAGAGTCGCAAAAATCGGGTTA
20	196	CGTCGATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
	197	GAGCTGACGTACCATCAGAGGAA	TTCTCTGATGGTGACGTCAGCTC
	198	GGAGGCTGGGGGTGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
	199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCACAA
	200	CCCTCGCACTGTGTTACCCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
25	201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA
	202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
	203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
	204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
	205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTCGTTTCATGTCCGCGC
30	206	CTTATTGGGTGCCGGTGTGCGGATT	AATCCGACACCGGCACCCAATAAG
	207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTTGGTAACCGCCCC
	4	CCGTGCGATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
	5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
	210	ACGAAAAAAGTGTGCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
35	211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTACTTGG
	212	ATCGTGCGTGGAGTGTGCGCATCTA	TAGATGCGACACTCCACGCACGAT
	213	TCCAGATACCGCCCCGAACTTTGA	TCAAAGTTCGGGGCGGTATCTGGA
	214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
	215	TTGAAATTGCTCTGCCGTCAGTCA	TGACTGACGGCAGAGCAATTTCAA
40	216	AGTCAGGCGAGATGTTTCAGGCAGC	GCTGCCTGAACATCTCGCCTGACT
	217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGGCTTAACGTGCGCTTGT

5	218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
	219	GTGAGACACACATCCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
	220	CGACGGATGCAGAGTTCAGTGGTC	GACCACTGAACTCTGCATCCGTCG
	221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
	222	TTAGCAAAGCGGCGCCGTTAGCAA	TTGCTAACGGCGCCGCTTTGCTAA
	223	CCCGACACGGGTCAGCGTAATAAT	ATTATTACGCTGACCCGTGTCTGGG
	224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
	225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
10	226	TCTCGAAGCACAGCCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
	227	ATGCTAACCGTTGGCCATGGAAT	AGTTCCATGGCCAACGGTTAGCAT
	228	CTTGCGGAGTGTTAGCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
	229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
	230	CCAATGCCTTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
	231	AGCAGATAACGTCCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
15	232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGCAACACGTAATGGTCAA
	233	TCGCGTATTTGCGGAATTCGTCTG	CAGACGAATTCGCAAATACGCGA
	234	CTGCGTGTCAACAATGTCCCGCAG	CTGCGGGACATTGTTGACACGCAG
	235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCGTGGCACCAGA
	236	CTCCGGGAGGTCACCTTAATTGCGG	CCGCAATTAAGTGACCTCCCGGAG
20	237	TTTTCGTGATTGCCCGGAGGAGGC	GCCTCCTCCGGGCAATCACGAAAA
	238	TCGGGATGTAGCTGGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
	239	CGAGCCAACGCAAACACGTCCCTG	CAAGGACGTGTTTGCCTTGGCTCG
	240	GCAAAGCCTTTGTGGGGCGGTAGT	ACTACCGCCCCACAAAGGCTTTGC
	241	ATTCGACCGGAAATGAGGTCTTCG	CGAAGACCTCATTTCCGGTCGAAT
25	242	TTGCTTGCTGAGTTGCTCTGTTT	GAACAGAGCAACTCAGCAAGCGAA
	243	CGCGTGAAGACCCCATTCGCGAGT	ACTCGGGAATGGGGTCTTCACGCG
	244	AACCGTATTCGCGGTCACTTGTTG	CCACAAGTGACCGCGAATACGGTT
	245	GGGGCCAACCGTTTCGAGGCGTAT	ATACGCCTCGAAACGGTTGGCCCC
	246	TTGCGGTGGCAGTCCAAACGGCTT	AAGCCGTTTGACTGCCAGCCGAA
30	247	GGGTGTGGTTAGAATGCACGGTTC	GAACCGTGCAATTCTAACCACACCC
	248	GCGAGGACCGAACTAGACAAACGG	CCGTTTGTCTAGTTCGGTCTCTCG
	249	ACGCACGCGTGACCGAAGTTGCTG	CAGCAACTTCGGTCACGCGTGCGT
	250	TAAAAGGTCGCTTTGAAAGGGGGA	TCCCCCTTTCAAAGCGACCTTTTA
	251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTTAGCGATCGCA
35	252	GGAGGTATAAGCGGAGCGGCCTCA	TGAGGCCGCTCCGCTTATACCTCC
	253	ATGCTGACATGTCGTGACCTCGT	ACGAGGTGCACGACATGTCAGCAT
	254	TGTGGTTAAAGCGTCCGTTCAACG	CGTTGAACGGACGCTTTAACCACA
	255	CGTTCACACCGGCGTAAGCTGCGT	ACGCAGCTTACGCCGGTGTGAACG
	256	CCTATCCCGGCGAGAACTTCTGTG	CACAGAAGTTCTCGCCGGGATAGG
40	257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTGACAGAC
	258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC

259	AACGTCGCACGACACACGTTTCGTC	GACGAACGTGTGTCGTGCGACGTT
260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
261	TCACGTTTTCGTCTCGACATGAGG	CCTCATGTGCGAGACGAAAACGTGA
262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCCTAAGGATGAGGCACA
263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCACCT
264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGCAGTCCCTTCGATCCAG
265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
266	GATCCTGCGGAGAAGAGAGTGCAG	CTGCACTCTCTTCTCCGCAGGATC
267	TACGTGTGGAGATGCCCCGAACCG	CGGTTGCGGGGCATCTCCACACGTA
268	GCGCTATGTCAATCGTGGGCGTAG	CTACGCCCACGATTGACATAGCGC
269	AGCGAGGTTTCTAGCGTCGACACC	GGTGTGCGACGCTAGAAACCTCGCT
270	ACCCAGGTTTTGCCGTTGTGGAAT	ATTCCACAACGGCAAAACCTGGGT
271	CCCTGTTAACGGCTGCGTAGTCTC	GAGACTACGCAGCCGTTAACAGGG
272	AGGCCGATTTACCCGCCAATTGC	GCAATTGGCGGGTGAAATCGGCCT
273	GAGCCCTCACTCCTTGCCCTTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
274	GGGTGGACATCCGCCCTCGCAGTCA	TGACTGCGAGGCGGATGTCCACCC
275	GATGGCTGAGAACCGTGCTACGAT	ATCGTAGCACGGTTCTCAGCCATC
276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTCGA
277	CGAATGGGTCTGGACCTTGCTATAG	CTATGCAAGGTCCAGACCCATTTCG
278	GTGCACCAGACATTGCAACTCGGA	TCCGAGTTCGAATGTCTGGTGCAC
279	AGAGGCCCGGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
280	AACGCCTGTTCAAGCATCAGCGG	CCGCTGATGCTCTGAACAGGCGTT
281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTTGAGCCTT
282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTTACATGGGACAT
284	ATGGAGTCTGCTCACGCCCAAAGG	CCTTTGGGCGTGAGCAGACTCCAT
285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTTGTTGGAGGCCG
286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
287	TCATTTGAATGAGGTGCGCACCGG	CCGGTGCGCACCTCATTCAAATGA
288	GACGTACCGGAAGCGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
289	ATGCGAGCAATGGGATCCGGATTTC	GAATCCGGATCCCATTGCTCGCAT
290	AGAGTGAGGCCTCCCTGACCACTG	CACTGGTCAGGGAGGCCTCACTCT
291	CGCACCGTAAGTAGATTTGCCCGC	GCGGGCAAATCTACTTACGGTGCG
292	TGAACCTTTGAGCACGTGCTGCGC	GCGCACGACGTGCTCAAAGGTTCA
293	TCCGCCTTTTGGTTACCTCGAAG	CTTCGAGGTAACCAAAAAGGCGGA
294	GAACGCCAACGGCACTAACACATC	GATGTGTTAGTGCCGTTGGCGTTC
295	CCGACAGCAGCCAAGACGTCCCAG	CTGGGACGTCTTGGCTGCTGTCGG
296	CATAAAAAACCTGGGGCTCTGCG	GCGAGAGCCCCAGTTTTTTTATG
297	TGCCAACTGTGCAGACCGGACTTA	TAAGTCCGGTCTGCACAGTTGGCA
298	GGCGAAAGAGCGAAACCGGCTCGT	ACGAGCCGGTTTCGCTCTTTTCGCC
299	GGGATGCGTATTTAGCGAACACG	CGTGTTGCTAAAATACGCATCCC

	300	TGGGATTCAGCGACCAGTACGCGA	TCGCGTACTGGTCGCTGAATCCCA
	301	CCCGATATTCGCCCCGGCCTATTTCG	CGAATAGGCCGGGCGAATATCGGG
	302	CGAGAAGATGCCTCACGCAACCAA	TTGGTTGCGTGAGGCATCTTCTCG
	303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
5	6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCGTTGCAA
	7	CGCATAGGTTGCCGATTTTCGTCAA	TTGACGAAATCGGCAACCTATGCG
	306	GCTTCCGGATGAACGGGATGGTTG	CAACCATCCCGTTCATCCGGAAGC
	307	CCCTCCATGTTCTTCGAACGGTTT	AAACCGTTTGAAGAACATGGAGGG
	308	TTGATGGGCGGCAATGCTCTTGCT	AGCAAGAGCATTGCCGCCCATCAA
10	309	ATTGTGAGATGCGCCAAATTCCCC	GGGGAATTTGGCGCATCTCACAAT
	310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
	311	ACTCCACTCCTCGGTGGCAAATA	TAGTTTGCCACCGAGGAGTGGAGT
	312	TCTGGGCATGCCTGGACGGAGACG	CGTCTCCGTCCAGGCATGCCCAGA
	313	TCTCAACTCCGTACGACGAAACA	TGTTTCGTTCGTACCGGAGTTGAGA
15	314	TTGCGTGGTCAAAGGCGCAACGTG	CACGTTGCGCCTTTGACCACGCAA
	315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGCGGATCGCTGTCT
	316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACGCG
	317	AGGCGCACATGTACGGACATTCAG	CTGAATGTCCGTACATGTGCGCCT
	318	GATGAGTGGCACGTGCGTGTGTAA	TTACACACCGACGTGCCACTCATC
20	319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
	320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
	321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAACGCCAATGCT
	322	GGTAATATTCAGCGCGACCGCTCA	TGAGCGGTTCGCGCTGAATATTACC
	323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
25	324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA
	325	ACTGCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGGCAGT
	326	CCTTTGGCCTGAAGTTGTCGTAGC	GCTACGACAACTTCAGGCCAAAGG
	327	GTGCCCCACGAGCGTATCGTTGTA	TACAACGATACGCTCGTGGGGCAC
	328	AGGCGCTACGTGGGCCTGGAGCAA	TTGCTCCAGGCCACGTAGCGCCT
30	329	GGGTGCTACCATTGCATTAGTCCG	CGGACTAATGCAATGGTAGCACCC
	330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGGT
	331	CCATGATGCATTGGGTGCATTTAG	CTAAATGCACCCAATGCATCATGG
	332	GGTCCGGCCCTACGAAACGTTTCA	TCGAACGTTTCGTAGGGCCGGACC
	333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGCCACACGG
35	334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
	335	GGGTGAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
	336	GCCGTGAAGTCGAATGCAGATCGA	TCGATCTGCATTGCACTTCACGGC
	337	GCCACCACCCAGTGCATTACGGTA	TACCTGAATGCACTGGGTGGTGGC
	338	GAGCTTAGTTTGCGGTATCGGGC	GCCCGATGACCGCAAACCTAAGCTC
40	339	TGTTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCAAACA
	340	GCTCCGCTGGATGTGCCGTTTAG	CTAAACCGGCACATCCAGCGGAGC

	341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTCGCATGCTACCG
	342	CTACGCTCTACCAGTTGCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
	343	GTGCCTCCTGCTGTATTTGCCAAG	CTTGGCAAATACAGCAGGAGGCAC
5	344	TTGCGACTCGACTTGGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
	345	TCTGGGAGCTGTTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
	346	TGCACGCGGAACCTCCCTTACCAT	ATGGTAAAGGGAGTTCCGCGTGCA
	347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTTCGATTCATTTGCTGCCA
	348	AACTGGTGACGCGGTACAGCGAAG	CTTCGCTGTACCGCGTCACCAAGTT
	349	AGACGATTACGCTGGACGCCGTCTG	CGACGGCGTCCAGCGTAATCGTCT
10	350	ATGCCCTCCTTCATGAAAGGGTT	AACCCCTTTCATGAAGGAGGGCAT
	351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATACGCTCCGAGAAT
	352	ATAGCGGAGTTTGGGTACGCGAAC	GTTGCGGTACCCAAACTCCGCTAT
	353	ACCTACGCATACCGCTTGGCGAGG	CCTCGCCAAGCGGTATGCGTAGGT
	354	GATTACCTGAATGGCCAAGCGAGC	GCTCGCTTGGCCATTCAAGTAATC
15	355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
	356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATCATTCCG
	357	TGAGAGAGGCGTTGGTTAAGGCAA	TTGCCTTAACCAACGCCTCTCTCA
	358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
	359	TCACGACAGACGGGCGGAGATTAC	GTAATCTCGGCCCCGTCTGTCGTGA
20	360	AAGCAATTTGGCCTCGTTTTGTGA	TCACAAAACGAGGGCCAAATTGCTT
	361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
	362	TTGTGAATCCGTTCTGTCCCCGAC	GTCGGGGACAGAACGGATTACAA
	363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTCGCCTCAGAGGAGCCCA
	364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTTCGATTCACTCTATCC
25	365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGACGTTTCGGTGCA
	366	GCCAGTATTCTCGGGTGTGGACG	CGTCCAACACCCGAGAATACTGGC
	367	TCGCTACCTAAGACCGGGCCATAC	GTATGGCCCGGTCTTAGGTAGCGA
	368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
	369	CGCGTCCCAGCGCCCTTGGAGTAT	ATACTCCAAGGGCGCTGGGACGCG
30	370	ATGAAGCCTACCGGGCGACTTCGT	ACGAAGTCGCCCGGTAGGCTTCAT
	371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCAGGCCATCTGTCTGG
	372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTTGAGATGGTCCCACGCCA
	373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
	374	GCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGGC
35	375	ATTACGGTCGTGATCCAGAAAGCG	CGCTTTCTGGATCACGACCGTAAT
	376	TGCGAGGTGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
	377	GGGCCGCATTCTTGATGTCCATTC	GAATGGACATCAAGAATGCGGCCC
	378	CCTCGGATGTGGGCTCTCGCCTAG	CTAGGCGAGAGCCCACATCCGAGG
	379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCTA
40	380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTTCGTATCG
	381	TACGCCGGTTAGCACGGTGCGCTA	TAGCGCACCGTGCTAACCGGCGTA

	382	CATACGATGTCCGGGCGGTGTCGC	GCGACACGGCCCGGACATCGTATG
	383	ATCCGCAGTTGTATGGCGCGTTAT	ATAACGCGCCATACAACCTGCGGAT
	384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATCTTTGTCCCTTACCC
5	385	ATTGGAGTGTTTTGGTGAATCCGC	GCGGATTCACCAAAACACTCCAAT
	386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTTT
	387	GCCGTCAAGCTTAAGTTTTGGGC	GCCCAAAACCTTAAGCTTGACGGC
	388	ACCTGCTTTTGGGTGGGTGATATG	CATATCACCCACCAAAAGCAGGT
	389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTTGCTGCGCCACGATT
10	390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
	391	ACCCGTCGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGGT
	392	ATCCGGGTGGGCGATAACAAGAGAT	ATCTCTTGATCGCCACCCGGAT
	393	TTCCGCATGAGTCAGCTTTGAAAA	TTTTCAAAGCTGACTCATGCGGAA
	394	GCAAAGTCCCACTGGCAAGCCGAT	ATCGGCTTGCCAGTGGGACTTTGC
	395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTCTG
15	396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAACCTGCGCTCATGAG
	397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
	398	TCAAAGGCTCTTGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTTGA
	399	TCCGCTAATTTCCAATCAGGGCTC	GAGCCCTGATTGGAAATTAGCGGA
20	8	CCGTTTGCGGTGCTCCTTGCTCAA	TTGAGCAAGGACGACCCGAAACGG
	9	TTGCTTTGCTGGCTGCACTTCAA	TTGAAGTGCAGCCACGAAAGCGAA
	402	CTTAGTTGGGCGCGGTATCCAGA	TCTGGATACGCGCCCCAACTAAG
	403	GCTCTAATGCCGTGGAGTCGGAAC	GTTCCGACTCCACGGCATTAGAGC
	404	CCGATTACAAATTGACTGACCGCA	TGCGGTCAGTCAATTTGTAATCGG
25	405	AGACGTACGTGAGCCTCCCGTGTC	GACACGGGAGGCTCACGTACGTCT
	406	AATGGAGCGATACGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT
	407	GGAGGCGCTGTACTGATAGGCGTA	TACGCCTATCAGTACAGCGCCTCC
	408	TGTTTTTGAATTGACCACACGGGA	TCCCGTGTGGTCAATTCAAAAACA
	409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
30	410	GCCCGCTAATCCGACACCCAGTTT	AAACTGGGTGTCGGATTAGCGGGC
	411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
	412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTCCGGTGATTC
	413	AACCAGCCGCAGTAGCTTACGTCTG	CGACGTAAGCTACTGCGGCTGGTT
	414	TTTTCTGAGGGACACGCGGGCGTT	AACGCCCCTGTGCCCTCAGAAAA
35	415	GGTGCTCCGTTTGATCGATCCTCC	GGAGGATCGATCAAACGGAGCACC
	416	CCGCTTAGGCCATACTCTGAGCCA	TGGCTCAGAGTATGGCCTAAGCGG
	417	TAAGACATACCGACGCCCTTGCTT	AGGCAAGGGCGTCGGTATGTCTTA
	418	GTTCCCGACGCCAGTCATTGAGAC	GTCTCAATGACTGGCGTCGGGAAC
	419	TAAAAGTTTCGCGGAGGTCGGGCT	AGCCCGACCTCCGCGAAACTTTTA
40	420	CGGTCCAGACGAGCTGAGTTCGGC	GCCGAACCTCAGCTCGTCTGGACCG
	421	CGGCGTAGCGGCTACGGACTTAAA	TTTAAGTCCGTAGCCGCTACGCCG
	422	GCTTGATGCCCATGCGGCAAGGT	ACCTTGCCGCATGGGCATCCAAGC

	423	AGCGGGATCCCAGAGTTTCGAAAA	TTTTCGAAACTCTGGGATCCCGCT
	424	GAGCTTGAGAGCGAGGTCATCCTC	GAGGATGACCTCGCTCTCAAGCTC
	425	GCATCGGCCGTTTTGACCATATTC	GAATATGGTCAAAACGGCCGATGC
	426	CATAGCGCTGCACGTTTCGACCGC	GCGGTGAAACGTGCAGCGCTATG
5	427	ACCCGACAACCACCAATTCAAAAA	TTTTGAATTGGTGGTTGTCGGGT
	428	GCGAACACTCATAAGAGCGCCCTG	CAGGGCGCTCTTATGAGTGTTCCG
	429	CCGCCGAGTGTAGAGAGACTCCGA	TCGGAGTCTCTTACACTCGGCGG
	430	GACATCGGGAGCCGGAACATGAG	CTCATGTTTCCGGCTCCCGATGTC
	431	TCGTGTAGACTCGGCGACAGGCGT	ACGCCTGTCGCCGAGTCTACACGA
10	432	ATGCGCATATACTGACTGCGCAGG	CCTGCGCAGTCAGTATATGCGCAT
	433	ACAAGCGAACCCGAGTTTTGATGA	TCATCAAAACTCGGGTTTCGTTGT
	434	GCATGAGACTCCGCGAAGACATGT	ACATGTCTTCGCGGAGTCTCATGC
	435	TCCTACATGTCGCGTCACGATCAC	GTGATCGTGACGCGACATGTAGGA
	436	GACCGATCGCGAAGTCGTACACAT	ATGTGTACGACTTCGCGATCGGTC
15	437	GTCGCCAGGACTGGGCCGATGTGA	TCACATCGGCCAGTCCTGGCGAC
	438	ACCGATAAGACTTGCATCCGAACG	CGTTCGGATGCAAGTCTTATCGGT
	439	TCCATAACCAGTCCGAAGTGCCGG	CCGGCACTTCGGACTGGTTATGGA
	440	ACGCGCCCTGCATCTCGTATTTAA	TTAAATACGAGATGCAGGGCGCGT
	441	AGACCGCATCAATTGGCGCGTACC	GGTACGCGCCAATTGATGCGGTCT
20	442	AGAGGCTTGCGAAGTAGGGACCCT	AGGGTCCCTACTTGCCAAGCCTCT
	443	GCAATGGACGCCAGACGATACCGG	CCGGTATCGTCTGGCGTCCATTGC
	444	GCTGGACTTAGTCGTGTTCCGGCGG	CCGCCGAACACGACTAAGTCCAGC
	445	AGGCATCGTGCCGGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCCT
	446	TGCGCATGTCGACGTTGAACAAAG	CTTTGTTCAACGTCGACATGCGCA
25	447	TTCGGGTCACATCCGATGCCATAC	GTATGGCATCGGATGTGACCCGAA
	448	ACCCATCGCCGGAAGCGATGTTG	CAACATCGCTTTCGGCGATGGGT
	449	AAGCGCTGACTCGGCTAAGAATCA	TGATTCTTAGCCGAGTCAGCGCTT
	450	ACTTCCAAGTCCTTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAAGT
	451	TCTCAATATTCGCGTAGTCGCCCA	TGGGCGACTACGGGAATATTGAGA
30	452	AACAGTTCCTCTTTTTCTGGCGC	GCGCCAGGAAAAAGAGGAACTGTT
	453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCTGTGACAACATGGAGGACG
	454	TGCGCAGACCTACCTGTCTTTGCT	AGCAAAGACAGGTAGGTCTGCGCA
	455	ATGGACGGCTTCGCAGTCCTCCTT	AAGGAGGACTGCGAAGCCGTCCAT
	456	TGAACGCTTTCTATGGGCCACGTA	TACGTGGCCCATAGAAAGCGTTCA
35	457	TGAACCCTGCCGCGAGCGATAACC	GGTTATCGCTCGCGGCAGGGTTCA
	458	GTTCTTGCGCGATGAATCAGGACC	GGTCCTGATTCATCGCGCAAGAAC
	459	AGGGTACGTGTCGAGCTTCGCGT	ACGCGAAGCTGCGACACGTACCCT
	460	ACCCTTGCTCCGCCATGTCTCTCA	TGAGAGACATGGCGGAGCAAGGGT
	461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTTCAATCCTTGTCCT
40	462	TGTCGTTGCTCCCGAGTACCATTG	CAATGGTACTCGGGAGCAACGACA
	463	GTTGTCCGAGACGTTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC



	464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTTCGTGAGTGTTACCAGC
	465	GCAGACAGGGCAAATCGGTGCAAA	TTTGCACCGATTGCCCCTGTCTGC
	466	CCCATCACAACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
	467	GCTTCTACAGCTGGCGTGCTAGCG	CGCTAGCACGCCAGCTGTAGAAGC
5	468	GAATGTGTGCCGACCATTCTAGCC	GGCTAGAATGGTCGGCACACATTC
	469	CCAGCGGAAGTTAGAGCTCTGTGG	CCACAGAGCTCTAACTCCGCTGG
	470	TTTTTACCGACCACTCCATGTCGG	CCGACATGGAGTGGTCGGTAAAA
	471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTCATCACATAGCCGC
	472	AGTACACGGGCGTGTTAGCGCTCC	GGAGCGCTAACACGCCCGTGTACT
10	473	TCCTGTGTGGTGGCGCACTCCCAC	GTGGGAGTGCGCCACCACACAGGA
	474	CCAACTAACCAATCGCGCGGATGA	TCATCCGCGCGATTGTTAGTTGG
	475	AGTGAGTGACCAAGGCAGGAGCAA	TTGCTCCTGCCTTGGTCACTCACT
	476	CATCTTTCGCGGAGTTTATTGCGG	CCGCAATAAACTCCGCGAAAGATG
	477	CTTCGTCCGGTTAGTGCGACAGCA	TGCTGTGCGACTAACCGGACGAAG
15	478	CTCACGAAAACGTGGGCCCGAAAT	ATTTCCGGGCCCACGTTTTCTGTAG
	479	CGCAGCAGCTGAACTCTAGCATTG	CAATGCTAGAGTTCAGCTGCTGCG
	480	AGGAGACATACGCCCAAATGGTGC	GCACCATTGTTGGCGTATGTCTCCT
	481	ATTGAGAACTCGTGCGGGAGTTTG	CAAACCTCCGCGACGAGTTCTCAAT
	482	CTCTTTGTAGGCCCAGGAGGAGCA	TGCTCCTCCTGGGCCTACAAAGAG
20	483	GCCGCAGGGTCGATAATTGGTCTA	TAGACCAATTATCGACCCTGCGGC
	484	AAACGCCGCCCTGAGACTATTGGG	CCCAATAGTCTCAGGGCGGCGTTT
	485	CTGAGTTGCCTGGAACGTTGGACT	AGTCCAACGTTCCAGGCAACTCAG
	486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
	487	CTGACCTTTGGGGGTTAGTGCGGT	ACCGCACTAACCCCCAAAGGTCAG
25	488	GGAAATGAGAACCTTACCCAGCG	CGCTGGGGTAAGGTTCTCATTTCC
	489	AACGCATCGTCCGTCAACTCATCA	TGATGAGTTGACGGACGATGCGTT
	490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCCCA
	491	TTGCGCTCATTGGATCTTGTCAGG	CCTGACAAGATCCAATGAGCGCAA
	492	AGCGCGTTAAAGCACGGCAACATT	AATGTTGCCGTGCTTTAACGCGCT
30	493	AGCCAGTAACTGTGGGCGGCTGT	ACAGCCGCCACAGTTTACTGGCT
	494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
	495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
	10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
	11	TTGCCGCACCGTCCGTCTCTCAA	TTGAGATGACGGACGGTGCGGCAA
35	498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCGCGGAGGTTCT
	499	AAAGGAGCTTTCGCCCAACGTACC	GGTACGTTGGGCGAAAGCTCCTTT
	500	AGTGATTGTGCCACTCCACAGCTC	GAGCTGTGGAGTGGCACAATCACT
	501	GCGATCGTCGAGGGTTGAGCTGAA	TTCAGCTCAACCCTCGACGATCGC
	502	GGGAGACAGCCATTATGGTCCTCG	CGAGGACCATAATGGCTGTCTCCC
40	503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTGCCGGAGTGACAGCGTCTC
	504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG

5

10

15

20

25

30

35

40

505	CGGCATAACGTCCAGTCCTGGGAC	GTCCCAGGACTGGACGTTATGCCG
506	AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
508	AGGGAACCGCGTTCAAACCTCAGTT	AACTGAGTTTGAACGCGGTTCCCT
509	GAATTACAACCACCCGCTCGTGTT	AACACGAGCGGGTGTTGTAATTC
510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
511	TTAGTTTGGCGTTGGGACTTCACC	GGTGAAGTCCCAACGCCAAACTAA
512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCCACGTTAACGGTTTCGG
514	TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTCGCCTTGTTACTTTA
515	TAATGATTTTAGTCGCGGGGTGGG	CCCACCCCGCGACTAAATCATTAA
516	GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCCGCCA
518	GGGCGTTAGGCGTAATAGACCGTC	GACGGTCTATTACGCCTAACGCCC
519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCGCTCTAAAGGTGGC
520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTTACACATCTC
521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGAGGGGCCACGAGCTA
522	GTGTCGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
523	CCAGGGAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTTCCCTGG
524	TTCCGAAACTAAGCCAGAACCGCT	AGCGGTTCTGGCTTAGTTTCGGAA
525	GCAAACCCGGTAACCCGAGAGTTC	GAAGTCTCGGGTTACCGGGTTTGC
526	GCAAATGGCGTCATGCACGAACGT	ACGTTCTGTCATGACGCCATTTGC
527	AGTACTTTTCGCGCCAGTTTAGGG	CCCTAAACTGGGCGCGAAAGTACT
528	AAGATCTGCGAGGCATCCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
529	GCAAGTGTATCGCACAGTGCGATT	AATCGCACTGTGCGATACACTTGC
530	CCGACAAGGCCTCAATTCATTCTG	CAGAAATGAATTGAGGCCTTGTCGG
531	GTCTCGTCTCAACTTTAAGGCGCG	CGCGCCTTAAAGTTGAGACGAGAC
532	ATCCAGAGATCCGTTTTGCAGCGT	ACGCTGCAAAACGGATCTCTGGAT
533	GTCACCAGGAGGGAAGTTTCACCC	GGGTGAAACTTCCCTCCTGGTGAC
534	TTCCGTCAGGCGGATCAACGGAAT	ATTCCGTTGATCCGCCTGACGGAA
535	ATGCCGGACACGCATTACACAGGC	GCCTGTGTAATGCGTGTCGGCAT
536	TGGGCCGCTTGGCGCTTTCATAGA	TCTATGAAAGCGCCAAGCGGCCCA
537	CCTAGCGCGAGCTTTACTGACCAG	CTGGTCAGTAAAGCTCGCGCTAGG
538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATATTCTGGCCAA
539	GTCTGCGGCCGACTTGCTATGCAT	ATGCATAGCAAGTCGGCCGCAGAC
540	AACTTGCTCATTCTCAAGCCGACG	CGTCGGCTTGAGAATGAGCAAGTT
541	ACGTCAGCGATTGTGGCGAAATAT	ATATTTTCGCCACAATCGCTGACGT
542	ACGGCCTGCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
543	ATACCTCCGCAGAACCATTCGGTT	AACGGAATGGTTCTGCGGAGGTAT
544	AGTTCGCGGTCCCACGATTCACTT	AAGTGAATCGTGGGACCGCGAACT
545	TGCTCAATTTGTGCAGAAAACGCC	GGCGTTTTCTGCACAAATTGAGCA

546	TTATCGCGAGAGACGACCGTGTC	GGACACGGTCGTCTCTCGCGATAA
547	GACGCGACGTGAGTAGTGAAGCG	CGCTTCCACTACTCACGTCGCGTC
548	ATGGTAGGGGCATTGGGCTTTCCT	AGGAAAGCCCAATGCCCCCTACCAT
549	CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGCTATATTTGG
550	GCAAACCCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
551	TAGCGTCTTGCGTGAAACCATGGG	CCCATGGTTTCACGCAAGACGCTA
552	CCACCCCGACAGCGCTGGACTCTT	AAGAGTCCAGCGCTGTCGGGGTGG
553	ACGAGCACTGAAGGCTGCTTTACG	CGTAAAGCAGCCTTCAGTGCTCGT
554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTGCGGGGCC
557	GGCTCCAGGGCGAGATTATGAATG	CATTCATAATCTCGCCCTGGAGCC
558	CAAAATCCGATGGGCGGAAATTA	TAATTTTCCGCCCATCGGATTTTG
559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
560	TAGCTATTGCCCGATGGGCTACT	AGTAGCCCATCGGGGCAATAGCTA
561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
562	GACGCTGTGGCTCGGAAACTGTTT	GAACAGTTTCCGAGCCACAGCGTC
563	CCTGGGTTGCGCGCGTGGAAGTCTG	CAGTTACCACGCGGCGAACCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
565	TTGCGCGATTGCTGCCGCATAACA	TGTTATGCGGCAGCAATCCGCGAA
566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTTCGGTGCCATTTTT
567	CATTCCGCGCGAGTTGAAATCCAG	CTGGATTTCAACTCGCGCGGAATG
568	ACGCACGTTTTTTGGCACGGTTAA	TTAACCGTGCCAAAAAACGTGCGT
569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
570	TCTCAGTCGGAAGTCGTATGCCAGA	TCTGGCATAACGAGTCCGACTGAGA
571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGTGCGTTTGGAG
572	TTCAACCAAGCGGGGTGTTCTGTA	TCACGAACACCCCGCTTGTTGAA
573	GGTGTGCGAGGGTGGTGACCTCGA	TCGAGGTCACCACCCTCCGACACC
574	AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAGCGCT
575	CCGAGGACTTACGTCTGCCAGGA	TCCTGGGCAGACGTAAGTCCCTCGG
576	GCCCAATCCAGTTCTTATGCGCCC	GGGCGCATAAGAACTGGATTGGGC
577	CGGGTTAACCACGCAAGTTATGA	TCATAACTTGCGTGGGTAAACCGG
578	TGATTAGCGCTCAATACACGCGTG	CACGCGTGATTGAGCGCTAATCA
579	AAGGGCAGACCTTTGGTTCGACTG	CAGTCGAACCAAAGGTCTGCCCTT
580	GCGCCACAAGATTCACATGTCATT	AATGACATGTGAATCTTGTGGCGC
581	GCCATGTTCAAGGGCCTTTGAAAG	CTTCGAAAGGCCCTTGAACATGGC
582	CGCGGTGTTTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
584	CGATACGCGCCGGTTTGTTAAATC	GATTTAAACAAACGGGCGCGTATCG
585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTTATAGCC
586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTACCCA

	587	GTCTTCATCGGCCCGCGCAAGCTA	TAGCTTGCGCGGGCCGATGAAGAC
	588	GCGACACACCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCCG
	589	GTAGCAGGGTCCGCAAGACCAAGC	GCTTGGTCTTGCGGACCCTGCTAC
	590	TCGCCAACGCAGGGTAACTGCCAT	ATGGCAGTTACCCTGCGTTGGCGA
5	591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGGAGT
	12	CATCGTCCCTTTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
	13	GCACGGGAGCTGACGACGTGTCAA	TTGACACGTCGTCAGCTCCCCTGC
	594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
	595	CGCTGGACTGGCCTATCCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
10	596	CGGTCTCAGCAACACTGTGCGAAA	TTTGCACAGTGTTGCTGAGACCG
	597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTTCG
	598	ATACCGTGCGACAAGCCCCCTCTGA	TCAGAGGGGCTTGTCGCACGGTAT
	599	AGCTCATTCCCGAGACGGAACACC	GGTGTTCGGTCTCGGGAATGAGCT
	600	TTTCATGCGGCCGTTGCAAATCAT	ATGATTTGCAACGGCCGCATGAAA
15	601	ACTCGAACGGACGTTCAATTCCCA	TGGGAATTGAACGTCCGTTTCGAGT
	602	CTGCATGGTGTGGGTGAGACTCCC	GGGAGTCTCACCCACACCATGCAG
	603	CCGCGAGTGTGGATGGCGTGTTGA	TCAACACGCCATCCACACTCGCGG
	604	AATGTGTGCGTCTAAGCCGGGTG	CACCCGGCTTAGGACCGACACATT
	605	TAAGACGAGCCTGCACAGCTTGCG	CGCAAGCTGTGCAGGCTCGTCTTA
20	606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCACGCC
	607	TGCTCCATGTTAGGAACGCACCAC	GTGGTGCGTTCCTAACATGGAGCA
	608	CGGTGTTGGTTCGACTGACGACTG	CAGTCGTCAGTCCGACCAACACCG
	609	CCGCGCGTATCTATCAGATCTGGG	CCCAGATCTGATAGATACGCGCGG
	610	AAAGCATGCTCCACCTGGAGCGAG	CTCGCTCCAGGTGGAGCATGCTTT
25	611	ACTTGCATCGCTGGGTAGATCCGG	CCGGATCTACCCAGCGATGCAAGT
	612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
	613	ATGCAGATGAACAAATCGCCGAAT	ATTCGGCGATTTGTTTCATCTGCAT
	614	GCAATTCTGGGCCATGTATTGCTC	GACGAATACATGGCCCAGAATTGC
	615	AGGGTTCCTTACGCGTCGACATGG	CCATGTCGACGCGTAAGGAACCCT
30	616	GTGGAGCTAATCGCGAGCCTCAGA	TCTGAGGCTCGCGATTAGCTCCAC
	617	TCGTAGTCTCACCGGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
	618	TTATAGCAGTGCGCCAATGCTTCG	CGAAGCATTGGCGCACTGCTATAA
	619	CGAACAGTGCTGTCCGTCGCTCAA	TTGAGCGACGGACAGCACTGTTTCG
	620	TCCGCGTGGACTGTTAGACGCTAT	ATAGCGTCTAACAGTCCACGCGGA
35	621	CATTAGCCCGCTGTCCGTAACGT	ACAGTTACCGACAGCGGGCTAATG
	622	GGAAAGAACTCAGACGCGCAATG	CATTGCGCGTCTGAGTTTCTTTCC
	623	CGACTCGCTGGACAGGAGAATCGT	ACGATTCTCCTGTCCAGCGAGTCG
	624	CATGATCCTCTGTTTCACCCGCGG	CCGCGGGTGAACAGAGGATCATG
	625	GGCGTAGCGCTCTAAAAGCTTCGG	CCGAAGCTTTTAGAGCGCTACGCC
40	626	AGTGATGCCATCAGGCCCGTATAC	GTATACGGGCCTGATGGCATCACT
	627	TATGGAAAGGGCAACAGCGCTATC	GATAGCGCTGTTGCCCTTTCCATA

	628	CTGTGGTTGATGGAGGATCCACAC	GTGTGGATCCTCCATCAACCACAG
	629	ACTCGCTGGAATTTGCGCTGACAC	GTGTCAGCGCAAATTCAGCGAGT
	630	CAGGCCCGAACCACGCGTTACAG	CTGTAACCGCGTGGTTCGGGCCTG
5	631	GGCGCAATGGGCGCATAAATACTA	TAGTATTTATGCGCCCATTGCGCC
	632	GGTCAATTCGCGCTACATGCCCTA	TAGGGCATGTAGCGCGAATTGACC
	633	GATGGTGGACTGGAGCCCTTCCGC	GCGGAAGGGCTCCAGTCCACCATC
	634	CCGCGCATAGCGCAATAGGGGAGA	TCTCCCCTATTGCGCTATGCGCGG
	635	TCTTCTGGCTGTCCGGCACCCGAA	TTCGGGTGCCGGACAGCCAGAAGA
	636	GCGTTCGCAATTCACGGGCCCTTA	TAAGGGCCCGTGAATTGCGAACGC
10	637	TCGTTTCGGCCTTGGAGAGTATCG	CGATACTCTCCAAGGCCGAAACGA
	638	AGGTGCAAGTGCAAGGCGAGAGGC	GCCTCTCGCCTTGCACTTGACCT
	639	CGCCAGTTTCGATGGCTGACGTTT	AAACGTCAGCCATCGAAACTGGCG
	640	GCTTTACCGCCGATCCCAGATATC	GATATCTGGGATCGGCGGTAAAGC
	641	GTGCTTGACGAAGAGGCGAAATGT	ACATTTGCGCTCTTCGTCAAGCAC
15	642	CAGTCCGTGCGCTTCATGTCCTCA	TGAGGACATGAAGCGCACGGACTG
	643	TACGCGTAAGAGCCTACCCTCGCG	CGCGAGGGTAGGCTCTTACGCGTA
	644	GGCGAGTCTTGTGGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
	645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTTCGCTTTGG
	646	GCCGTAGGTTGCTCTTCACCGAAC	GTTCTGGTGAAGAGCAACCTACGGC
20	647	AAATCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGCGGATTT
	648	GGCTTCGCACCCGTACCAATTTAG	CTAAATTGGTACGGGTGCGAAGCC
	649	TGTAGAGTCCACGTAGCCGGCAT	ATGCCGGCTACGTGGGACTCTACA
	650	CACTAGTCTGGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
	651	TGTACTCGGCAGGCGCAATAGATT	AATCTATTGCGCCTGCCGAGTACA
25	652	AACGGGTATCGGAAGCGTAAAAGC	GCTTTTACGCTTCCGATACCCGTT
	653	CGGACTGCCCGTTTGCAAGTTGAG	CTCAACTTGCAAACGGGCAGTCCG
	654	ATCGTTCAGCACTGGAGCCCGTAA	TTACGGGCTCCAGTGCTGAACGAT
	655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
	656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
30	657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGCAC
	658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTTAGGACGATGAG
	659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACCGCCGAAGTGCCATT
	660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCCACGG
	661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTCACCAACGAGAATTT
35	662	TTGCTCTTATCCTTGCTCTGGGCG	CGCCCAGGACAAGGATAAGAGCAA
	663	TTAAGGATCAGGCGGAGCTTGCA	CTGCAAGCTCCGCTGATCCTTAA
	664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGCAGCACCTTAGTCGCG
	665	GCTCGATTTACGGCCCGTTGTTT	GAACAACGGGCCGTGAAATCGAGC
	666	AGCAGAGTGCGTTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
40	667	TGGAGGTGAGGACGACGTGCACTA	TAGTGCACGTCGTCTCACCTCCA
	668	AACCGTTTAGGGTACATTCGCGGT	ACCGCGAATGTACCCTAAACGGTT

	669	TATGATCGCTCGGCTCACAGTTTG	CAAACGTGAGCCGAGCGATCATA
	670	GACTTTTTGCGAAACGTCATGGT	ACCATGACGTTTCCGCAAAAAGTC
	671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAAGGTGGAATAACCGACA
5	672	CTATGGTTTGCACTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
	673	AGCAGGGAAATTCAATCGTTCGCA	TGCGAACGATTGAATTTCCCTGCT
	674	CCTAACCGAGCGCTTAGCATTTCC	GGAAATGCTAAGCGCTCGGTTAGG
	675	CCCGACCCTAACTCGCATTGAATA	TATTCAATGCGAGTTAGGGTCGGG
	676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAAGCAA
10	677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAATAAACACGGCGAGCATC
	678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAACTCGTCATCCGA
	679	ATGCGGTCTACTTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
	680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
	681	AACTTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAATTAAGTT
15	682	GTGACCGCGAACTTGTTCCGACAG	CTGTCGGAACAAGTTCCGCGTCAC
	683	TGCGGATTACCGATTGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
	684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
	685	TCGCTCCGTAGCGATTCATCGTAG	CTACGATGAATCGCTACGGAGCGA
	686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
20	687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
	14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
	15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
	690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGCAGAATGCGAC
	691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
25	692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTCACCCAAGGTCCCTT
	693	TCAAATGGCCACCGCGTGTCAATC	GAATGACACGCGGTGGCCATTGA
	694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
	695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGGAATAGCC
	696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
30	697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
	698	GCCACAGAGTTTTAGCAGGGACCC	GGGTCCCTGCTAAACTCTGTGGC
	699	CCCACGCTTTCCGACCACTGACCT	AGGTCAGTGGTCGGAAAGCGTGGG
	700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCAATG
	701	AGCCACTCGACAGGGTTCCAAAGC	GCTTTGGAACCCTGTGAGTGGCT
35	702	CAGGATGAGCAAAGCGACTCTCCA	TGGAGAGTCGCTTTGCTCATCCTG
	703	CAAGGTATGGTCTGGGGCCTAAGC	GCTTAGGCCCCAGACCATACCTTG
	704	GGTGTTGCGCCTAAACTCTTTCGG	CCGAAAGAGTTTAGGCCGAACACC
	705	TTTAGTCGGACCCTGTGGCAATTC	GAATTGCCACAGGGTCCGACTAAA
	706	CACACGTTTCCGACCAGCCTGAAC	GTTACAGCTGGTCGGAAACGTGTG
40	707	CTGGACGAACTGGCTTCCTCGTAC	GTACGAGGAAGCCAGTTTCGTCCAG
	708	TTCACAATCCGCCGAAAACCTGACC	GGTCAGTTTTTCGGCGGATTGTGAA
	709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATATCCTGTT

5

10

15

20

25

30

35

40

710	TACGTCGGATCCATTGCGCCGAGT	ACTCGGCGCAATGGATCCGACGTA
711	CATGGATCTCTCGGTTTGATCGCC	GGCGATCAAACCGAGAGATCCATG
712	AGCCAGGCGCGTATATACGCTCGG	CCGAGCGTATATACGCGCCTGGCT
713	ATTTGGCACGTGTCGTGCCATGTT	AACATGGCACGACACGTGCCAAAT
714	CCGCGTTGCACCACTTTGAGGTGC	GCACCTCAAAGTGGTGCAACGCGG
715	TTGGACGTGACAAGCATGGCGCTC	GAGCGCCATGCTTGTCACGTCCAA
716	CTGAATCGCGCAAGTAAATGGGGG	CCCCATTTACTTGCGCGATTGAG
717	GATAAGGTCCACCAGATTGCGCGC	GCGCGCAATCTGGTGGACCTTATC
718	CTAACAATTGCCAACCGGGACGGC	GCCGTCCCGGTTGGCAATTGTTAG
719	GGTAACCTGGGTGCTTGCAAGTTA	TAACCTGCAAGCACCCAGGTTACC
720	ATCGGAGCCACCATTGCGATTGGG	CCCAATGCGAATGGTGGCTCCGAT
721	GTGAACTGGCTTGCCCCAGGATTA	TAATCCTGGGGCAAGCCAGTTCAC
722	AGGCGATAGCATGGTCCCATATGA	TCATATGGGACCATGCTATCGCCT
723	AACGGTATCGTGGCTAATGCACGA	TCGTGCATTAGCCACGATACCGTT
724	AGTAGTGGTCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCACTACT
725	CCGTTGAATTGGACGGGAGGTTAG	CTAACCTCCCGTCCAATTCAACGG
726	GCATAAGTGCGGCATCGCGAAGGG	CCCTTCGCGATGCCGCACCTTATGC
727	CGACAAGATGCAGCTGCTACATGC	GCATGTAGCAGCTGCATCTTGTCG
728	TCGCAGTGATTCCCGACCGATAAG	CTTATCGGTGCGGAATCACTGCGA
729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCTCGAGTGGACTCGCCTTG
730	GCAACTTGCACGGCATAAGTGGCC	GGCCACTTATGCCGTGCAAGTTGC
731	TCCGAGCTTGACGTTGCGGACGTC	GACGTGCGGAACGTCAAGCTCGGA
732	AGCGCTGGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
733	TTCATGTCGCTGAGTAACCCTCGC	GCGAGGGTTACTCAGCGACATGAA
734	CGAACCGCTAATGCCATTGTCAG	CTGACAATGGGCATTAGCGGTTTCG
735	CACGGAAGGTGGGACAAATCGCCG	CGGCGATTTGTCCCACCTTCCGTG
736	CACAGATGGAGACAAACGCGCCTT	AAGGCGCGTTTGTCTCCATCTGTG
737	TTTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAAA
738	ACGTTACGTTTCCGGCGCCTCTAA	TTAGAGGCGCCGAAACGTAACGT
739	TATCGGATTGCGTGGGTTTCAATC	GATTGAAACCCACGCAATCCGATA
740	CTTCCACAATTGTCTGCGACGCAC	GTGCGTCGCAGACAATTGTGGAAG
741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACCTTTGTGCA
742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
743	CTGAAACCGTGCGAATCGAGGTGA	TCACCTCGATTGCGACGGTTTCAG
744	CGGTGTTCCGCGTGTGAAAAAAT	ATTTTTTCGACACGCGGAACACCG
745	TCTAGCAGGCCTTTTGAATCGCCA	TGGCGATTCAAAGGCCTGCTAGA
746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
747	TCTTCTGTCATCCTGCAGCAGCAT	ATGCTGCTGCAGGATGACAGAAGA
748	GCGGATGAAACCTGAAAGGGGCCT	AGGCCCTTTTCAGGTTTCATCCGC
749	GGGGCCCCAACTGGTATCAAGCC	GGCTTGATACCAGTTTGGGGCCCC
750	GCATTGGCTTCGGATTCTCCTACA	TGTAGGAGAATCCGAAGCCAATGC

	751	AGGCGGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGGCCGCCT
	752	ACACCATGTGCTCCGCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
	753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCGATTTCATGTTTCATCGT
	754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
5	755	GTGCCGTATTTGACCTGTGCGTT	AACGCACAGGTGCGAAATACGGCAC
	756	GCAGTGCGCACTTCAGTTCAAAG	CTTTTGAAGTGAAGTGCAGCACTGC
	757	GCGATTTTAAGCGATGCCTTGACG	CGTCAAGGCATCGCTTAAATCGC
	758	TAGGTGACCTAGGCTTGCTTGCGG	CCGCAAGCAAGCCTAGGTCACCTA
	759	CTGGATACCTTGCTGTGCGGCGC	GCGCCGCACAGGCAAGGTATCCAG
10	760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
	761	GCGCTTGCCCGATGCGATGCATTA	TAATGCATCGCATCGGGCAAGCGC
	762	TTTCTGTAAGCGGCCTGGGGTTCA	TGAACCCAGGCGCTTACAGAAA
	763	GGCTGAGGTGAGCGGTAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
	764	TCTTGGCCTCCCCGATCTAATTTG	CAAATTAGATCGGGGAGGCCAAGA
15	765	GGAGGTAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
	766	GTAATCCATTTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
	767	CAAACCCATTCCAGCAGACGCCTG	CAGGCGTCTGCTGGAATGGGTTTG
	768	TAGGAGGAATTTGGCATGCGGGCG	CGCCCGCATGCCAAATTCCTCCTA
	769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGGCACATCCTACCTAT
20	770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
	771	CTGGCTGTGTGCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
	772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
	773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
	774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTTCGTCTCCTGCT
25	775	TTCAAGCACCATCGTGCAATCCAA	TTGGATTGCACGATGGTGCTTGAA
	776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
	777	TACATTCCCTGCCTCCGTGGGCTT	AAGCCACGGAGGCAGGGAATGTA
	778	CGCTTCGCGTATTCAGTAGCGGTT	AACCGCTACTGAATACGCGAAGCG
	779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTCGACGCGTCCGA
30	780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGCTCAGA
	781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGAATTCAA
	782	AGTTTTCGCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAAC
	783	GTTTCATAGGCCACGCGTGCTAAA	TTTAGCACGCGTGGCCTATGAAAC
	16	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCGGTACTTGACGCGATG



TABLE 4

Seq. ID No.	Decoder Sequence (5'-3') + 5' T	Probe Sequence (5'-3') + 5' T
17	TTTCGCCGTCGTGTAGGCTTTTCAA	TTTGAAAAGCCTACACGACGGCGAA
18	TGTTCCAGTGAAGCTGCGATCTGG	TCCAGATCGCAGCTTCACTGGAAC
19	TTACTTGGCATGGAATCCCTTACGC	TGCGTAAGGGATTCCATGCCAAGTA
20	TACTAGCATATTTACAGGGCACC GGC	TGCCGGTGCCCTGAAATATGCTAGT
21	TGAACGGTCAATGAACCCGCTGTGA	TTACACAGCGGGTTCATTGACCGTTC
22	TGCGGCCCTTGGTTCAATATGAATCG	TCGATTCATATTGAACCAAGGCCGC
23	TGATCGTTAGAGGGACCTTGCCCGA	TTGCGGCAAGGTCCCTCTAACGATC
24	TTGGACCTAGTCCGGCAGTGACGAA	TTTCGTCACTGCCGGACTAGGTCCA
25	TATAAACTACCCAGGACGGGCGGAA	TTTCCGCCCGTCTCTGGGTAGTTTAT
26	TCATCGGTTGCGGCCAATCCAGATA	TTATCTGGATTGGCGCGAACCGATG
27	TGTCGGGCATAGAGCCGACCACCCT	TAGGGTGGTCGGCTCTATGCCCGAC
28	TCTTGGGTCATGATTACCGTGCTA	TTAGCACGGTGAATCATGACCCAAG
29	TTGCCTAACGTGCTAATCAGCAGCG	TCGCTGCTGATTAGCACGTTAGGCA
30	TCGCATGTTGGAGCATATGCCCTGA	TTCAGGGCATATGCTCCAACATGCG
31	TAGCCACTGCATCAGTGCTGTTCAA	TTTGAACAGCACTGATGCAGTGGCT
32	TGGTTGTTTTGAGGCGTCCCACACT	TAGTGTGGGACGCCTCAAACAACC
33	TTCGACCAAGAGCAAGGGCGGACCA	TTGGTCCGCCCTTGCTCTTGGTCTGA
34	TGACATCGCTATTGCGCATGGATCA	TTGATCCATGCGCAATAGCGATGTC
35	TGAAATACGAAGTCTGCGGGAGTCG	TCGACTCCCGCAGACTTCGTATTTTC
36	TTGTCATGAATGATTGATCGCGCGA	TTGCGCGCATCAATCATTATGACA
37	TATATCGGGATTTCGTTCCCGGTGAA	TTTCACCGGGAACGAATCCCGATAT
38	TGCGAGCGTACCGAAGGGCCTAGAA	TTTCTAGGCCCTTCGGTACGCTCGC
39	TTTACCGGCAGCGGACTTCCGAATT	TAATTTCGGAAGTCCGCTGCCGGTAA
40	TGTAATCGAGAGCTGCGCGCCGTCT	TAGACGGCGCGCAGCTCTCGATTAC
41	TCCTGTTAGCGTAGGCGAGTCGATC	TGATCGACTCGCCTACGCTAACAGG
42	TTAGCGGACCGGCAGAATGAGTTCC	TGGAACCTATTCTGCCGGTCCGCTA
43	TGGTACATGCACTACGCGCACTCGG	TCCGAGTGCGCGTAGTGCATGTACC
44	TAATTCATCTCGGACTCCCGCGGTA	TTACCGCGGGAGTCCGAGATGAATT
45	TGCCAAATCTGGATTGGCAGGAATG	TCATTCCTGCCAATCCAGATTTGGC
46	TTGCATTTTCGGTTGAGGCACATCC	TGGATGTGCCTCAACCGAAAATGCA
47	TCCGCTCAATTCACCATGCTTCGCT	TAGCGAAGCATGGTGAATTGAGCGG
48	TCTCGGAAAGGTGCAACTTTGGTGT	TACACCAAAGTTGCACCTTTCCGAG
49	TAATTCGACCAGCAGAACGTCCCAT	TATGGGACGTTCTGCTGGTCTGAATT
50	TGCCAGAGTCTCAACCTCACGGGAT	TATCCCGTGAGGTTGAGACTCTGGC
51	TCCAACAACCTGGAACGGGAACCCGC	TGCGGGTTCCCGTTCAGTTGTTGG
52	TGAGAACTGATCGCTGAGGGGCATG	TCATGCCCCCTCAGCGATCAGTTCTC
53	TGGCACACTAGACTTGTGGCACCGA	TTCCGGTGCCACAAGTCTAGTGTGCC

54	TTCACATCCAAATATGGTCCGCGAA	TTTCGCGGACCATATTTGGATGTGA
55	TGTCTGCCGGTGTGACCGCTTCATT	TAATGAAGCGGTACACCGGCAGAC
56	TCATCGCAGAGCATAAACACCCTCA	TTGAGGGTGTATGCTCTGCGATG
57	TGTTGGTATCTATGGCAGAGGCGGA	TTCCGCCTCTGCCATAGATACCAAC
58	TACGAGGTGCCGCTGAGGTTCCATT	TAATGGAACCTCAGCGGCACCTCGT
59	TGGAATGAGTGGACCCAGGCACATT	TAATGTGCCTGGGTCCACTCATTCC
60	TTGTCAATATGCGTCCGTGTCGTCT	TAGACGACACGGACGCATATTGACA
61	TTGATGAGCCTCAGGGTACGAGGCA	TTGCCTCGTACCCTGAGGCTCATCA
62	TCACCGCGGTGTTCTACAGAATGA	TTCATTCTGTAGGAACACCGCGGTG
63	TTTGTGGCAATGGTGTCCGCTCGG	TCCGAGCGGACACCATTGGCAACAA
64	TTTAACCTGCGTCTGCCCTTTTCT	TAGGAAAGGGGCAGACGCAGGTTAA
65	TAGGCGCGTTCTGCCTTAGTGACG	TCGTCACTAAGGCAGGAACGCGCCT
66	TTAGGGCGATGGCACGAAGCTTCAA	TTTGAAGCTTCGTGCCATCGCCCTA
67	TTGCATAGAGCCAAAGTCGGCGATG	TCATCGCCGACTTTGGCTCTATGCA
68	TTTGAGAGGCAGGTGGCCACACGGA	TTCCGTGTGGCCACCTGCCTCTCAA
69	TTCCGCATTGTGAGAAAAACGAGC	TGCTCGTTTTTTCTCACAATGCGGA
70	TGGCGGTTTCCGTAGCTATAGGTGC	TGCACCTATAGCTACGAAACCGCC
71	TGGTGAAAATTCGTAGCCACGGGC	TGCCCGTGGCTACGAAATTTTACC
72	TCCGACGGAGGATGAAGACAATCAC	TGTGATTGTCTTCATCCTCCGTCGG
73	TCCAGTTTGGCCCAATTCGCCAAAA	TTTTTGCGAATTGGGCCAACTGG
74	TGGATCTATTAGGCCGTGCGCACAG	TCTGTGCGCACGGCCTAATAGATCC
75	TCGGATGTCACCGTTTGGACTTTCA	TTGAAAGTCAAACGGTGACATCCG
76	TATCGCAAATCCTGCTCGTCCCTAA	TTTAGGGACGAGCAGGATTGCGAT
77	TCAGGGCATGCAATAATCGAGGTTC	TGAACCTCGATTATTGCATGCCCTG
78	TCATGCGTTGATATATGGGCCCAAG	TCTTGGGCCCATATATCAACGCATG
79	TCAGCTGCAGCTTGTGACCAACCAC	TGTGGTTGGTCACAAGCTGCAGCTG
80	TTTGTATGTCTGCCGACCGGCGACC	TGGTCGCCGGTCGGCAGACATACAA
81	TGATGGCGCCCGTTGATAGGTATGG	TCCATACCTATCAACGGGCGCCATC
82	TATGAGAATCGCCGGCAATCTGCTA	TTAGCAGATTGCCGGCGATTCTCAT
83	TATTTGCACTGACCGCAGGCTCGTG	TCACGAGCCTGCGGTCAAGTGCAAAT
84	TCAGGGAGAACGGTTAAGTTCCCGT	TACGGGAACCTAACCGTTCTCCCTG
85	TAGGCCGGCGATCGAGGAGTTTGGT	TACCAAACCTCCTCGATCGCCGGCCT
86	TACACGGTGGTCTCTGATAGCGACC	TGGTCGCTATCAGAGACCACCGTGT
87	TGTGCAACGCCGAGGACTTCCATCA	TTGATGGAAGTCTCGGCGTTGCAC
88	TTCCGGTGCCTGATAGCCATTCCGAT	TATCGGAATGGCTATCAGGCACCGA
89	TTGAAATACCACACAGCCAATTGGC	TGCCAATTGGCTGTGTGGTATTTCA
90	TGCATCGTGTACATGACTGCCGCGA	TTCCGCGGCAGTCATGTACACGATGC
91	TCAGTGTTCTAACGGCGCGCGTGAA	TTTACGCGCGCCGTTAGAACACTG
92	TCGCTTGCAACGTTGCACCTACTCT	TAGAGTAGGTGCAACGTTGCAAGCG
93	TCGAAAACTAGTGGGCTCGCCGCG	TCGCGGCGAGCCCACTAGTTTTTCG
94	TCTTTCAGGGGAACCTGCCGGAGTCG	TCGACTCCGGCAGTTCCCCTGAAAG

5	95	TTTGTGGCCTTCTTGTAAGGCACG	TCGTGCCTTTACAAGAAGGCCACAA
	96	TTCCACGAACGGCGACCCGTTGTCT	TAGACAACGGGTGCGCGTTTCGTGGA
	97	TCGACCTTGACGAAACCTAACGAG	TCTCGTTAGGTTTCGTGCAAGGTCG
	98	TGTGCAGCTTCACGAGCCAGCCTGA	TTCAGGCTGGCTCGTGAAGCTGCAC
	99	TCGCTTTCGTGCGAATAGACGATGA	TTCATCGTCTATTCGCACGAAAGCG
	100	TTGCGCTTACAGGCTCCTAGTGGTC	TGACCACTAGGAGCCTGTAAGCGCA
	101	TCACGCGCTTAGTCGCGATCGCATA	TTATGCGATCGCGACTAAGCGCGTG
	102	TCGGAGGGAGGGAGCTAGCCTTCGA	TTCGAAGGCTAGCTCCCTCCCTCCG
10	103	TGCATCCGGCCTGTTGATGACGCCT	TAGGCGTCATCAACAGGCCGGATGC
	104	TAGGCCAATCGATCTTATTGCCGAG	TCTCGGCAATAAGATCGATTGGCCT
	105	TCCTTCCAATGATTGCATACGCCCA	TTGGGCGTATGCAATCATTGGAAGG
	106	TAACACTTGATCAGGCGGGTCGTCT	TAGACGACCCGCCTGATCAAGTGTT
	107	TTGGAATCAAGGCCGTAAAGGACAG	TCTGTCCTTTACGGCCTTGATTCCA
15	108	TGCTCCCGTAACCTGTCCACCAGTG	TCACTGGTGGACAGGTTACGGGAGC
	109	TAGTGGTGAATGGCCGCTACCCTGA	TTCAGGGTAGCGGCCATTCACTACT
	110	TTGTTGAAGCGAGCTAAACGGCCA	TTGGCCGTTTTAGCTCGCTTCAACA
	111	TCAGCGCTCCAGAATTGACAGCAAT	TATTGCTGTCAATTCTGGAGCGCTG
	2	TTTGAAGCGCACGTCCCTTTTCAA	TTTGAAAAGGGACGTGCGCTTCGAA
	3	TAACGCGTGGGGAATGGGACATCAA	TTTGATGTCCCATTTCCCAACGCGTT
20	114	TCACGAGATACCGGCGTAAGGGTGG	TCCACCCTTACGCCGGTATCTCGTG
	115	TCTACGGCAAACGTGTGGAATGGGT	TACCCATTCCACACGTTTGCCGTAG
	116	TGTAGGGCGATGACGGGCGAACTAC	TGTAGTTCGCCCCTCATCGCCCTAC
	117	TAATCGACCTCCGCACACATTCGCA	TTGCGAATGTGTGCGGAGGTGATT
	118	TGAGTCAGCATGGCGGCGGAGATTC	TGAATCTCCGCCGCCATGCTGACTC
25	119	TAGATAAAGACGCTGGCAACACGGG	TCCCGTGTTGCCAGCGTCTTTATCT
	120	TGGTACCTCAACGCGAACCATTGT	TACAAGTGGTTCGCGTTGAGGTACC
	121	TAAGCGATGGCTACCCAAGAGCGAT	TATCGCTCTTGGGTAGCCATCGCTT
	122	TAGAGCTTATGCAGAACCAGGCGCC	TGGCGCCTGGTTCTGCATAAGCTCT
	123	TATCGGTCTCACGCAGGGTTGGATA	TTATCCAACCCTGCGTGAGACCGAT
30	124	TTAGGTTGCCCGCCAGAAGAAACAT	TATGTTTCTTCTGGCGGGCAACCTA
	125	TCGGTGCTGTTGCAAAAGCCTGTAG	TCTACAGGCTTTTGCAACAGCACCG
	126	TTGATGAAAGTTTGCGGCAGGACAC	TGTGTCCTGCCGCAAACTTTCATCA
	127	TGTTGAGTGCAGGATGCAGCGATAG	TCTATCGCTGCATCCTGCACTCAAC
	128	TAACATTGCGCGGTCCACCAGGGTT	TAACCCTGGTGGACCGCGCAATGTT
35	129	TGGGCAGTTAGAGAGGGCCAGAAGT	TACTTCTGGCCCTCTCTAACTGCCC
	130	TTGAGCTGGTCCCGTGAACGTGT	TACACGTTACGGGGACCAGCTCGA
	131	TGTCTTGGGGGCGCTTAGTGAAAA	TTTTTCACTAAGCGGGCCCCCAAGAC
	132	TACTGTTGGCTTGCTCTCATGTCCA	TTGGACATGAGAGCAAGCCAACAGT
	133	TAGGACCATTCGGAAGGCGAAGATA	TTATCTTCGCCTTCCGAATGGTCCT
40	134	TCTTGGGAGGCATCCGCTATAAGGA	TTCTTATAGCGGATGCCTCCCAAG
	135	TAATAAACGGAACGCACCGCTACAG	TCTGTAGCGGTGCGTTCGGTTTATT

	136	TTTGTACGTGCGGTCCCCATAAGCA	TTGCTTATGGGGACCGCACGTACAA
	137	TCGCACCAAACCTGAGTTTCCCAGAC	TGTCTGGGAAACCTCAGTTTGGTGCG
	138	TACCTGATCGTTCCCTATTGGGAA	TTTCCCAATAGGGGAACGATCAGGT
	139	TGGAACAGAGGCGAGGGGACTGAGC	TGCTCAGTCCCCTCGCCTCTGTTCC
5	140	TCCCTGCCTTGCGGTGTCGGCTTAT	TATAAGCCGACACGCCAAGGCAGGG
	141	TACTCTGACACGCCAACTCCGGAAG	TCTTCCGGAGTTGGCGGTGTCAGAGT
	142	TCTGACGGTTTTCAATCGGCGTGCC	TGGCACGCCGAATGAAAACCGTCAG
	143	TTGCGGTGGTTCATTGGAGCTGGCC	TGGCCAGCTCCAATGAACCACCGCA
	144	TGCATGGCCAACTAGTGA CTGCGAA	TTTGCGAGTCACTAGTTGGCCATGC
10	145	TAGGCCGTAAAGCGAATCTCACCTG	TCAGGTGAGATTGCGTTTACGGCCT
	146	TCGAATATTATGCCGAGAATCCGCG	TCGCGGATTCTCGGCATAATATTG
	147	TACAGACGAGCTCCCAACCACATGA	TTCATGTGGTTGGGAGCTCGTCTGT
	148	TGGACGGTTTGTGCTGGATTGTCTG	TCAGACAATCCAGCACAAACCGTCC
	149	TAAAGGCTATTGAGTTGGTTGGGCG	TCGCCCCAACCAACTCAATAGCCTTT
15	150	TGATGGCCTATTCGGAGATCGGGCC	TGGCCCGATCTCCGAATAGGCCATC
	151	TGATCCAGTAGGCAGCTTCATCCA	TTGGGATGAAGCTGCCTACTGGATC
	152	TAATAACTCGCGCGGTATGCTTCT	TAGAAGCATACCCGCGCGAGTTATT
	153	TGGAGGAGGTTTGTCTCGGAAAGCA	TTGCTTTCCGAGACAAACCTCCTCC
	154	TCTTTGGTATGGCACATGCTGCCCG	TCGGGCAGCATGTGCCATACCAAAG
20	155	TAGAAAGGCTCGAGCAACGGGAACT	TAGTTCCCGTTGCTCGAGCCTTTCT
	156	TAATCTACCGCACTGGTCCGCAAGT	TACTTGCGGACCAGTGCGGTAGATT
	157	TCGTGGCGGCCACAGTTTTTGGAGG	TCCTCCAAAACTGTGGCCGCCACG
	158	TTTGAGTTCAATCCATACGCACGT	TACGTGCGTATGGATTGAACTGCAA
	159	TGGCCCAAAGCCCCAGACCATTTTA	TTAAATGGTCTGGGGCTTTGGGCC
25	160	TCGCCTGTCTTTGTCTCCGACAAT	TATTGTCCGGAGACAAAGACAGGCG
	161	TTGAGGCAACAGGGGCCAAAACTA	TTAGTTTTTGCCCCTGTTGCCTCA
	162	TAGCGGAAGTAGTCCTCGGCTCGTC	TGACGAGCCGAGGACTACTTCCGCT
	163	TGGCCCCAAGGCTTAGAGATAGTGG	TCCACTATCTCTAAGCCTTGGGGCC
	164	TGCACGTGAAGTTTAACCGCGATTG	TGAATCGCGGTTAACTTCACGTGC
30	165	TAGCGGCAGAAACGTTCTTGACGG	TCCGTCAAGGAACGTTTCTGCCGCT
	166	TTCTGTCGAGCAGACGAGATTGCACG	TCGTGCAATCTCGTCTGCTCGACGA
	167	TTCTTTGCCGCGTAACTGACTGCTT	TAAGCAGTCAGTTACGCGGCAAGA
	168	TTTTATGTGCCAAGGGGTTAACCGA	TTCGGTTAACCCTTGGCACATAAA
	169	TTGTTACTGTGGTTCACGGCAGTCC	TGGACTGCCGTGAACCACAGTAACA
35	170	TCGCGCCTCGCTAGACCTTTTATTG	TCAATAAAAGGTCTAGCGAGGCGCG
	171	TACAAATGCGTGAGAGCTCCCAACT	TAGTTGGGAGCTCTCACGCATTGT
	172	TCGCGCAGATTATAGACCCGAATGT	TACATTCGGGTCTATAATCTGCGCG
	173	TCAAATAACGCCGCTGAATCGGCGT	TACGCCGATTACGCGGCGTTATTTG
	174	TCCTTCGTGCATCGGTGATGATGTT	TAACATCATCACCGATGCACGAAGG
40	175	TTGAACACGAGCAACACTCCAACGC	TGCGTTGGAGTGTTGCTCGTGTTCA
	176	TCAGCAGATCCTTCGTAGCGGTCGT	TACGACCGCTACGAAGGATCTGCTG

	177	TGGAACCTGGTGAGTTGTGCCTCAT	TATGAGGCACAACCTCACCAGGTTCC
	178	TTCATAAGCGACAATCGCGGGCTTA	TTAAGCCCGCGATTGTGCGTTATGA
	179	TCCCAACGTCACTGAAGCTCACAGT	TACTGTGAGCTTCAGTGACGTTGGG
5	180	TTGTCAGAGCCCGCGACTCAGACGG	TCCGTCTGAGTCGCGGGCTCTGACA
	181	TTACACGAAGCCTCTCCGTGGTCCA	TTGGACCACGGAGAGGCTTCGTGTA
	182	TCTCAGAAGTCCTCGGCCAACTGGG	TCCCAGTTCGCCGAGGACTTCTGAG
	183	TATCCTTTTATCTACTCCGCGGCGA	TTCGCCGCGGAGTAGATAAAAAGGAT
	184	TAGGCGTGACGCAACAGGATAAAACC	TGGTTTATCCTGTTGCTGCACGCCT
10	185	TACTCTCGAGGGAGTCTCTGGCACA	TTGTGCCAGAGACTCCCTCGAGAGT
	186	TTTGCCAGGTCCATCGAGACCTGTT	TAACAGGTCTCGATGGACCTGGCAA
	187	TTCCACTATAACTGCGGGTCCGTGT	TACACGGACCCGCGAGTTATAGTGGA
	188	TGCCCAGTCGGCTCTAACAAGTTCTG	TCGAACTTGTTAGAGCCGACTGGGC
	189	TCGGAACGGATAATCGGCGTCAGGT	TACCTGACGCCGATTATCCGTTCCG
15	190	TTAAAATAAGCGCCTGGCGGGAGGA	TTCTCCCGCCAGGCGCTTATTTTA
	191	TGCGCACTCGTGAAACCTTTCTCGC	TGCGAGAAAGGTTTCACGAGTGC GC
	192	TAGTTTGCCAGGTACTGGCAAGTGC	TGCACTTGCCAGTACCTGGCAAAC T
	193	TACAACGAGGGATGTCCAGCGGCAT	TATGCCGCTGGACATCCCTCGTTGT
	194	TTTCGCAGCACCCGCTAGGTACAGT	TACTGTACCTAGCGGGTGCTGCGAA
	195	TTAACCCGATTTTTCGCACTCTGCC	TGGCAGAGTCGCAAAAATCGGGTTA
20	196	TCGTGCGATTGCAAGCGTAGGCTTG	TCAAGCCTACGCTTGCAATGCGACG
	197	TGAGCTGACGTCACCATCAGAGGAA	TTTCCTCTGATGGTGACGTCAGCTC
	198	TGGAGGCTGGGGGTGCGCTTAAGT	TACTTAAGCGCGACCCCCAGCCTCC
	199	TTTGTGGGAACCGCACTAGCTGGCT	TAGCCAGCTAGTGCGGTTCCACAA
	200	TCCCTCGCACTGTGTTCAACCCTCTT	TAAGAGGGTGAACACAGTGCGAGGG
25	201	TTCAATTGACTCGAATCCGCACAACG	TCGTTGTGCGGATTTCGAGTCAATGA
	202	TACAGGGGTTGGCCTTCGTACGTAC	TGTACGTACGAAGGCCAACCCCTGT
	203	TAGGCCGTGCAACATCACACAGGAT	TATCCTGTGTGATGTTGCACGGCCT
	204	TGGGCCGTGGTCACGTAATATTGGC	TGCCAATATTACGTGACCACGGCCC
	205	TGCGCGGACATGAAACGACAAGGCC	TGGCCTTGTCGTTTCATGTCCGCGC
30	206	TCTTATTGGGTGCCGGTGTCCGATT	TAATCCGACACCGGCACCCAATAAG
	207	TGGGGCGGTTACCAAAAAATCCGAT	TATCGGATTTTTTGGTAACCGCCCC
	4	TCCGTGCGATACCGGCTACGATCAA	TTTGATCGTAGCCGGTATGCGACGG
	5	TATGGCCGTGCTGGGGACAAGTCAA	TTTGA CTGTCCCCAGCACGGCCAT
35	210	TACGAAAAAAGTGTGCGGATCCCCT	TAGGGGATCCGCACACTTTTTTCGT
	211	TCCAAGTACACCGCACGCATGTTTA	TTAAACATGCGTGCGGTGTACTTGG
	212	TATCGTGCGTGGAGTGTGCGCATCTA	TTAGATGCGACACTCCACGCACGAT
	213	TTCCAGATACCGCCCCGAAC TTTGA	TTCAAAGTTCGGGGCGGTATCTGGA
	214	TTCTGCTGGCAGCACGTGAAGTGGC	TGCCACTTCACGTGCTGCCAGCAGA
	215	TTTGAAATTGCTCTGCCGTCA GTCA	TTGACTGACGGCAGAGCAATTTCAA
40	216	TAGTCAGGCGAGATGTTCAAGGCAGC	TGCTGCCTGAACATCTCGCCTGACT
	217	TACAAGCCGACGTAAAGCCCGCCCA	TTGGGCGGGCTTAACGTGCGCTTGT

5	218	TCCCTAATGAGGCCAGTAACCTGCA	TTGCAGGTTACTGGCCTCATTAGGG
	219	TGTGAGACACACATCCCCTCCAATG	TCATTGGAGGGGATGTGTGTCTCAC
	220	TCGACGGATGCAGAGTTCAGTGGTC	TGACCACTGAACTCTGCATCCGTCG
	221	TCCCGCATGCCTGGCGGTATTACAA	TTTGTAAATACCGCCAGGCATGCGGG
	222	TTTAGCAAAGCGGCGCCGTTAGCAA	TTTGCTAACGGCGCCGCTTTGCTAA
	223	TCCCGACACGGGTCAGCGTAATAAT	TATTATTACGCTGACCCGTGTGCGGG
	224	TGCGACGGCCCTGAGGTATGTCGTC	TGACGACATACCTCAGGGCCGTCGC
	225	TCAAAAGTGTGTTCCCTTGCGCTTG	TCAAGCGCAAGGGAACACACTTTTG
10	226	TTCTCGAAGCACAGCCCGGTTATTG	TCAATAACCGGGCTGTGCTTCGAGA
	227	TATGCTAACCGTTGGCCATGGAAT	TAGTTCCATGGCCAACGGTTAGCAT
	228	TCTTGCGGAGTGTTAGCCCAGCGGT	TACCGCTGGGCTAACACTCCGCAAG
	229	TTGCTCCCTAGGCGCTCGGAGGAGT	TACTCCTCCGAGCGCCTAGGGAGCA
	230	TCCAATGCCTTTGAGTAAGCGATGG	TCCATCGCTTACTCAAAGGCATTGG
	231	TAGCAGATAACGTCCCAATGACGCC	TGGCGTCATTGGGACGTTATCTGCT
15	232	TTTGACCATTACGTGTTGCGCCCAT	TATGGGCGCAACACGTAATGGTCAA
	233	TTGCGGTATTTGCGGAATTCGTCTG	TCAGACGAATTCGCAAATACGCGA
	234	TCTGCGTGTCAACAATGTCCCGCAG	TCTGCGGGACATTGTTGACACGCAG
	235	TTCTGGTGCCACGCAAGGTCCACAG	TCTGTGGACCTTGCGTGGCACCAGA
	236	TCTCCGGGAGGTCACTTAATTGCGG	TCCGCAATTAAGTGACCTCCCGGAG
20	237	TTTTTCGTGATTGCCCGGAGGAGGC	TGCCTCCTCCGGGCAATCACGAAAA
	238	TTCCGGGATGTAGCTGGGGCTACCGG	TCCGGTAGCCCCAGCTACATCCCGA
	239	TCGAGCCAACGCAAACACGTCCTTG	TCAAGGACGTGTTGCGTTGGCTCG
	240	TGCAAAGCCTTTGTGGGGCGGTAGT	TACTACCGCCCCACAAAGGCTTTGC
	241	TATTCGACCGGAAATGAGGTCTTCG	TCGAAGACCTCATTTCCGGTCTGAAT
25	242	TTTCGCTTGCTGAGTTGCTCTGTTT	TGAACAGAGCAACTCAGCAAGCGAA
	243	TCGCGTGAAGACCCCATTCGAGT	TACTCGGGAATGGGGTCTTCACGCG
	244	TAACCGTATTCGCGGTCACTTGTGG	TCCACAAGTGACCGCGAATACGGTT
	245	TGGGGCCAACCGTTTCGAGGCGTAT	TATACGCCTCGAAACGGTTGGCCCC
	246	TTTCGGCTGGCAGTCCAAACGGCTT	TAAGCCGTTTGGACTGCCAGCCGAA
30	247	TGGGTGTGGTTAGAATGCACGGTTC	TGAACCGTGCATTCTAACCACACCC
	248	TGCGAGGACCGAACTAGACAAACGG	TCCGTTTGTCTAGTTCGGTCTCTCG
	249	TACGCACGCGTGACCGAAGTTGCTG	TCAGCAACTTCGGTCACGCGTGCGT
	250	TTAAAAGGTGCTTTGAAAGGGGGA	TTCCCCCTTTCAAAGCGACCTTTTA
35	251	TTGCGATCGCTAACTGCTGGGACAA	TTTGTCCCAGCAGTTAGCGATCGCA
	252	TGGAGGTATAAGCGGAGCGGCCTCA	TTGAGGCCGCTCCGCTTATACCTCC
	253	TATGCTGACATGTCGTGCACCTCGT	TACGAGGTGCACGACATGTCAGCAT
	254	TTGTGGTTAAAGCGTCCGTTCAACG	TCGTTGAACGGACGCTTTAACCACA
	255	TCGTTACACCCGGCGTAAGCTGCGT	TACGCAGCTTACGCCGGTGTGAACG
	256	TCCTATCCCGGCGAGAACTTCTGTG	TCACAGAAGTTCTCGCCGGGATAGG
40	257	TGTCTGCACTCACGCAGCGGAGGGA	TTCCCTCCGCTGCGTGAGTGCAGAC
	258	TGCACGAGTTGGTGCTCGGCAGATT	TAATCTGCCGAGCACCAACTCGTG

5	259	TAACGTCGCACGACACACGTTGTC	TGACGAACGTGTGTCGTGCGACGTT
	260	TATGCGCGCTTATCCTAGCATGGTC	TGACCATGCTAGGATAAGCGCGCAT
	261	TTCACGTTTTCTCTCGACATGAGG	TCCTCATGTCGAGACGAAAACGTGA
	262	TTGTGCCTCATCCTTAGGATACGGC	TGCCGTATCCTAAGGATGAGGCACA
	263	TAGGTGGTGTGGGTCAACCGCTTTA	TTAAAGCGGTTGACCCACACCACCT
	264	TCTGGATCGAAGGGACTGCAAGCTC	TGAGCTTGCAAGTCCCTTCGATCCAG
	265	TTAGATCAACTCGCGTACGCATGGA	TTCCATGCGTACGCGAGTTGATCTA
	266	TGATCCTGCGGAGAAGAGAGTGCAG	TCTGCACTCTCTTCTCCGCAGGATC
10	267	TTACGTGTGGAGATGCCCCGAACCG	TCGGTTCGGGGCATCTCCACACGTA
	268	TGCGCTATGTCAATCGTGGGCGTAG	TCTACGCCCACGATTGACATAGCGC
	269	TAGCGAGGTTTCTAGCGTCGACACC	TGGTGTGACGCTAGAAACCTCGCT
	270	TACCCAGGTTTTGCCGTTGTGGAAT	TATTCCACAACGGCAAAACCTGGGT
	271	TCCCTGTAAACGGCTGCGTAGTCTC	TGAGACTACGCAGCCGTTAACAGGG
	272	TAGGCCGATTTACCCGCCAATTGC	TGCAATTGGCGGGTGAAATCGGCCCT
15	273	TGAGCCCTCACTCCTTGCCCTTTGA	TTCAAAGGGCAAGGAGTGAGGGCTC
	274	TGGGTGGACATCCGCCTCGCAGTCA	TTGACTGCGAGGCGGATGTCCACCC
	275	TGATGGCTGAGAACCGTGCTACGAT	TATCGTAGCACGGTTCTCAGCCATC
	276	TTCGACGTTAGGAGTGCTGCCAGAA	TTTCTGGCAGCACTCCTAACGTCGA
	277	TCGAATGGGTCTGGACCTTGCTAG	TCTATGCAAGGTCCAGACCCATTG
20	278	TGTGCACCAGACATTGCAACTCGGA	TTCCGAGTTCGAATGTCTGGTGAC
	279	TAGAGGCCCCGTATATCCCATCCAT	TATGGATGGGATATACGGGGCCTCT
	280	TAACGCCTGTTGAGAGCATCAGCGG	TCCGCTGATGCTCTGAACAGGCGTT
	281	TAAGGCTCAACACGCCTATGTGCGC	TGCGCACATAGGCGTGTTGAGCCTT
	282	TAGTCCGTGTTGCCAGATTGGCTCG	TCGAGCCAATCTGGCAACACGGACT
25	283	TATGTCCCATGTAAAGACGCGTGTG	TCACACGCGTCTTTACATGGGACAT
	284	TATGGAGTCTGCTACGCCCCAAAGG	TCCTTTGGGCGTGAGCAGACTCCAT
	285	TCGGCCTCCAACAAGGAGCACTAAC	TGTTAGTGCTCCTTGTTGGAGGCCG
	286	TCAGAGCCGTGGCAACATTGCGAGC	TGCTCGCAATGTTGCCACGGCTCTG
	287	TTCATTTGAATGAGGTGCGCACCCG	TCCGGTGCGCACCTCATTCAAATGA
30	288	TGACGTACCGGAAGCGCCGTATAAA	TTTTATACGGCGCTTCCGGTACGTC
	289	TATGCGAGCAATGGGATCCGGATTC	TGAATCCGGATCCCATGCTCGCAT
	290	TAGAGTGAGGCCTCCCTGACCAGTG	TCACTGGTCAGGGAGGCCTCACTCT
	291	TCGCACCGTAAGTAGATTGCCCCG	TGCGGGCAAATCTACTTACGGTGCG
	292	TTGAACCTTTGAGCACGTGCTGCGC	TGCGCACGACGTGCTCAAAGGTTCA
35	293	TTCCGCCTTTTGGTTACCTCGAAG	TCTTCGAGGTAACCAAAAAGGCGGA
	294	TGAACGCCAACGGCACTAACACATC	TGATGTGTTAGTGCCGTTGGCGTTC
	295	TCCGACAGCAGCCAAGACGTCCAG	TCTGGGACGTCTTGGCTGCTGTCGG
	296	TCATAAAAAACCTGGGGCTCTGCG	TCGCAGAGCCCCAGTTTTTTTATG
	297	TTGCCAACTGTGCAGACCGGACTTA	TTAAGTCCGGTCTGCACAGTTGGCA
40	298	TGGCGAAAGAGCGAAACCGGCTCGT	TACGAGCCGGTTTCGCTCTTCGCC
	299	TGGGATGCGTATTTAGCGAACACG	TCGTGTTGCTAAAATACGCATCCC

	300	TTGGGATT CAGCGACCAGTACGCGA	TTCGCGTACTGGTCGCTGAATCCCA
	301	TCCCCGATATTCGCCGGCCTATTCTG	TCGAATAGGCCGGGCGAATATCGGG
	302	TCGAGAAGATGCCTCACGCAACCAA	TTTGGTTGCGTGAGGCATCTTCTCG
	303	TAACCTTGACCCGTGGATGACGCTA	TTAGCGTCATCCACGGGTCAAGGTT
5	6	TTTGCAACGGGCTGGTCAACGTCAA	TTTGACGTTGACCAGCCC GTTGCAA
	7	TCGCATAGGTTGCCGATTTCGTCAA	TTTGACGAAATCGGCAACCTATGCG
	306	TGCTTCCGGATGAACGGGATGGTTG	TCAACCATCCCGTTTCATCCGGAAGC
	307	TCCCTCCATGTTCTTCGAACGGTTT	TAAACCGTTCGAAGAACATGGAGGG
10	308	TTTGATGGGCGGCAATGCTCTTGCT	TAGCAAGAGCATTGCCGCCCATCAA
	309	TATTGTGAGATGCGCCAAATCCCC	TGGGGAATTTGGCGCATCTCACAAT
	310	TTCAGCACAGCCAGACGGTCAACTT	TAAGTTGACCGTCTGGCTGTGCTGA
	311	TACTCCACTCCTCGGTGGCAAACCTA	TTAGTTTGCCACCGAGGAGTGGAGT
	312	TTCTGGGCATGCCTGGACGGAGACG	TCGTCTCCGTCCAGGCATGCCCAGA
	313	TTCTCAACTCCGGTACGACGAAACA	TTGTTTCGTCTGACCGGAGTTGAGA
15	314	TTTGCGTGGTCAAAGGCGCAACGTG	TCACGTTGCGCCTTTGACCACGCAA
	315	TAGACAGCGATCCGCGGCTCATGAT	TATCATGAGCCGCGGATCGCTGTCT
	316	TCGCGTCTCTAACTGAGAGCAGCCA	TTGGCTGCTCTCAGTTAGAGACGCG
	317	TAGGCGCACATGTACGGACATTCAAG	TCTGAATGTCCGTACATGTGCGCCT
20	318	TGATGAGTGGCACGTCGGTGTGTAA	TTTACACACCGACGTGCCACTCATC
	319	TTGATCCATATTGTCCGACGTTGCG	TCGCAACGTCCGACAATATGGATCA
	320	TACCTGCCGGGAGTTCATAGGCTAG	TCTAGCCTATGAACTCCCGGCAGGT
	321	TAGCATTGGCGTTTTTCCGCAACGA	TTCGTTGCGGAAAAACGCCAATGCT
	322	TGGTAATATTCAGCGCGACCGCTCA	TTGAGCGGTGCGCGCTGAATATTACC
	323	TATAGCGTACGACGAGGTGACGCGC	TGCGCGTCACCTCGTCTGACGCTAT
25	324	TTAGGTCACGATGCGTTTGACGCTA	TTAGCGTCAAACGCATCGTGACCTA
	325	TACTGCCCCGTACCTCTGGTTCTGGC	TGCCAGAACCAGAGGTACGGGCAGT
	326	TCCTTTGGCCTGAAGTTGTCTGAGC	TGCTACGACAACCTCAGGCCAAAGG
	327	TGTGCCCCACGAGCGTATCGTTGTA	TTACAACGATACGCTCGTGGGGCAC
	328	TAGGCGCTACGTGGGCCTGGAGCAA	TTTGCTCCAGGCCACGTAGCGCCT
30	329	TGGGTGCTACCATTGCATTAGTCCG	TCGGACTAATGCAATGGTAGCACCC
	330	TACCACGCGCGTACGTGTAACCGAG	TCTCGGTTACACGTACGCGCGTGGT
	331	TCCATGATGCATTGGGTGCATTTAG	TCTAAATGCACCCAATGCATCATGG
	332	TGGTCCGGCCCTACGAAACGTTCTGA	TTCGAACGTTTCGTAGGGCCGGACC
	333	TCCGTGTGGCTGGAGATTTCGTGTGA	TTACACGAATCTCCAGCCACACGG
35	334	TGTTAGGGCGACGCATATTGGCACA	TTGTGCCAATATGCGTCGCCCTAAC
	335	TGGGTGAGTCAGGTGCGTTAGGATC	TGATCCTAACGCACCTGACTGACCC
	336	TGCCGTGAAGTCGAATGCAGATCGA	TTCGATCTGCATTGACTTCACGGC
	337	TGCCACCACCCAGTGCATTCAGGTA	TTACCTGAATGCACTGGGTGGTGGC
	338	TGAGCTTAGTTTGGCGTCATCGGGC	TGCCCCGATGACCGCAAACCTAAGCTC
40	339	TTGTTTGCCGCCATTAGGGAGTAAC	TGTTACTCCCTAATGGCGGCAAACA
	340	TGCTCCGCTGGATGTGCCGGTTTAG	TCTAAACCGGCACATCCAGCGGAGC



5	341	TCGGTAGCATGCGAGATCCCTGTTA	TTAACAGGGATCTCGCATGCTACCG
	342	TCTACGCTCTACCAGTTGCCTGCGA	TTCGCAGGCAACTGGTAGAGCGTAG
	343	TGTGCCTCCTGCTGTATTGCCAAG	TCTTGGCAAATACAGCAGGAGGCAC
	344	TTTGCGACTCGACTTGGACGAGTAG	TCTACTCGTCCAAGTCGAGTCGCAA
	345	TTCTGGGAGCTGTTTACTCCAGCCA	TTGGCTGGAGTAAACAGCTCCCAGA
	346	TTGCACGCGGAACCTCCCTTTACCAT	TATGGTAAAGGGAGTTCCGCGTGCA
	347	TTGGCAGCAAATGAATCGAAAGCAC	TGTGCTTTCGATTCATTTGCTGCCA
	348	TAAGTGGTGACGCGGTACAGCGAAG	TCTTCGCTGTACCGCGTCACCAAGTT
10	349	TAGACGATTACGCTGGACGCCGTCG	TCGACGGCGTCCAGCGTAATCGTCT
	350	TATGCCCTCCTTCATGAAAAGGGTT	TAACCCCTTCCATGAAGGAGGGCAT
	351	TATTCTCGGAGCGTATGCGCCAGAA	TTTCTGGCGCATACGCTCCGAGAAT
	352	TATAGCGGAGTTTGGGTACGCGAAC	TGTTGCGGTACCCAACTCCGCTAT
	353	TACCTACGCATACCGCTTGGCGAGG	TCCTCGCCAAGCGGTATGCGTAGGT
15	354	TGATTACCTGAATGGCCAAGCGAGC	TGCTCGCTTGGCCATTACAGGTAATC
	355	TCCTGTTAGCATCACGGCGCTTAGG	TCCTAAGCGCCGTGATGCTAACAGG
	356	TCGGAATGATGCGCTCGACAACGCT	TAGCGTTGTCGAGCGCATCATTCCG
	357	TTGAGAGAGGCGTTGGTTAAGGCAA	TTTGCCCTTAACCAACGCCTCTCTCA
	358	TAAGCAGGCGAAGGGATACTCCTCG	TCGAGGAGTATCCCTTCGCCTGCTT
20	359	TTACGACAGACGGGCCGAGATTAC	TGTAATCTCGGCCCGTCTGTCGTGA
	360	TAAGCAATTTGGCCTCGTTTTGTGA	TTACAAAAACGAGGCCAAATTGCTT
	361	TGCTGGTTGCGGTAGGATCGCATAT	TATATGCGATCCTACCGCAACCAGC
	362	TTTGTGAATCCGTTCTGTCCCCGAC	TGTCGGGGACAGAACGGATTACAA
	363	TTGGGCTCCTCTGAGGCGAGATGGC	TGCCATCTCGCCTCAGAGGAGCCCA
	364	TGGATAGAGTGAATCGACCGGCAAC	TGTTGCCGGTTCGATTCACTCTATCC
25	365	TTGCACCGAACGTGCACGAGTAATT	TAATTACTCGTGACGTTCCGGTGCA
	366	TGCCAGTATTCTCGGGTGTTGGACG	TCGTCCAACACCCGAGAATACTGGC
	367	TTGCTACCTAAGACCGGGCCATAC	TGTATGGCCCGGTCTTAGGTAGCGA
	368	TTGGCATTGACGAGCAGCAGTCAGT	TACTGACTGCTGCTCGTCAATGCCA
	369	TCGCGTCCAGCGCCCTTGGAGTAT	TATACTCCAAGGGCGCTGGGACGCG
30	370	TATGAAGCCTACCGGGCGACTTCGT	TACGAAGTCGCCCCGTAGGCTTCAT
	371	TCCAGACAGATGGCCTGGAACCATG	TCATGGTTCCAGGCCATCTGTCTGG
	372	TTGGCGTGGGACCATCTCAAAGCTA	TTAGCTTTGAGATGGTCCCACGCCA
	373	TCCGCATGGGAACACGTGTCAAGGT	TACCTTGACACGTGTTCCCATGCGG
35	374	TGCCCCACTCGTCAGCTGGACGTAAT	TATTACGTCCAGCTGACGAGTGGGC
	375	TATTACGGTCGTGATCCAGAAAGCG	TCGCTTTCTGGATCACGACCGTAAT
	376	TTGCGAGGTGAGCACCTACGAGAGA	TTCTCTCGTAGGTGCTCACCTCGCA
	377	TGGGCCCGCATTCTTGATGTCCATT	TGAATGGACATCAAGAATGCGGCCC
	378	TCCTCGGATGTGGGCTCTCGCCTAG	TCTAGGCGAGAGCCCACATCCGAGG
40	379	TTAGGCATGTTGGCGTGAGCGCTAT	TATAGCGCTCACGCCAACATGCCTA
	380	TCGATACGAACGAGGATGTCCGCCT	TAGGCGGACATCCTCGTTTCGTATCG
	381	TTACGCCGGTTAGCACGGTGCGCTA	TTAGCGCACCGTGCTAACCGGCGTA

5	382	TCATACGATGTCCGGGCCGTGTGCGC	TGCGACACGGCCCCGGACATCGTATG
	383	TATCCGCAGTTGTATGGCGCGTTAT	TATAACGCGCCATACAACCTGCGGAT
	384	TGGGTAAGGGACAAAGATGGGATGG	TCCATCCCATCTTTGTCCCTTACCC
	385	TATTGGAGTGTTTTGGTGAATCCGC	TGCGGATTCACCAAAACACTCCAAT
	386	TGAACCGAGCCAACGTATGGACACG	TCGTGTCCATACGTTGGCTCGGTTC
	387	TGCCGTCAAGCTTAAGGTTTTGGGC	TGCCCAAACCTTAAGCTTGACGGC
	388	TACCTGCTTTTGGGTGGGTGATATG	TCATATCACCCACCCAAAAGCAGGT
	389	TAATCGTGGGCGCAGCAAACGTATA	TTATACGTTTTGCTGCGCCACGATT
10	390	TGTCGCCGGATTGCTCAGTATAAGC	TGCTTATACTGAGCAATCCGGCGAC
	391	TACCCGTCGATGCTTCCTCCTCAGA	TTCTGAGGAGGAAGCATCGACGGGT
	392	TATCCGGGTGGGCGATACAAGAGAT	TATCTCTTGATCGCCACCCGGAT
	393	TTTCCGCATGAGTCAGCTTTGAAA	TTTTTCAAAGCTGACTCATGCGGAA
	394	TGCAAAGTCCCACTGGCAAGCCGAT	TATCGGCTTGCCAGTGGGACTTTGC
	395	TCGACCTCGGCTTCATCGTACACAT	TATGTGTACGATGAAGCCGAGGTCTG
15	396	TCTCATGAGCGCAGTTGTGCGTGAG	TCTCACGCACAACCTGCGCTCATGAG
	397	TCAGATGAAGGATCCACGGCCGGAG	TCTCCGGCCGTGGATCCTTCATCTG
	398	TTCAAAGGCTCTTGGATACAGCCGT	TACGGCTGTATCCAAGAGCCTTTGA
	399	TTCCGCTAATTTCCAATCAGGGCTC	TGAGCCCTGATTGGAAATTAGCGGA
20	8	TCCGTTTGCGGTCGTCTTGCTCAA	TTTGAGCAAGGACGACCGCAAACGG
	9	TTTCGCTTTCGTGGCTGCACTTCAA	TTTGAAGTGCAGCCACGAAAGCGAA
	402	TCTTAGTTGGGGCGCGGTATCCAGA	TTCTGGATACCGCGCCCCAACTAAG
	403	TGCTCTAATGCCGTGGAGTCGGAAC	TGTTCCGACTCCACGGCATTAGAGC
	404	TCCGATTACAAATTGACTGACCGCA	TTGCGGTCAGTCAATTTGTAATCGG
	405	TAGACGTACGTGAGCCTCCCGTGTC	TGACACGGGAGGCTCACGTACGTCT
25	406	TAATGGAGCGATACGATCCAACGCA	TTGCGTTGGATCGTATCGCTCCATT
	407	TGGAGGCGCTGTACTGATAGGCGTA	TTACGCCTATCAGTACAGCGCCTCC
	408	TTGTTTTGAATTGACCACACGGGA	TTCCCGTGTGGTCAATTCAAAAACA
	409	TCATGTCTGGATGCGCTCAATGAAG	TCTTCATTGAGCGCATCCAGACATG
	410	TGCCCGCTAATCCGACACCCAGTTT	TAAACTGGGTGTGCGATTAGCGGGC
30	411	TCCATTGACAGGAGAGCCATGAGCC	TGGCTCATGGCTCTCCTGTCAATGG
	412	TGAATCACCGAATCACCAGCTCGTT	TAACGAGTCGGTGATTCCGTGATTCT
	413	TAACCAGCCGCAGTAGCTTACGTCG	TCGACGTAAGCTACTGCGGCTGGTT
	414	TTTTTCTGAGGGACACGCGGGCGTT	TAACGCCCCGCGTGCCCTCAGAAAA
	415	TGGTGCTCCGTTTGATCGATCCTCC	TGGAGGATCGATCAAACGGAGCACC
35	416	TCCGCTTAGGCCATACTCTGAGCCA	TTGGCTCAGAGTATGGCCTAAGCGG
	417	TTAAGACATACCGACGCCCTTGCCCT	TAGGCAAGGGCGTCGGTATGTCTTA
	418	TGTTCCCGACGCCAGTCATTGAGAC	TGTCTCAATGACTGGCGTCGGGAAC
	419	TTAAAAGTTTCGCGGAGTCCGGGCT	TAGCCCGACCTCCGCGAAACTTTTA
	420	TCGGTCCAGACGAGCTGAGTTCGGC	TGCCGAACCTCAGCTCGTCTGGACCG
40	421	TCGGCGTAGCGGCTACGGACTTAAA	TTTTAAGTCCGTAGCCGCTACGCCG
	422	TGCTTGATGCCCATGCGGCAAGGT	TACCTTGCCGCATGGGCATCCAAGC

423	TAGCGGGATCCCAGAGTTTCGAAAA	TTTTTCGAAACTCTGGGATCCCGCT
424	TGAGCTTGAGAGCGAGGTCATCCTC	TGAGGATGACCTCGCTCTCAAGCTC
425	TGCATCGGCCGTTTTGACCATATTC	TGAATATGGTCAAACGGCCGATGC
426	TCATAGCGCTGCACGTTTCGACCGC	TGCGGTGGAACGTGCAGCGCTATG
427	TACCCGACAACCACCAATTCAAAAA	TTTTTTGAATTGGTGGTTGTCGGGT
428	TGCGAACACTCATAAGAGCGCCCTG	TCAGGGCGCTCTTATGAGTGTTCCG
429	TCCGCCGAGTGTAGAGAGACTCCGA	TTCGGAGTCTCTCTACACTCGGCCG
430	TGACATCGGGAGCCGGAACATGAG	TCTCATGTTTCCGGCTCCCGATGTC
431	TTCGTGTAGACTCGGCCGACAGGCGT	TACGCCTGTCGCCGAGTCTACACGA
432	TATGCGCATATACTGACTGCGCAGG	TCCTGCGCAGTCAGTATATGCGCAT
433	TACAAGCGAACCCGAGTTTTGATGA	TTTATCAAAACTCGGGTTTCGTTGT
434	TGCATGAGACTCCGCGAAGACATGT	TACATGTCTTCGCGGAGTCTCATGC
435	TTCCTACATGTCGCGTCACGATCAC	TGTGATCGTGACGCGACATGTAGGA
436	TGACCGATCGCGAAGTCGTACACAT	TATGTGTACGACTTCGCGATCGGTC
437	TGTCGCCAGGACTGGGCCGATGTGA	TTACATCGGCCCAGTCTTGCGCAG
438	TACCGATAAGACTTGCATCCGAACG	TCGTTCCGATGCAAGTCTTATCGGT
439	TTCCATAACCAGTCCGAAGTGCCGG	TCCGGCACTTCGGAAGTGTATGGA
440	TACGCGCCCTGCATCTCGTATTTAA	TTTAAATACGAGATGCAGGGCGCGT
441	TAGACCGCATCAATTGGCGCGTACC	TGGTACGCGCCAATTGATGCGGTCT
442	TAGAGGCTTGGAAGTAGGGACCCT	TAGGGTCCCTACTTGCCAAGCCTCT
443	TGCAATGGACGCCAGACGATACCGG	TCCGGTATCGTCTGGCGTCCATTGC
444	TGCTGGACTTAGTCGTGTTCCGGCGG	TCCGCCGAACACGACTAAGTCCAGC
445	TAGGCATCGTGCCGGATTGCTCCCT	TAGGGAGCAATCCGGCACGATGCCT
446	TTGCGCATGTCGACGTTGAACAAAG	TCTTTGTTCAACGTCGACATGCGCA
447	TTTCGGGTCACATCCGATGCCATAC	TGTATGGCATCGGATGTGACCCGAA
448	TACCCATCGCCGGAAGCGATGTTG	TCAACATCGCTTTCGGCGATGGGT
449	TAAGCGCTGACTCGGCTAAGAATCA	TTGATTCTTAGCCGAGTCAGCGCTT
450	TACTTCCAAGTCCTTGACCGTCCGA	TTCCGACGGTCAAGGACTTGGAAGT
451	TTCTCAATATTCCCGTAGTCGCCCA	TTGGGCGACTACGGGAATATTGAGA
452	TAACAGTTCCTCTTTTTCTGGCGC	TGCGCCAGGAAAAAGAGGAACTGTT
453	TCGTCTCCATGTTGTCACGAACAG	TCTGTTCTGTGACAACATGGAGGACG
454	TTGCGCAGACCTACCTGTCTTTGCT	TAGCAAAGACAGGTAGGTCTGCGCA
455	TATGGACGGCTTCGCAGTCCTCCTT	TAAGGAGGACTGCGAAGCCGTCCAT
456	TTGAACGCTTTCTATGGGCCACGTA	TTACGTGGCCCATAGAAAGCGTTCA
457	TTGAACCCTGCCGCGAGCGATAACC	TGGTTATCGCTCGCGGCAGGGTTCA
458	TGTTCTTGCGCGATGAATCAGGACC	TGGTCCTGATTCATCGCGCAAGAAC
459	TAGGGTACGTGTCGCAGCTTCGCGT	TACGCGAAGCTGCGACACGTACCCT
460	TACCCTTGCTCCGCCATGTCTCTCA	TTGAGAGACATGGCGGAGCAAGGGT
461	TGGGACAAGGATTGAAGCTGGCGTC	TGACGCCAGCTTCAATCCTTGTCCT
462	TTGTCTGTTGCTCCCGAGTACCATTG	TCAATGGTACTCGGGAGCAACGACA
463	TGTTGTCCGAGACGTTTGTGTCAGC	TGCTGACACAAACGTCTCGGACAAC

382	TCATACGATGTCCGGGCCGTGTGCGC	TGCGACACGGCCCGGACATCGTATG
383	TATCCGCAGTTGTATGGCGCGTTAT	TATAACGCGCCATACAACGCGGAT
384	TGGGTAAGGGACAAAGATGGGATGG	TCCATCCCATCTTTGTCCCTTACCC
385	TATTGGAGTGTTTTGGTGAATCCGC	TGCGGATTCACCAAAACACTCCAAT
386	TGAACCGAGCCAACGTATGGACACG	TCGTGTCCATACGTTGGCTCGGTTT
387	TGCCGTCAAGCTTAAGGTTTTGGGC	TGCCCCAAACCTTAAGCTTGACGGC
388	TACCTGCTTTTGGGTGGGTGATATG	TCATATCACCCACCCAAAAGCAGGT
389	TAATCGTGGGCGCAGCAAACGTATA	TTATACGTTTGCTGCGCCACGATT
390	TGTCGCCGGATTGCTCAGTATAAGC	TGCTTATACTGAGCAATCCGGCGAC
391	TACCGTCGATGCTTCCTCCTCAGA	TTCTGAGGAGGAAGCATCGACGGGT
392	TATCCGGGTGGGCGATACAAGAGAT	TATCTCTTGATCGCCCACCCGGAT
393	TTTCCGCATGAGTCAGCTTTGAAAA	TTTTTCAAAGCTGACTCATGCGGAA
394	TGCAAAGTCCCACTGGCAAGCCGAT	TATCGGCTTGCCAGTGGGACTTTGC
395	TCGACCTCGGCTTCATCGTACACAT	TATGTGTACGATGAAGCCGAGGTCTG
396	TCTCATGAGCGCAGTTGTGCGTGAG	TCTCACGCACAACTGCGCTCATGAG
397	TCAGATGAAGGATCCACGGCCGGAG	TCTCCGGCCGTGGATCCTTCATCTG
398	TTCAAAGGCTCTTGATACAGCCGT	TACGGCTGTATCCAAGAGCCTTTGA
399	TTCCGCTAATTTCCAATCAGGGCTC	TGAGCCCTGATTGGAAATTAGCGGA
8	TCCGTTTGCGGTGCTCCTTGCTCAA	TTTGAGCAAGGACGACCGCAAACGG
9	TTTCGCTTTCGTGGCTGCACTTCAA	TTTGAAGTGCAGCCACGAAAGCGAA
402	TCTTAGTTGGGGCGCGGTATCCAGA	TTCTGGATACCGCGCCCCAACTAAG
403	TGCTCTAATGCCGTGGAGTCGGAAC	TGTTCCGACTCCACGGCATTAGAGC
404	TCCGATTACAAATTGACTGACCGCA	TTGCGGTCAGTCAATTTGTAATCGG
405	TAGACGTACGTGAGCCTCCCGTGTC	TGACACGGGAGGCTCACGTACGTCT
406	TAATGGAGCGATACGATCCAACGCA	TTGCGTTGGATCGTATCGCTCCATT
407	TGGAGGCGCTGTACTGATAGGCGTA	TTACGCCTATCAGTACAGCGCCTCC
408	TTGTTTTTGAATTGACCACACGGGA	TTCCCGTGTGGTCAATTCAAAAACA
409	TCATGTCTGGATGCGCTCAATGAAG	TCTTCATTGAGCGCATCCAGACATG
410	TGCCCGCTAATCCGACACCCAGTTT	TAAACTGGGTGTCGGATTAGCGGGC
411	TCCATTGACAGGAGAGCCATGAGCC	TGGCTCATGGCTCTCCTGTCAATGG
412	TGAATCACCGAATCACCGACTCGTT	TAACGAGTCGGTGATTCCGGTGATTC
413	TAACCAGCCGCAGTAGCTTACGTCG	TCGACGTAAGCTACTGCGGCTGGTT
414	TTTTTCTGAGGGACACGCGGGCGTT	TAACGCCCCGCGTGTCCCTCAGAAAA
415	TGGTGCTCCGTTTGATCGATCCTCC	TGGAGGATCGATCAAACGGAGCACC
416	TCCGCTTAGGCCATACTCTGAGCCA	TTGGCTCAGAGTATGGCCTAAGCGG
417	TTAAGACATACCGACGCCCTTGCCCT	TAGGCAAGGGCGTCCGTATGTCTTA
418	TGTTCCCGACGCCAGTCATTGAGAC	TGTCTCAATGACTGGCGTCGGGAAC
419	TTAAAAGTTTCGCGGAGGTCGGGCT	TAGCCCGACCTCCGCGAAACTTTTA
420	TCGGTCCAGACGAGCTGAGTTCGGC	TGCCGAACCTCAGCTCGTCTGGACCG
421	TCGGCGTAGCGGCTACGGACTTAAA	TTTTAAGTCCGTAGCCGCTACGCCG
422	TGCTTGGATGCCCATGCGGCAAGGT	TACCTTGCCGCATGGGCATCCAAGC

5	423	TAGCGGGATCCCAGAGTTTCGAAAA	TTTTTCGAAACTCTGGGATCCCGCT
	424	TGAGCTTGAGAGCGAGGTCATCCTC	TGAGGATGACCTCGCTCTCAAGCTC
	425	TGCATCGGCCGTTTTGACCATATTC	TGAATATGGTCAAACGGCCGATGC
	426	TCATAGCGCTGCACGTTTCGACCGC	TGCGGTGCAAACGTGCAGCGCTATG
	427	TACCCGACAACCACCAATTCAAAAA	TTTTTTGAATTGGTGGTTGTCGGGT
	428	TGCGAACACTCATAAGAGCGCCCTG	TCAGGGCGCTCTTATGAGTGTTCCG
	429	TCCGCCGAGTGTAGAGAGACTCCGA	TTCCGAGTCTCTCTACACTCGGCGG
	430	TGACATCGGGAGCCGGAACATGAG	TCTCATGTTCCGGCTCCCGATGTC
10	431	TTCGTGTAGACTCGGCGACAGGCGT	TACGCCTGTCGCCGAGTCTACACGA
	432	TATGCGCATATACTGACTGCGCAGG	TCCTGCGCAGTCAGTATATGCGCAT
	433	TACAAGCGAACCCGAGTTTTGATGA	TTTCATCAAACTCGGGTTCGCTTGT
	434	TGCATGAGACTCCGCGAAGACATGT	TACATGTCTTCGCGGAGTCTCATGC
	435	TTCTTACATGTCGCGTCACGATCAC	TGTGATCGTGACGCGACATGTAGGA
	436	TGACCGATCGCGAAGTCGTACACAT	TATGTGTACGACTTCGCGATCGGTC
15	437	TGTCGCCAGGACTGGGCCGATGTGA	TTACATCGGCCCAGTCTTGCGCAG
	438	TACCGATAAGACTTGCATCCGAACG	TCGTTCCGATGCAAGTCTTATCGGT
	439	TTCCATAACCAGTCCGAAGTGCCGG	TCCGGCACTTCGGAAGTGTATGGA
	440	TACGCGCCCTGCATCTCGTATTTAA	TTTAAATACGAGATGCAGGGCGCGT
	441	TAGACCGCATCAATTGGCGCGTACC	TGGTACGCGCCAATTGATGCGGTCT
20	442	TAGAGGCTTGCGCAAGTAGGGACCT	TAGGGTCCCTACTTGCCAAGCCTCT
	443	TGCAATGGACGCCAGACGATACCGG	TCCGGTATCGTCTGGCGTCCATTGC
	444	TGCTGGACTTAGTCGTGTTCCGGCGG	TCCGCCGAACACGACTAAGTCCAGC
	445	TAGGCATCGTGCCGATTGCTCCCT	TAGGGAGCAATCCGGCACGATGCCT
	446	TTGCGCATGTGACGTTGAACAAAG	TCTTTGTTCAACGTCGACATGCGCA
25	447	TTTCGGGTACATCCGATGCCATAC	TGTATGGCATCGGATGTGACCCGAA
	448	TACCCATCGCCGGAAGCGATGTTG	TCAACATCGCTTCCGGCGATGGGT
	449	TAAGCGCTGACTCGGCTAAGAATCA	TTGATTCTTAGCCGAGTCAGCGCTT
	450	TACTTCCAAGTCCTTGACCGTCCGA	TTCCGACGGTCAAGGACTTGGAAGT
	451	TTCTCAATATTTCCCGTAGTCGCCCA	TTGGGCGACTACGGGAATATTGAGA
30	452	TAACAGTTCCTCTTTTCTGCGCG	TGCGCCAGGAAAAAGAGGAACTGTT
	453	TCGTCTCCATGTTGTCACGAACAG	TCTGTTCTGTGACAACATGGAGGACG
	454	TTGCGCAGACCTACCTGTCTTTGCT	TAGCAAAGACAGGTAGGTCTGCGCA
	455	TATGGACGGCTTCGCAGTCTCCTT	TAAGGAGGACTGCGAAGCCGTCCAT
	456	TTGAACGCTTTCTATGGGCCACGTA	TTACGTGGCCCATAGAAAGCGTTCA
35	457	TTGAACCCTGCCGCGAGCGATAACC	TGGTTATCGCTCGCGGCAGGGTTCA
	458	TGTTCTTGCGCGATGAATCAGGACC	TGGTCCTGATTCATCGCGCAAGAAC
	459	TAGGGTACGTGTGCGAGCTTCGCGT	TACGCGAAGCTGCGACACGTACCCT
	460	TACCCTTGCTCCGCCATGTCTCTCA	TTGAGAGACATGGCGGAGCAAGGGT
	461	TGGGACAAGGATTGAAGCTGGCGTC	TGACGCCAGCTTCAATCCTTGTCCC
40	462	TTGTCGTTGCTCCCGAGTACCATTG	TCAATGGTACTCGGGAGCAACGACA
	463	TGTTGTCCGAGACGTTTGTGTCAGC	TGCTGACACAAACGTCTCGGACAA

5	464	TGCTGGTGAACACTCACGAACCGCT	TAGCGGTTCGTGAGTGTTCAACCAGC
	465	TGCAGACAGGGCAAATCGGTGCAAA	TTTTGCACCGATTGGCCCTGTCTGC
	466	TCCCATCACAAACGAGTGGCGACTTT	TAAAGTCGCCACTCGTTGTGATGGG
	467	TGCTTCTACAGCTGGCGTGCTAGCG	TCGCTAGCACGCCAGCTGTAGAAGC
	468	TGAATGTGTGCCGACCATTCTAGCC	TGGCTAGAATGGTCGGCACACATTC
	469	TCCAGCGGAAGTTAGAGCTCTGTGG	TCCACAGAGCTCTAACTTCCGCTGG
	470	TTTTTTACCGACCACTCCATGTGG	TCCGACATGGAGTGGTCGGTAAAAA
	471	TGCGGCTATGTGATGACGGCCTAGC	TGCTAGGCCGTCATCACATAGCCGC
10	472	TAGTACACGGGCGTGTTAGCGCTCC	TGGAGCGCTAACACGCCCCGTGTACT
	473	TTCCTGTGTGGTGGCGCACTCCAC	TGTGGGAGTGCGCCACCACACAGGA
	474	TCCAACTAACCAATCGCGCGGATGA	TTCATCCGCGCGATTGGTTAGTTGG
	475	TAGTGAGTGACCAAGGCAGGAGCAA	TTTGCTCCTGCCTTGGTCACTCACT
	476	TCATCTTTCGCGGAGTTTATTGCGG	TCCGCAATAAACTCCGCGAAAGATG
	477	TCTTCGTCCGGTTAGTGCGACAGCA	TTGCTGTGCGACTAACCGGACGAAG
15	478	TCTCACGAAAACGTGGGCCCCGAAAT	TATTCGGGCCCCACGTTTTCGTGAG
	479	TCGCAGCAGCTGAACTCTAGCATTG	TCAATGCTAGAGTTCAGCTGCTGCG
	480	TAGGAGACATACGCCCAAATGGTGC	TGCACCATTTGGGCGTATGTCTCCT
	481	TATTGAGAACTCGTGCGGGAGTTTG	TCAAACCTCCCGCACGAGTTCTCAAT
	482	TCTCTTTGTAGGCCCAGGAGGAGCA	TTGCTCCTCCTGGGCCCTACAAAGAG
20	483	TGCCCGCAGGGTCGATAATTGGTCTA	TTAGACCAATTATCGACCCTGCGGC
	484	TAAACGCCGCCCTGAGACTATTGGG	TCCAATAGTCTCAGGGCGGCGTTT
	485	TCTGAGTTGCCTGGAACGTTGGACT	TAGTCCAACGTTCCAGGCAACTCAG
	486	TCGGATGGGTTGCAGAGTATGGGAT	TATCCCATACTCTGCAACCCATCCG
	487	TCTGACCTTTGGGGGTTAGTGCGGT	TACCGCACTAACCCCCAAAGGTCAG
25	488	TGGAAATGAGAACCTTACCCAGCG	TCGCTGGGGTAAGGTTCTCATTTC
	489	TAACGCATCGTCCGTCAACTCATCA	TTGATGAGTTGACGGACGATGCGTT
	490	TTGGAGAGAGACTTCGGCCATTGTT	TAACAATGGCCGAAGTCTCTCTCCA
	491	TTTGCGCTCATTGGATCTTGTGAGG	TCCTGACAAGATCCAATGAGCGCAA
30	492	TAGCGCGTTAAAGCACGGCAACATT	TAATGTTGCCGTGCTTTAACGCGCT
	493	TAGCCAGTAACTGTGGGCGGCTGT	TACAGCCGCCACAGTTTACTGGCT
	494	TCGACTGATGTGCAACCAGCAGCTG	TCAGCTGCTGGTTGCACATCAGTCG
	495	TGGTTGCTCATACGACGAGCGAGTG	TCACTCGCTCGTCGTATGAGCAACC
	10	TGTCCAACGCGCAACTCCGATTCAA	TTTGAATCGGAGTTGCGCGTTGGAC
	11	TTTGCCGCACCGTCCGTCATCTCAA	TTTGAGATGACGGACGGTGCGGCAA
35	498	TAGAACCTCCGCGCCTCCGTAGTAG	TCTACTACGGAGGCGCGGAGGTTCT
	499	TAAAGGAGCTTTCGCCCAACGTACC	TGGTACGTTGGGCGAAAGCTCCTTT
	500	TAGTGATTGTGCCACTCCACAGCTC	TGAGCTGTGGAGTGGCACAATCACT
	501	TGCGATCGTCGAGGGTTGAGCTGAA	TTTCAGCTCAACCCTCGACGATCGC
	502	TGGGAGACAGCCATTATGGTCTCTCG	TCGAGGACCATAATGGCTGTCTCCC
40	503	TGAGACGCTGTCACTCCGGCAGAAC	TGTTCTGCCGGAGTGACAGCGTCTC
	504	TCCACCGGTCGCTTAAGATGCACTT	TAAGTGATCTTAAGCGACCGGTGG

505	TCGGCATAACGTCCAGTCCTGGGAC	TGTCCCAGGACTGGACGTTATGCCG
506	TAAGCGGAACGGGTTATACCGAGGT	TACCTCGGTATAACCCGTTCCGCTT
507	TTGCACACTAGGTCCGTCGCTTGAT	TATCAAGCGACGGACCTAGTGTGCA
508	TAGGGAACCGCGTTCAAACCTCAGTT	TAACTGAGTTTGAACGCGGTTCCCT
509	TGAATTACAACCACCCGCTCGTGTT	TAACACGAGCGGGTGGTTGTAATTC
510	TTTCAGTGCTCACGAAGCATGGATT	TAATCCATGCTTCGTGAGCACTGAA
511	TTTAGTTTGGCGTTGGGACTTCACC	TGGTGAAGTCCCAACGCCAACTAA
512	TAATGCGACCTCGACGAGCCTCATA	TTATGAGGCTCGTCGAGGTCGCATT
513	TCCGAAACCGTTAACGTGGCGCACA	TTGTGCGCCACGTTAACGGTTTCGG
514	TTAAAGTAACAAGGCGACCTCCCGC	TGCGGGAGGTCGCCTTGTTACTTTA
515	TTAATGATTTTAGTCGCGGGGTGGG	TCCCACCCCGCGACTAAAATCATT
516	TGGCTACTCTAAGTGCCCGCTCAGG	TCCTGAGCGGGCACCTTAGAGTAGCC
517	TTGGCGGACGACTCAATATCTCACG	TCGTGAGATATTGAGTCGTCCGCCA
518	TGGGCGTTAGGCGTAATAGACCGTC	TGACGGTCTATTACGCCTAACGCC
519	TGCCACCTTTAGACGGCGGCTCTAG	TCTAGAGCCGCCGTCTAAAGGTGGC
520	TGAGATGTGTAAACGTGCAGGCACC	TGGTGCCTGCACGTTTACACATCTC
521	TTAGCTCGTGGCCCTCCAAGCGTGT	TACACGCTTGAGGGCCACGAGCTA
522	TGTGTCGGCGCTATTTGGCCTTACC	TGGTAAGGCCAAATAGCGCCGACAC
523	TCCAGGGAAGCAACTGGTTGCCATT	TAATGGCAACCAGTTGCTTCCCTGG
524	TTTCCGAAACTAAGCCAGAACCCT	TAGCGGTTCTGGCTTAGTTTCGGAA
525	TGCAAACCCGTAACCCGAGAGTTC	TGAACTCTCGGGTTACCGGGTTTGC
526	TGCAAATGGCGTCATGCACGAACGT	TACGTTTCGTGCATGACGCCATTTGC
527	TAGTACTTTCGCGCCAGTTTAGGG	TCCCTAAACTGGGCGCGAAAGTACT
528	TAAGATCTGCGAGGCATCCCGGCTT	TAAGCCGGGATGCCTCGCAGATCTT
529	TGCAAGTGTATCGCACAGTGCGATT	TAATCGCACTGTGCGATACACTTGC
530	TCCGACAAGGCCTCAATTCATTCTG	TCAGAATGAATTGAGGCCTTGTCGG
531	TGTCTCGTCTCAACTTTAAGGCGCG	TCGCGCCTTAAAGTTGAGACGAGAC
532	TATCCAGAGATCCGTTTTGCAGCGT	TACGCTGCAAAACGGATCTCTGGAT
533	TGTCACCAGGAGGGAAGTTTCACCC	TGGGTGAACTTCCCTCCTGGTGAC
534	TTTCGTCAGGCGGATCAACGGAAT	TATTCCGTTGATCCGCCTGACGGAA
535	TATGCCGGACACGCATTACACAGGC	TGCCTGTGTAATGCGTGTCCGGCAT
536	TTGGGCCGCTTGGCGCTTTCATAGA	TTCTATGAAAGCGCCAAGCGGCCCA
537	TCCTAGCGCGAGCTTTACTGACCAG	TCTGGTCAGTAAAGCTCGCGCTAGG
538	TTTGGCCAGGAATATGGTCTCGAGA	TTCTCGAGACCATATTCCTGGCCAA
539	TGTCTGCGGCCGACTTGCTATGCAT	TATGCATAGCAAGTCGGCCGCAGAC
540	TAACTTGCTCATTCTCAAGCCGACG	TCGTGCGCTTGAGAATGAGCAAGTT
541	TACGTGAGCGATTGTGGCGAAATAT	TATATTTGCCACAATCGCTGACGT
542	TACGGCCTGCGTCAGCACATGCATC	TGATGCATGTGCTGACGCAGGCCGT
543	TATACCTCCGCAGAACCATTCCGTT	TAACGGAATGGTTCTGCGGAGGTAT
544	TAGTTCGCGGTCCACGATTCACTT	TAAGTGAATCGTGGGACCGCGAACT
545	TTGCTCAATTTGTGCAGAAAACGCC	TGGCGTTTTCTGCACAAATTGAGCA

546	TTTATCGCGAGAGACGACCGTGTCC	TGGACACGGTCGTCTCTCGCGATAA
547	TGACGCGACGTGAGTAGTGGAAGCG	TCGCTTCCACTACTCACGTCGCGTC
548	TATGGTAGGGGCATTGGGCTTTCCT	TAGGAAAGCCCAATGCCCTACCAT
549	TCCAAATATAGCCGCGCGGAGACAT	TATGTCTCCGCGCGGCTATATTTGG
550	TGCAAACCCCTGATTGAATCGTGCCC	TGGGCACGATTCAATCAGGGTTTGC
551	TTAGCGTCTTGCGTGAAACCATGGG	TCCCATGGTTTCACGCAAGACGCTA
552	TCCACCCCGACAGCGCTGGACTCTT	TAAGAGTCCAGCGCTGTCGGGGTGG
553	TACGAGCACTGAAGGCTGCTTTACG	TCGTAAAGCAGCCTTCAGTGCTCGT
554	TCATATCAGCGTCGTCTAGCTCGCG	TCGCGAGCTAGACGACGCTGATATG
555	TTGATCCCGGACCGGCTAGACTAAT	TATTAGTCTAGCCGGTCCGGGATCA
556	TGGCCCCGACACTACAGGGTAATCA	TTGATTACCCTGTAGTGTCGGGGCC
557	TGGCTCCAGGGCGAGATTATGAATG	TCATTCATAATCTCGCCCTGGAGCC
558	TCAAAATCCGATGGGCGGAAATTA	TTAATTTTCCGCCCATCGGATTTTG
559	TCACAGGCGCATAGGGAGCAAGCTA	TTAGCTTGCTCCCTATGCGCCTGTG
560	TTAGCTATTGCCCCGATGGGCTACT	TAGTAGCCCATCGGGGCAATAGCTA
561	TTGGTACGCGGTCCATAGCAAGTCG	TCGACTTGCTATGGACCGCGTACCA
562	TGACGCTGTGGCTCGGAACTGTTC	TGAACAGTTTCCGAGCCACAGCGTC
563	TCCTGGGTTGCGCGGTGGTAAGTG	TCAGTTACCACGCGGCGAACCCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TTATAGCTGTTGGGCTACGCGGGAA
565	TTTCGCGGATTGCTGCCGCATAACA	TTGTTATGCGGCAGCAATCCGCGAA
566	TAAAAATGGCACCGAAGTTGAGGCA	TTGCCTCAACTTCGGTGCCATTTT
567	TCATTCCGCGCGAGTTGAAATCCAG	TCTGGATTTCAACTCGCGCGGAATG
568	TACGCACGTTTTTTGGCACGGTTAA	TTTAACCGTGCCAAAAACGTGCGT
569	TTGTCCATGACGTCGTTTCTCTGGT	TACCAGAGAAACGACGTCATGGACA
570	TTCTCAGTCGGAATCGTATGCCAGA	TTCTGGCATAACGAGTCCGACTGAGA
571	TCTCCAAACGCACACATCAAGCATC	TGATGCTTGATGTGTGCGTTTGGAG
572	TTTCAACCAAGCGGGGTGTTGCGTGA	TTACGAACACCCCGCTTGTTGAA
573	TGGTGTGCGAGGGTGGTGACCTCGA	TTGAGGTCACCACCCTCCGACACC
574	TAGCGCTTTTGGTCATGATTTGCAA	TTTGCAAATCATGACCAAAAGCGCT
575	TCCGAGGACTTACGTCTGCCAGGA	TTCTTGGGCAGACGTAAGTCTCGG
576	TGCCCAATCCAGTTCTTATGCGCCC	TGGGCGCATAAGAACTGGATTGGGC
577	TCGGGTAAACCCACGCAAGTTATGA	TTCATAACTTGCGTGGGTAAACCCG
578	TTGATTAGCGCTCAATACACGCGTG	TCACGCGTGTATTGAGCGCTAATCA
579	TAAGGGCAGACCTTTGGTTCGACTG	TCAGTCGAACCAAAGGTCTGCCCTT
580	TGCGCCACAAGATTCACATGTCATT	TAATGACATGTGAATCTTGTGGCGC
581	TGCCATGTTCAAGGGCCTTTGGAAG	TCTTCGAAAGGCCCTTGAACATGGC
582	TCGCGGTGTTTTGTCTAGGTGCCGG	TCCGGCACCTAGACAAAACACCGCG
583	TCAACATTGTGGTGGCACTCCATCC	TGGATGGAGTGCCACCACAATGTTG
584	TCGATACGCGCCGGTTTGTTAAATC	TGATTTAACAAACCGGCGCGTATCG
585	TGGCTATAAACGTGCGGACTGCTCC	TGGAGCAGTCCGCACGTTTATAGCC
586	TTGGGTAAATCACTATTGCGCGGTT	TAACCGCGCAATAGTGATTTACCCA



	587	TGTCTTCATCGGCCCCGCGCAAGCTA	TTAGCTTGCGCGGGCCGATGAAGAC
	588	TGCGACACACCCTGTACTCTGATGC	TGCATCAGAGTACAGGGTGTGTGCG
	589	TGTAGCAGGGTCCGCAAGACCAAGC	TGCTTGGTCTTGCGGACCCTGCTAC
5	590	TTGCCAACGCAGGGTAACTGCCAT	TATGGCAGTTACCCTGCGTTGGCGA
	591	TACTCCGAAGCTTCGAGCGGCACGA	TTCGTGCCGCTCGAAGCTTCGGAGT
	12	TCATCGTCCCTTTTCGATGGGATCAA	TTTGATCCCATCGAAAGGGACGATG
	13	TGCACGGGAGCTGACGACGTGTCAA	TTTGACACGTCGTCAGCTCCCCTGTC
	594	TATCATCCCACGGCAGAGTGAAGAG	TCTCTTCACTCTGCCGTGGGATGAT
	595	TCGCTGGACTGGCCTATCCGAGTCG	TCGACTCGGATAGGCCAGTCCAGCG
10	596	TCGGTCTCAGCAACACTGTGCGAAA	TTTTGCGACAGTGTTGCTGAGACCG
	597	TCGAACGTTCTCCGATGTAATGGCC	TGGCCATTACATCGGAGAACGTTCCG
	598	TATACCGTGCGACAAGCCCCTCTGA	TTGAGAGGGGCTTGTCGCACGGTAT
	599	TAGCTCATTCCCGAGACGGAACACC	TGGTGTTCCGTCTCGGGAATGAGCT
	600	TTTTCATGCGGCCCGTTGCAAATCAT	TATGATTTGCAACGGCCGCATGAAA
15	601	TACTCGAACGGACGTTCAATTCCCA	TTGGGAATTGAACGTCCGTTTCGAGT
	602	TCTGCATGGTGTGGGTGAGACTCCC	TGGGAGTCTCACCCACACCATGCAG
	603	TCCGCGAGTGTGGATGGCGTGTTGA	TTCAACACGCCATCCACACTCGCGG
	604	TAATGTGTGCGGTCCTAAGCCGGGTG	TCACCCGGCTTAGGACCGACACATT
	605	TTAAGACGAGCCTGCACAGCTTGCG	TCGCAAGCTGTGCAGGCTCGTCTTA
20	606	TGGCGTGGGAGGATAAGACGATGTC	TGACATCGTCTTATCCTCCCACGCC
	607	TTGCTCCATGTTAGGAACGCACCAC	TGTGGTGCGTTCCTAACATGGAGCA
	608	TCGGTGTTGGTCGGACTGACGACTG	TCAGTCGTGAGTCCGACCAACACCG
	609	TCCGCGCGTATCTATCAGATCTGGG	TCCCAGATCTGATAGATACGCGCGG
	610	TAAAGCATGCTCCACCTGGAGCGAG	TCTCGCTCCAGGTGGAGCATGCTTT
25	611	TACTTGATCGCTGGGTAGATCCGG	TCCGGATCTACCCAGCGATGCAAGT
	612	TTGCTTACGCAGTGGATTGGTCAGA	TTCTGACCAATCCACTGCGTAAGCA
	613	TATGCAGATGAACAAATCGCCGAAT	TATTCGCGGATTTGTTTCATCTGCAT
	614	TGCAATTCTGGGCCATGTATTCGTC	TGACGAATACATGGCCCAGAATTGC
	615	TAGGGTTCCTTACGCGTCGACATGG	TCCATGTCGACGCGTAAGGAACCCT
30	616	TGTGGAGCTAATCGCGAGCCTCAGA	TTCTGAGGCTCGCGATTAGCTCCAC
	617	TTCGTAGTCTCACCGGCAATGATCC	TGGATCATTGCCGGTGAGACTACGA
	618	TTTATAGCAGTGCGCCAATGCTTCG	TCGAAGCATTGGCGCACTGCTATAA
	619	TCGAACAGTGCTGTCCGTGCTCAA	TTTGAGCGACGGACAGCACTGTTCCG
	620	TTCCGCGTGGACTGTTAGACGCTAT	TATAGCGTCTAACAGTCCACGCGGA
35	621	TCATTAGCCCGCTGTCCGTAAGTGT	TACAGTTACCGACAGCGGGCTAATG
	622	TGGAAGAAAGTCTCAGACGCGCAATG	TCATTGCGCGTCTGAGTTTCTTTCC
	623	TCGACTCGCTGGACAGGAGAATCGT	TACGATTCTCCTGTCCAGCGAGTCG
	624	TCATGATCCTCTGTTTACCCGCGG	TCCGCGGGTGAAACAGAGGATCATG
	625	TGGCGTAGCGCTCTAAAAGCTTCGG	TCCGAAGCTTTTAGAGCGCTACGCC
40	626	TAGTGATGCCATCAGGCCCCGTATAC	TGTATACGGGCCTGATGGCATCACT
	627	TTATGGAAAGGGCAACAGCGCTATC	TGATAGCGCTGTTGCCCTTCCATA

	628	TCTGTGGTTGATGGAGGATCCACAC	TGTGTGGATCCTCCATCAACCACAG
	629	TACTCGCTGGAATTTGCGCTGACAC	TGTGTCAGCGCAAATTCAGCGAGT
	630	TCAGGCCCGAACCACGCGGTTACAG	TCTGTAACCGCGTGGTTCGGGCCTG
5	631	TGGCGCAATGGGCGCATAAATACTA	TTAGTATTTATGCGCCCATTGCGCC
	632	TGGTCAATTCGCGCTACATGCCCTA	TTAGGGCATGTAGCGCGAATTGACC
	633	TGATGGTGGACTGGAGCCCTTCCGC	TGCGGAAGGGCTCCAGTCCACCATC
	634	TCCGCGCATAGCGCAATAGGGGAGA	TTCTCCCCTATTGCGCTATGCGCGG
	635	TTCTTCTGGCTGTCCGGCACCCGAA	TTTCGGGTGCCGGACAGCCAGAAGA
10	636	TGCGTTCGCAATTCACGGGCCCTTA	TTAAGGGCCCGTGAATTGCGAACGC
	637	TTCGTTTCGGCCTTGAGAGTATCG	TCGATACTCTCCAAGGCCGAAACGA
	638	TAGGTGCAAGTGCAAGGCGAGAGGC	TGCCTCTCGCCTTGCACTTGACCT
	639	TCGCCAGTTTCGATGGCTGACGTTT	TAAACGTCAGCCATCGAACTGGCG
	640	TGCTTTACCGCCGATCCCAGATATC	TGATATCTGGGATCGGCGGTAAAGC
15	641	TGTGCTTGACGAAGAGGCGAAATGT	TACATTTGCGCTCTTCGTCAAGCAC
	642	TCAGTCCGTGCGCTTCATGTCCTCA	TTGAGGACATGAAGCGCACGGACTG
	643	TTACGCGTAAGAGCCTACCCTCGCG	TCGCGAGGGTAGGCTCTTACGCGTA
	644	TGGCGAGTCTTGTTGGGGACATGTGT	TACACATGTCCCCACAAGACTCGCC
	645	TCCAAAGCGAAGCGAGCGTGCTAT	TATAGACACGCTCGCTTCGCTTTGG
20	646	TGCCGTAGGTTGCTCTTCACCGAAC	TGTTCCGGTGAAGAGCAACCTACGGC
	647	TAAATCCGCGATGTGCCGTGAGGCT	TAGCCTCACGGCACATCGCGGATTT
	648	TGGCTTCGCACCCGTACCAATTTAG	TCTAAATTGGTACGGGTGCGAAGCC
	649	TTGTAGAGTCCCACGTAGCCGGCAT	TATGCCGGCTACGTGGGACTCTACA
	650	TCACTAGTCTGGGGCAAGGTGCATT	TAATGCACCTTGCCCCAGACTAGTG
25	651	TTGTACTCGGCAGGCGCAATAGATT	TAATCTATTGCGCCTGCCGAGTACA
	652	TAACGGGTATCGGAAGCGTAAAAGC	TGCTTTTACGCTTCCGATACCCGTT
	653	TCGGACTGCCCGTTTGCAAGTTGAG	TCTCAACTTGCAAACGGGCAGTCCG
	654	TATCGTTCAGCACTGGAGCCCGTAA	TTTACGGGCTCCAGTGCTGAACGAT
	655	TATGCATCGAACTAGTCGTGACGGC	TGCCGTACGACTAGTTCGATGCAT
30	656	TTTCCAGGCATTAAGGAGAGGGAGC	TGCTCCCTCTCCTTAATGCCTGGAA
	657	TGTGCGACATCTACTCCACGATCCC	TGGGATCGTGGAGTAGATGTCGCAC
	658	TCTCATCGTCCTAACACGAGAGCCC	TGGGCTCTCGTGTTAGGACGATGAG
	659	TAATGGCACTTCGGCGGTGATGCAA	TTTGCATCACCGCCGAAGTGCCATT
	660	TCCGTGGGAGGGAATCCAACCGAGG	TCCTCGGTTGGATTCCCTCCCACGG
35	661	TAAATTCTCGTTGGTGACGGCTCAT	TATGAGCCGTCACCAACGAGAATTT
	662	TTTGCTCTTATCCTTGTCCTGGGCG	TCGCCCAGGACAAGGATAAGAGCAA
	663	TTTAAGGATCAGGCGGAGCTTGCA	TCTGCAAGCTCCGCCTGATCCTTAA
	664	TCGCGACTAAGGTGCTGCAACTCGA	TTGAGTTGCAGCACCTTAGTCGCG
	665	TGCTCGATTTACGGCCCGTTGTTT	TGAACAACGGGCCGTGAAATCGAGC
40	666	TAGCAGAGTGCGTTGAGAGGCTAA	TTTAGCCTCTGCAACGCACTCTGCT
	667	TTGGAGGTGAGGACGACGTGCACTA	TTAGTGCACGTGCTCCTCACCTCCA
	668	TAACCGTTTAGGGTACATTCGCGGT	TACCGCGAATGTACCCTAAACGGTT

	669	TTATGATCGCTCGGCTCACAGTTTG	TCAAACGTGTGAGCCGAGCGATCATA
	670	TGACTTTTTGCGGAAACGTCATGGT	TACCATGACGTTTCCGCAAAAAGTC
	671	TTGTGCGTTATTCCACCTGCAAGGA	TTCTTGACAGGTGGAATAACCGACA
5	672	TCTATGGTTTGCACTGCGCCGTCGA	TTGACGCGCAGTGCAAACCATAG
	673	TAGCAGGGAAATTCAATCGTTCGCA	TTGCGAACGATTGAATTTCCCTGCT
	674	TCCTAACCGAGCGCTTAGCATTTCC	TGGAAATGCTAAGCGCTCGGTTAGG
	675	TCCCGACCCCTAACTCGCATTGAATA	TTATTCAATGCGAGTTAGGGTCGGG
	676	TTTGCTTAATGGTGACGCCACGGAT	TATCCGTGGCGTCACCATTAAGCAA
10	677	TGATGCTCGCCGTGTTTAGTTCACG	TCGTGAACTAAACACGGCGAGCATC
	678	TTCCGATGACGAGTTTCCATGACGG	TCCGTCATGGAACTCGTCATCCGA
	679	TATGCGGTCTACTTTCTCGATCGGG	TCCCGATCGAGAAAGTAGACCGCAT
	680	TTTGCGAGGCTAAGCACACGGTAAA	TTTTACCGTGTGCTTAGCCTCGCAA
	681	TAACCTTAATTACCGCCTCTGGCGCC	TGGCGCCAGAGGCGGTAATTAAGTT
15	682	TGTGACCGCGAACTTGTTCCGACAG	TCTGTGCGAACAAGTTCGCGGTCAC
	683	TTGCGGATTACCGATTGCTCTTAA	TTTAAGAGCGAATCGGTAATCCGCA
	684	TTGATAGGGGGCCACGTTGATCAGA	TTCTGATCAACGTGGCCCCCTATCA
	685	TTGCTCCGTAGCGATTATCGTAG	TCTACGATGAATCGCTACGAGCGA
	686	TTGTCAGCTGGTAGCCTCCGTTTGA	TTCAAACGGAGGCTACCAGCTGACA
20	687	TAGCGTCGCATGACGCTTACGGCAC	TGTGCCGTAAGCGTCATGCGACGCT
	14	TAGACGCACCGCAACAGGCTGTCAA	TTTGACAGCCTGTTGCGGTGCGTCT
	15	TCGTGTAGGGGTCCCGTGCTGTCAA	TTTGACAGCACGGGACCCCTACACG
	690	TGTCGCATTCTGCACTGGCTTCGCC	TGGCGAAGCCAGTGCAGAATGCGAC
	691	TTGATTAGGTGCGGTCCCGTAGTCC	TGGACTACGGGACCGCACCTAATCA
25	692	TAAGGGACCTTGGGTGACGGCGAGA	TTCTCGCCGTCACCCAAGGTCCCTT
	693	TTCAAATGGCCACCGCGTGTCAATC	TGAATGACACGCGGTGGCCATTTGA
	694	TCTCCGACGACCAATAAATAGCCGC	TGCGGCTATTTATTGGTCGTCGGAG
	695	TGGCTATTCCCGTAGAGAGCGTCCA	TTGGACGCTCTCTACGGGAATAGCC
	696	TTGGATAACCTCTCGGTCCATCCAC	TGTGGATGGACCGAGAGGTTATCCA
30	697	TGACCGCTGTACGGGAGTGTGCCTT	TAAGGCACACTCCCGTACAGCGGTC
	698	TGCCACAGAGTTTTAGCAGGGACCC	TGGGTCCCTGCTAAAACTCTGTGGC
	699	TCCCACGCTTTCCGACCACTGACCT	TAGGTCAGTGGTCGGAAAGCGTGGG
	700	TCATTGACACAATGCGGGGACTGAT	TATCAGTCCCCGCATTGTGTCAATG
	701	TAGCCACTCGACAGGGTTCCAAAGC	TGCTTTGGAACCCTGTCGAGTGGCT
35	702	TCAGGATGAGCAAAGCGACTCTCCA	TTGGAGAGTCGCTTTGCTCATCCTG
	703	TCAAGGTATGGTCTGGGGCCTAAGC	TGCTTAGGCCCCAGACCATACTTG
	704	TGGTGTTTCGGCCTAAACTCTTTCGG	TCCGAAAGAGTTTAGGCCGAACACC
	705	TTTTAGTCGGACCCTGTGGCAATTC	TGAATTGCCACAGGGTCCGACTAAA
	706	TCACACGTTTCCGACCAGCCTGAAC	TGTTACAGGCTGGTCGGAAACGTGTG
40	707	TCTGGACGAACTGGCTTCCTCGTAC	TGTACGAGGAAGCCAGTTCGTCCAG
	708	TTTCACAATCCGCCGAAACTGACC	TGGTCAGTTTTCGGCGGATTGTGAA
	709	TAACAGGATATCCGCGATCACGACA	TTGTGCTGATCGCGGATATCCTGTT

	710	TTACGTCGGATCCATTGCGCCGAGT	TACTCGGCGCAATGGATCCGACGTA
	711	TCATGGATCTCTCGGTTTGATCGCC	TGGCGATCAAACCGAGAGATCCATG
	712	TAGCCAGGCGCGTATATACGCTCGG	TCCGAGCGTATATACGCGCCTGGCT
5	713	TATTTGGCACGTGTCGTGCCATGTT	TAACATGGCACGACACGTGCCAAAT
	714	TCCGCGTTGCACCACTTTGAGGTGC	TGCACCTCAAAGTGGTGAACGCGG
	715	TTTGGACGTGACAAGCATGGCGCTC	TGAGCGCCATGCTTGTCACGTCCAA
	716	TCTGAATCGCGCAAGTAAATGGGGG	TCCCCCATTTACTTGCGCGATTGAG
	717	TGATAAGGTCCACCAGATTGCGCGC	TGCGCGCAATCTGGTGGACCTTATC
10	718	TCTAACAATTGCCAACCGGGACGGC	TGCCGTCCCGGTTGGCAATTGTTAG
	719	TGGTAACCTGGGTGCTTGCAAGTTA	TTAACCTGCAAGCACCCAGGTTACC
	720	TATCGGAGCCACCATTCGCATTGGG	TCCAATGCGAATGGTGGCTCCGAT
	721	TGTGAACTGGCTTGCCCCAGGATTA	TTAATCCTGGGGCAAGCCAGTTCAC
	722	TAGGCGATAGCATGGTCCCATATGA	TTCATATGGGACCATGCTATCGCCT
15	723	TAACGGTATCGTGGCTAATGCACGA	TTCGTGCATTAGCCACGATACCGTT
	724	TAGTAGTGGTCCTCCAGATCGGCAA	TTTGCCGATCTGGAGGACCACTACT
	725	TCCGTTGAATTGGACGGGAGGTTAG	TCTAACCTCCCGTCCAATTCAACGG
	726	TGCATAAGTGCGGCATCGCGAAGGG	TCCCTTCGCGATGCCGCACTTATGC
	727	TCGACAAGATGCAGCTGCTACATGC	TGCATGTAGCAGCTGCATCTTGTCG
	728	TTCGCAGTGATTCCCGACCGATAAG	TCTTATCGGTGCGGAATCACTGCGA
20	729	TCAAGGCGAGTCCACTCGAGGGGAC	TGTCCCCTCGAGTGGACTCGCCTTG
	730	TGCAACTTGACCGGCATAAGTGGCC	TGGCCACTTATGCCGTGCAAGTTGC
	731	TTCCGAGCTTGACGTTGCGGACGTC	TGACGTGCGGAACGTCAAGCTCGGA
	732	TAGCGCTGGGCTGTGCTGCCATCTC	TGAGATGGCAGCACAGCCCAGCGCT
	733	TTTCATGTCGCTGAGTAACCCTCGC	TGCGAGGGTTACTCAGCGACATGAA
25	734	TCGAACCGCTAATGCCATTGTCAG	TCTGACAATGGGCATTAGCGGTTG
	735	TCACGGAAGGTGGGACAAATCGCCG	TCGGCGATTTGTCCACCTTCCGTG
	736	TCACAGATGGAGACAAACGCGCCTT	TAAGGCGCGTTTGTCTCCATCTGTG
	737	TTTTTCGCAACTCGCTCCATAACCC	TGGGTTATGGAGCGAGTTGCGAAAA
	738	TACGTTACGTTTCCGGCGCCTCTAA	TTTAGAGGCGCCGAAACGTAACGT
30	739	TTATCGGATTGCGTGGGTTTCAATC	TGATTGAAACCCACGCAATCCGATA
	740	TCTTCCACAATTGTCTGCGACGCAC	TGTGCGTGCAGACAAATTGTGGAAG
	741	TTGCACAAAGGTATGGCTGTCCGGC	TGCCGGACAGCCATACCTTTGTGCA
	742	TTCCGATGCCAGTCCCATCTTAAGA	TTCTTAAGATGGGACTGGCATCGGA
	743	TCTGAAACCGTGCGAATCGAGGTGA	TTACCTCGATTGCGACGGTTTCAG
35	744	TCGGTGTTCCGCGTGTCGAAAAAT	TATTTTTTCGACACGCGGAACACCG
	745	TTCTAGCAGGCCTTTTGAATCGCCA	TTGGCGATTCAAAGGCCTGCTAGA
	746	TGAGTCACCTCTGAGACGGACGCCA	TTGGCGTCCGTCTCAGAGGTGACTC
	747	TTCTTCTGTCATCCTGCAGCAGCAT	TATGCTGCTGCAGGATGACAGAAGA
	748	TGCGGATGAAACCTGAAAGGGGCCT	TAGGCCCTTTTCAAGTTTCATCCGC
40	749	TGGGGCCCCAACTGGTATCAAGCC	TGGCTTGATACCAGTTTGGGGCCCC
	750	TGCATTGGCTTCGGATTCTCCTACA	TTGTAGGAGAATCCGAAGCCAATGC

	751	TAGGCGGCCCAACTGTGAGGTCTTG	TCAAGACCTCACAGTTGGGCCGCCT
	752	TACACCATGTGCTCCGCGCTGCAGT	TACTGCAGCGCGGAGCACATGGTGT
	753	TACGATGAACATGAATCGGGAGTCG	TCGACTCCCGATTTCATGTTTCATCGT
5	754	TCTGCATCCCTGTAGCAGCGCTCCG	TCGGAGCGCTGCTACAGGGATGCAG
	755	TGTGCCGTATTTGACCTGTGCGTT	TAACGCACAGGTCGAAATACGGCAC
	756	TGCAGTGCGCACTTCAGTTCAAAAG	TCTTTTGAAGTGAAGTGCGCACTGC
	757	TGCGATTTTAAGCGATGCCCTTGACG	TCGTCAAGGCATCGCTTAAAATCGC
	758	TTAGGTGACCTAGGCTTGCTTGCGG	TCCGCAAGCAAGCCTAGGTCACCTA
10	759	TCTGGATACCTTGCTGTGCGGCGC	TGCGCCGCACAGGCAAGGTATCCAG
	760	TCCCCTTACGGCTCGTCGTCTATGC	TGCATAGACGACGAGCCGTAAGGGG
	761	TGCGCTTGCCCGATGCGATGCATTA	TTAATGCATCGCATCGGGCAAGCGC
	762	TTTTCTGTAAGCGGCCTGGGGTTCA	TTGAACCCCAGGCCGCTTACAGAAA
	763	TGGCTGAGGTGAGCGGTAAGGATGA	TTCATCCTTACCGCTCACCTCAGCC
15	764	TTCTTGCCCTCCCGATCTAATTTG	TCAAATTAGATCGGGGAGGCCAAGA
	765	TGGAGGTAACGCCGTGTACGTAGGA	TTCTTACGTACACGGCGTTACCTCC
	766	TGTAATCCATTTGTGGCTGCGTCAA	TTTGACGCAGCCACAAATGGATTAC
	767	TCAAACCCATTCCAGCAGACGCCTG	TCAGGCGTCTGCTGGAATGGGTTTG
	768	TTAGGAGGAATTTGGCATGCGGGCG	TCGCCCCGATGCCAAATTCCTCCTA
20	769	TATAGGTAGGATGTGCCCGGCGTTG	TCAACGCCGGGCACATCCTACCTAT
	770	TGCAAGTGCTTAGCTCGTCAGCCTC	TGAGGCTGACGAGCTAAGCACTTGC
	771	TCTGGCTGTGTGCGATCTCGTTAAC	TGTTAACGAGATGCGACACAGCCAG
	772	TCTAACGTCGTCTCGCGCAATCACT	TAGTGATTGCGCGAGACGACGTTAG
	773	TTTTTCATAAACGTTGTCCCCGAGC	TGCTCGGGGACAACGTTTATGAAAA
25	774	TAGCAGGAGGACGAACCTCCGCTCC	TGGAGCGGAGGTTTCGTCTCTCTGCT
	775	TTTCAAGCACCATCGTGCAATCCAA	TTTGATTGCACGATGGTGCTTGAA
	776	TAGCGTCGCCAGTGATCGCTAGTGG	TCCACTAGCGATCACTGGCGACGCT
	777	TTACATTCCCTGCCTCCGTGGGCTT	TAAGCCCACGGAGGCAGGGAATGTA
	778	TCGCTTCGCGTATTTCAGTAGCGGTT	TAACCGCTACTGAATACGCGAAGCG
	779	TTCGGACGCGTCGACACTCATTATA	TTATAATGAGTGTGACGCGTCCGA
30	780	TTCTGAGCAGGCCAGCGCTCCAGCT	TAGCTGGAGCGCTGGCCTGCTCAGA
	781	TTTGAATTGCCAAGCCCTGAAAGCC	TGGCTTTCAGGGCTTGCCAATTCAA
	782	TAGTTTTCGCCTTGATGCGTCGGTG	TCACCGACGCATCAAGGCGAAAAC
	783	TGTTTCATAGGCCACGCGTGCTAAA	TTTTAGCACGCGTGGCCTATGAAAC
	16	TCATCGCTGCAAGTACCGCACTCAA	TTTGAGTGCGGTACTTGCAGCGATG

## CLAIMS

We claim:

5

1. An oligonucleotide array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

10

2. An array according to claim 1, wherein said capture probes are microspheres.

3. An array according to claim 1 or 2 wherein said array is a liquid array.

4. An array according to claim 1, 2 or 3, wherein said array further comprises a solid support.

15

5. An array according to claim 1, 2, 3 or 4, wherein said addresses are microspheres and wherein said solid support comprises wells into which said microspheres are individually distributed.

20

6. An array according to claim 1, 2, 3 or 4, wherein each address is a different known location, and wherein each capture probe is attached to one of said known locations.

7. An array according to claim 1, 2, 3, 4, 5 or 6, wherein said array comprises at least 50 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

25

8. An array according to claim 1, 2, 3, 4, 5 or 6 wherein said array comprises at least 100 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

30

9. A kit comprising at least twenty-five nucleic acids selected from the group consisting of sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

35

10. A kit according to claim 9, wherein said kit comprises at least 50 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

11. A kit according to claim 9 or 10, wherein said kit comprises at least 100 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.
- 5 12. A kit according to claim 9, 10 or 11, wherein said nucleic acids further comprise at least a first universal priming sequence.
13. A kit according to claim 9, 10, 11 or 12, wherein said nucleic acid sequence further comprises a sequence substantially complementary to a target domain.
- 10 14. A method of immobilizing a target nucleic acid sequence, said method comprising:
- a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
- 15 b) contacting said modified first target nucleic acid sequence with an array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4, whereby said target nucleic acid sequence is immobilized.
- 20 15. A method of detecting a target nucleic acid sequence, said method comprising:
- a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
- 25 b) contacting said modified first target nucleic acid sequence with an array comprising: an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4; and
- 30 c) detecting the presence of said modified first target nucleic acid sequence.
16. A method of detecting a target nucleic acid, said method comprising:
- a) hybridizing a first adapter probe with a first target nucleic acid, said first adapter probe comprising a first domain that is complementary to said first target nucleic acid and a second domain, said second domain comprising a first sequence substantially complementary to a selected from the group consisting of the sequences set forth in Table I, Table II, Table III and Table IV to form a first hybridization complex;
- 35

- 5
- b) contacting said first hybridization complex with an enzyme such that when said first domain of said adapter probe is perfectly complementary with said first target nucleic acid, said first adapter probe is altered resulting in a modified first adapter probe;
  - c) contacting said modified first adapter probe with a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that said first capture probe and said modified first adapter probe form a second hybridization complex; and
  - d) detecting the presence of said modified first adapter probe as an indication of the presence of said target nucleic acid.



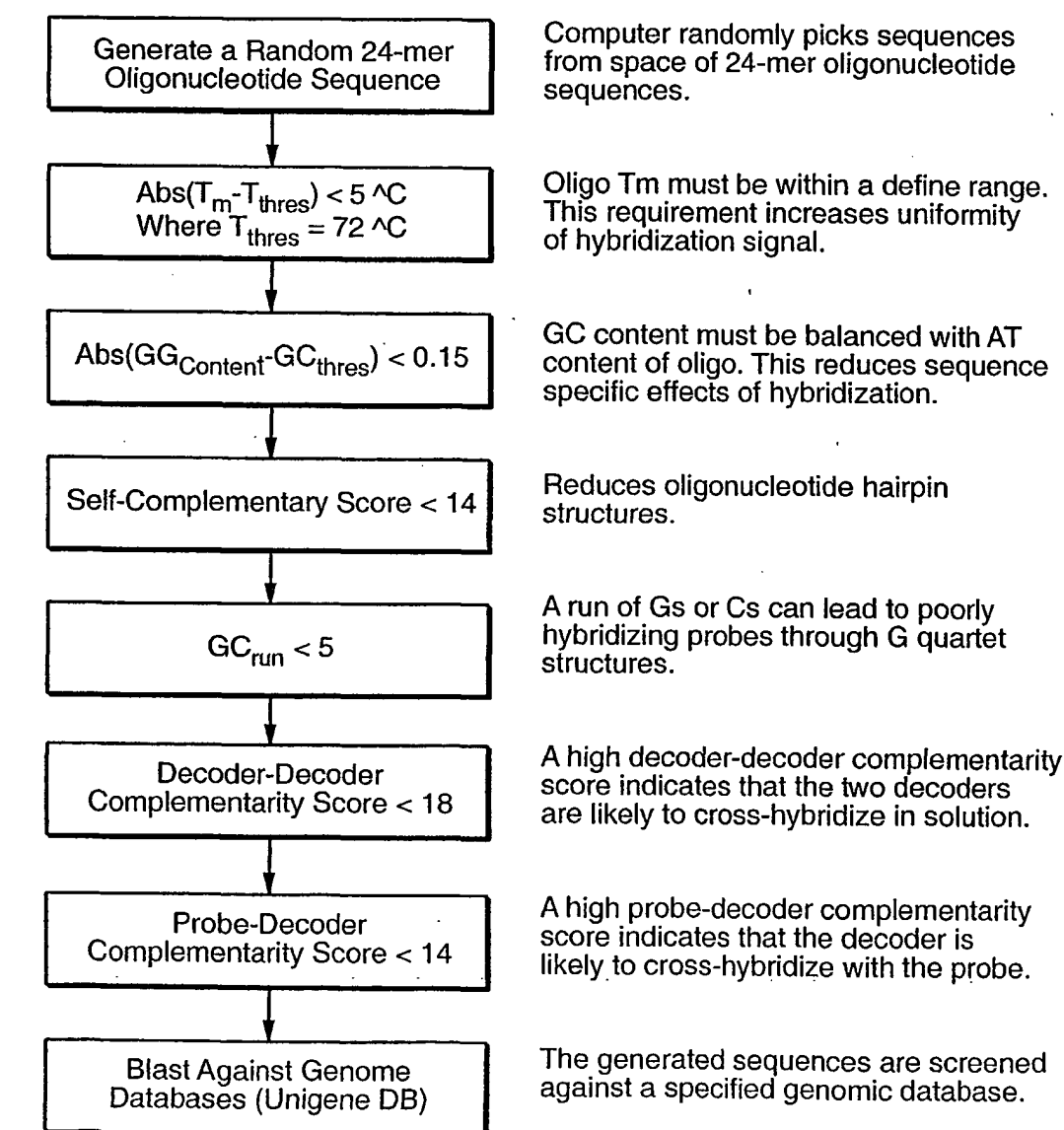
1 / 3

**Description of algorithm to select "best" oligonucleotide adapter sequences.**

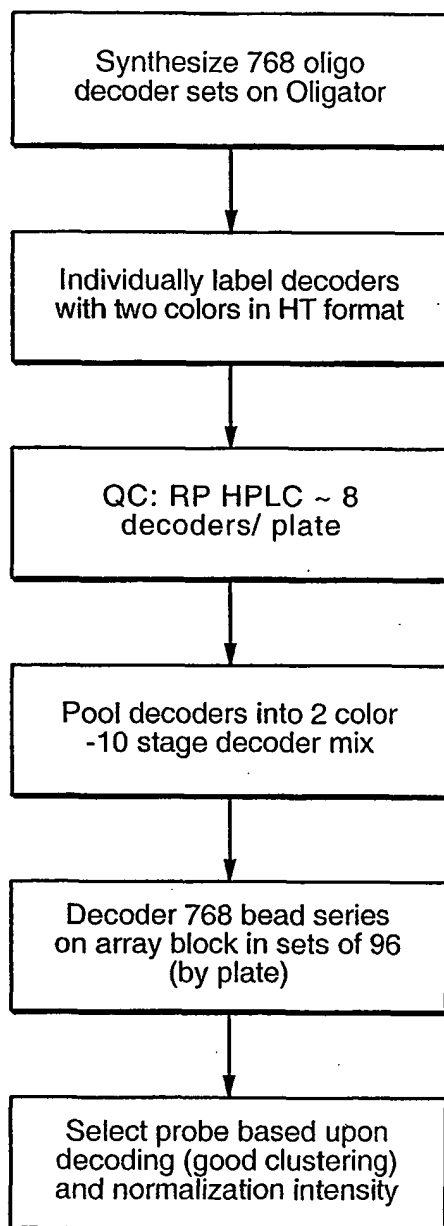
Requirements for good sequences:

- Generates adequate hybridization signal intensity when employed in an experiment.
- Exhibits minimal cross-reactivity with other adapter sequences.
- Unique within the human genome sequence. This requirement can be extended to the genomic sequence of other organisms such as the fruit fly, the mouse, etc.

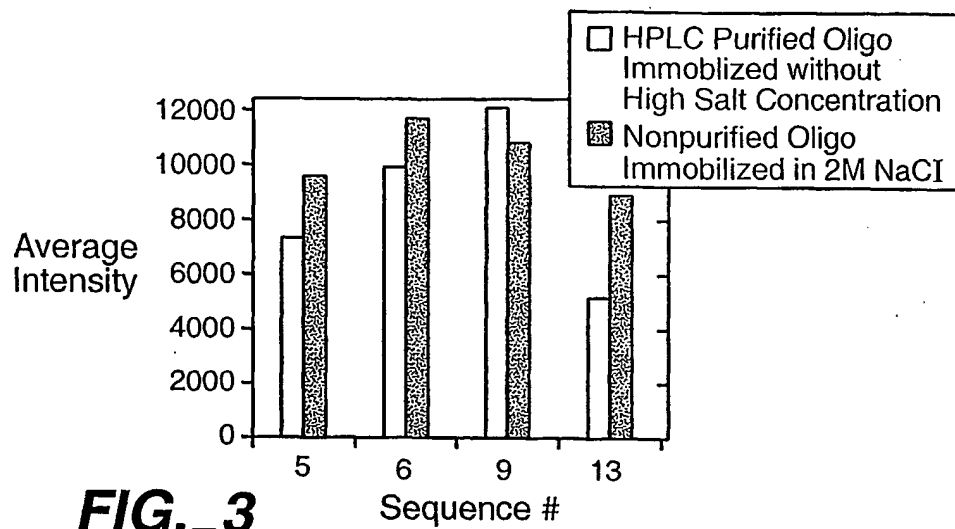
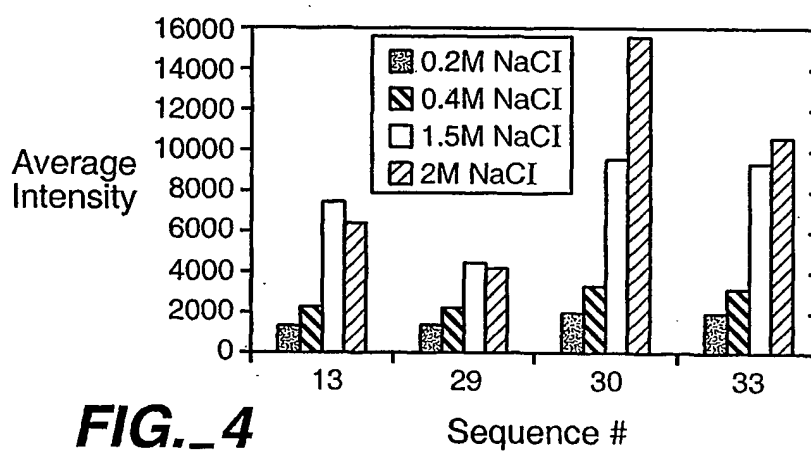
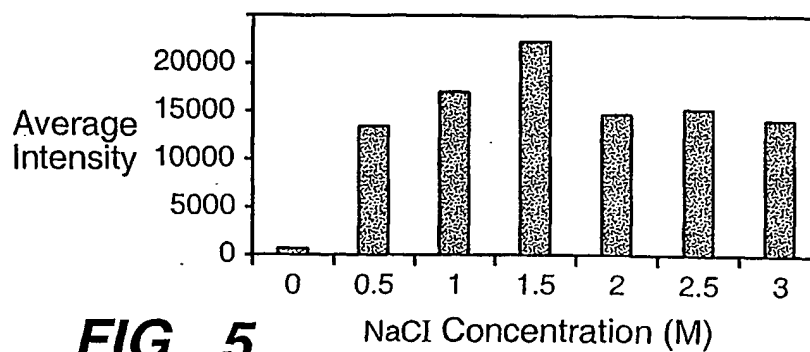
One method of generating sequences that meet the above requirements is to randomly generate sequences of given lengths and then pass these filters through a set of heuristic acceptance filters. In particular, the 24-mer Illumina Adapter sequences (IllumaCodes) were chosen as follows.

**FIG. 1**

2 / 3

**Flow diagram for selection  
of probes sequences****FIG. 2**

3 / 3

**FIG.\_3****FIG.\_4****FIG.\_5**

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**